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Patentanmeldung Nr. Patent application No. Demande de brevet n°

99870141.1

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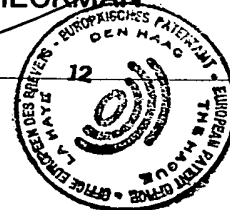
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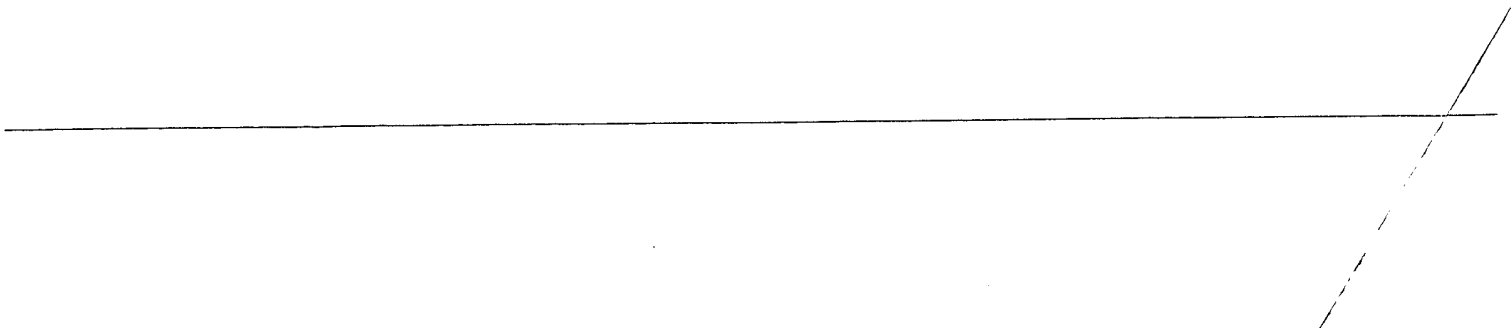
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Sheet 2 of the certificate
Page 2 de l'attestation

Anmeldung Nr.:
Application no.: 99870141.1
Demande n°:

Anmeldetag:
Date of filing: 01/07/99
Date de dépôt:

Anmelder:
Applicant(s):
Demandeur(s):
JANSSEN PHARMACEUTICA N.V.
2340 Beerse
BELGIUM

Bezeichnung der Erfindung:
Title of the invention:
Titre de l'invention:

Genetic sequences related to programmed cell death in yeast and fungi

In Anspruch genommene Priorität(en) / Priority(ies) claimed / Priorité(s) revendiquée(s)

Staat:
State:
Pays:

Tag:
Date:
Date:

Aktenzeichen:
File no.
Numéro de dépôt:

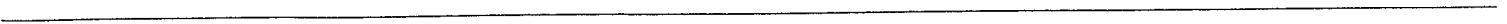
Internationale Patentklassifikation:
International Patent classification:
Classification internationale des brevets:

C12Q1/68, C12N15/81, A61P31/04, A61P31/10, C07K14/395, C07K14/40, C07K16/14

Am Anmeldetag benannte Vertragsstaaten:
Contracting states designated at date of filing: AT/BE/CH/CY/DE/DK/ES/FI/FR/GB/GR/IE/IT/LI/LU/MC/NL/PT/SE
Etats contractants désignés lors du dépôt:

Bemerkungen:
Remarks:
Remarques:

See for original title of the application
page 1 of the description



CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI

The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon
5 programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi.

Invasive fungal infections (e.g. *Candida* spp, *Aspergillus* spp., *Fusarium* spp., *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two
10 decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in
15 several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the
20 production of unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botritis*, spp., *Cladosporium* spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses, expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal
25 agents is thus an essential element of any new antifungal therapy.

Classical approaches for identifying anti-fungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic, or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic
5 model organism. These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular target.

10 Cells from multicellular organisms can commit suicide in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. To survive, all cells from multicellular organisms depend on the constant repression of this suicide program by signals from other cells (Raff, 1992). It has
15 been assumed that such an altruistic form of cell survival arose with multicellularity and would have been counterselected in unicellular organisms. Recent findings indicate, however, that a similar process of cell survival also operates in single-celled eukaryotes.

It has been found that expression of the mammalian *Bax* gene triggers cell
20 death in *Saccharomyces cerevisiae* and the fission yeast *Schizosaccharomyces pombe* with morphological changes similar to apoptosis (Jürgensmeier *et al.*, 1997). However, the mechanism of *Bax* lethality in *S. cerevisiae* remains unclear.

Since it has been discovered that the mammalian *Bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the

molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes.

It is an aim of the present invention to provide nucleic acid as well as polypeptide sequences which represent potential molecular targets for the
5 identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungi infections.

It is a further aim of the present invention to provide uses of these nucleic acid and amino acid molecules for the preparation of a medicament for treating diseases associated with yeast or fungi.

10 It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

15 It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicine for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds capable of inhibiting or activating expression of such polypeptides in
20 yeast or fungi infections. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds.

It is also an aim of the invention to provide a method of preventing infection with yeast or fungi.

It is also an aim of the invention to provide probes and primers derived from
25 the nucleic acid sequences of the invention.

All the aims of the present invention have been met by the embodiments as set out below.

The present inventors identified a range of specific nucleotide sequences which are involved in the molecular pathways eventually leading to programmed
5 cell death.

According to a first embodiment, the invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

- 10 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136,
15 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286,
20 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436,

438, 440, 442, 444, 446, 448, 450, 452, 454 or 456, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456;

- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID

NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42,
44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84,
86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118,
120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148,
5 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178,
180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208,
210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238,
240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268,
270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298,
10 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328,
330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358,
360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388,
390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418,
420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448,
15 450, 452, 454 or 456; and

(d) a nucleic acid molecule comprising a sequence as represented in any of SEQ

ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39,
41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81,
83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117,
20 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147,
149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177,
179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207,
209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237,
239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267,
25 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297,

299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327,
329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357,
359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387,
389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417,
5 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447,
449, 451, 453 or 455;

(e) a nucleic acid sequence which is more than 70% identical, preferably more
than 75 or 80% identical, more preferably more than 85%, or 90% or 95%
identical and most preferably more than 97% identical to any of the nucleic acid
10 sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25,
27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67,
69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105,
107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135,
137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165,
15 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195,
197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225,
227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255,
257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285,
287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315,
20 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345,
347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375,
377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405,
407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435,
437, 439, 441, 443, 445, 447, 449, 451, 453 or 455; and

25 ~~(f) the complement of any of the nucleic acid sequences as specified in a) to),~~

for the preparation of a medicament for treating diseases associated with yeast or fungi.

Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using
5 BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means the degree of sequence relatedness between
10 two polypeptide or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton,
15 1988). Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in
20 computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The nucleic acid sequences to be used according to this aspect of the
25 ~~invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 1, 3, 5, 7, 9,~~

11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 5 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281 and 283. The invention also relates to nucleic acid sequences from *Candida albicans*, as represented by 10 the SEQ ID NOs 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 15 439, 441, 443, 445, 447, 449, 451, 453 and 455.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, and hydrogen peroxide.

20 The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic 25 ~~reactions caused by said organisms, such as the so-called "professional diseases"~~

in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic".

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455, but isolated from other yeast and fungi which are also involved in a pathway eventually leading to programmed cell death.

According to the invention, these sequences and their homologues in other yeast and fungi as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides and their potential use in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp.,

Microsporium spp., Trichophyton spp., Fusarium spp., Zygomycetes spp., Botritis,
 spp., Cladosporium spp., Malassezia spp., *Epidermophyton floccosum*,
Blastomyces dermatitidis, *Coccidioides immitis*, *Histoplasma capsulatum*,
Paracoccidioides brasiliensis, *Cryptococcus neoformans*, and *Sporothrix*
 5 *schenckii*.

The present inventors were able to identify via macro array screening a
 range of genes involved in a pathway eventually leading to programmed cell death
 in the yeast *Saccharomyces cerevisiae*. As explained in Example 3, genes
 showing a difference of a factor 5 or more in expression as a result of Bax-induced
 10 cell death, were identified as differentially expressed candidate genes. Some of
 these genes are clearly down-regulated in a *Bax*-expressing strain, while other
 genes show an upregulated expression (Table 1).

According to another embodiment, the invention also relates to a nucleic acid
 sequence encoding a polypeptide which is involved in a pathway eventually
 15 leading to programmed cell death of yeast or fungi selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as
 represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302,
 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338,
 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372,
 20 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408,
 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442,
 444, 446, 448, 450, 452 or 454, or encoding a functional equivalent, derivative
 or bioprecursor of said protein;

(b) a nucleic acid molecule encoding a protein having an amino acid sequence
 25 ~~which is more than 70% similar, preferably more than 75% or 80% similar,~~

more preferably more than 85% , 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454;

(c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454;

(d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;

(e) a nucleic acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95%

identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 5 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455; and,

(f) the complement of any of the nucleic acid sequences as specified in a) to e).

10 According to a more specific embodiment, these nucleic acid sequences are derived from *Saccharomyces cerevisiae*, *Candida albicans* or *Aspergillus fumigatus*.

A nucleic acid sequence according to the invention may comprise an mRNA sequence or alternatively a DNA sequence and preferably a cDNA sequence. A 15 nucleic acid sequence according to the invention may also comprise any modified nucleotide known in the art.

The present invention further relates to a nucleic acid molecule capable of specifically hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof, under high stringency conditions.

20 The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given, or the antisense version thereof.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid sequence capable of hybridizing to any of the above defined nucleic acid sequences.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

5 The present invention also advantageously provides nucleic acid sequences of at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according
10 to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically with any of the nucleic acid molecules of the invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

 The probes or primers according to the invention may also be used in
15 diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

 According to the present invention these probes may be anchored to a solid
20 support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can be used to screen for compounds interacting with said
25 probes.

Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene
5 which is desired to be cloned, bringing the primers into contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as
10 described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P or ^{35}S , enzyme labels or other protein labels such as biotin or fluorescent markers. Such labels
15 may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable expression vector which may be transformed, transfected or
20 infected into a host cell. In such an expression vector the nucleic acid is operably linked to a control sequence, such as a suitable inducible promotor, or the like, to ensure expression of the proteins according to the invention in a suitable host cell. The expression vector may also comprise a reporter molecule. The expression vector may advantageously be a plasmid, cosmid, virus or other suitable vector
25 which is known to those skilled in the art. The expression vector and the host cell

defined herein also form part of the present invention. Preferably the host cell is a lower eukaryotic cell such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

The invention further relates to any nucleic acid as defined above for use as a medicament.

Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides, leading to impaired growth or death of yeast and fungi with reductions of associated illnesses or diseases.

According to another embodiment, the invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

(a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178,

180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208,
210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238,
240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268,
270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298,
5 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328,
330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358,
360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388,
390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418,
420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448,
10 450, 452, 454 or 456, or encoding a functional equivalent, derivative or
bioprecursor of said protein;

(b) a protein having an amino acid sequence which is more than 70% similar,
preferably more than 75% or 80% similar, more preferably more than 85%,
90% or 95% similar and most preferably more than 97% similar to any of the
15 amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20,
22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62,
64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102,
104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132,
134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162,
20 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192,
194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222,
224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252,
254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282,
284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312,
25 ~~314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342,~~

344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456;

- 5 (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456; and,
- (d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

Functional fragments include those comprising an epitope which is specific for the proteins according to the invention. Epitopes may be determined using, for example, peptide scanning techniques as described in Geysen *et al.* (1996). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 100, 150 or 200 amino acids.

The polypeptides to be used according to this aspect of the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, and 284. Also according to the invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative amino acid changes.

The nucleic acid molecule as defined in claim 1 or the polypeptide as
5 defined in claim 2 of the invention may be provided in a pharmaceutically acceptable carrier, diluent or excipient therefor.

The present invention also relates to a vaccine for immunizing a mammal against infections caused by yeast and fungi, comprising at least one (recombinant) nucleic acid molecule as defined in claim 1, or at least one
10 (recombinant) polypeptide as defined in claim 2, in a pharmaceutically acceptable carrier.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing
15 macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete. A vaccine
20 may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions.

The term "therapeutic" refers to a composition capable of treating infections
25 caused by yeast or fungi.

According to another embodiment, the present invention provides a method of identifying compounds which selectively inhibit, induce or interfere with the expression of the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound, (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

According to the invention, the term "mutation" includes deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as
5 monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

The invention also relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway
10 eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1,
15 which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective
20 action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective
25 ~~action of said compound on a polypeptide in the same or a parallel pathway, (d)~~

alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

The invention further relates to a method of identifying compounds which
5 bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2, (b) detecting the complex formed between the compound to be tested and said polypeptide, (c) alternatively, examining the
10 diminution of complex formation between said polypeptide and a receptor, caused by the addition of the compound being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

The invention also relates to a method of identifying compounds which
15 selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene and (b) monitoring
20 increased or decreased expression of said reporter gene caused by the addition of the compound being tested.

According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus*

25 *fumigatus*.

The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of
5 endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

According to the invention, alternative methods for identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in
10 metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell
15 death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

The compounds to be screened may be of extracellular, intracellular,
20 biologic or chemical origin. The protein or peptide fragments according to the invention employed in such a method may be for example in solution, affixed to a solid support, borne on a cell or phage surface or located intracellularly. One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine th

diminution of complex formation between the protein according to the invention and a receptor caused by the compound being tested.

Another technique for compound identification provides high throughput screening for compounds having suitable binding affinity to the polypeptides
5 according to the invention. Hereby, large numbers of compounds are fixed to a solid substrate and tested for their binding affinity.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

10 This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid
15 DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating
20 domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the GAL4 protein in yeast. GAL4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of GAL4.

These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of GAL4.

10 These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL-4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated

15 upon restoration of transcription of the yeast galactose metabolism genes.

The invention also relates to a compound identified using any of the methods of the invention.

Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament, or in the preparation of

20 a medicament to treat diseases or conditions associated with yeast and fungi infections, for instance *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*,

25 ~~*Cryptococcus neoformans*, and *Sporothrix schenckii*~~ infections. These

compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

5 A medicament according to the invention not only relates to fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

The invention also relates to genetically modified yeast or fungi in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or the polypeptides as defined in claim 2, which
10 overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungi. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament
15 for prophylactic or therapeutic use.

Also according to the invention is the use of a compound according to claim
10 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

According to another embodiment, the invention also relates to an isolated
20 protein which is involved in a pathway for programmed cell death of yeast or fungi selected from:

(a) a protein having an amino acid sequence as represented in any of SEQ ID

NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316,

318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354,

25 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386,

388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a protein having an amino acid sequence which is more than 70% similar,

5 preferably more than 75% or 80% similar, more preferably more than 85%, 90 or 95% similar and most preferably more than 90% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 10 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454;

(c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%,

15 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 20 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454; and,

(d) a functional fragment of any of said proteins as defined in a) to c).

According to the invention, the polypeptides as defined above may be used as a medicament.

Also encompassed within the present invention are antibodies, monoclonal or polyclonal, capable of specifically binding to one or more epitopes of the proteins of the invention. The term "specific binding" implies that there is substantially no cross-reaction of the antibody with other proteins.

5 The antibodies according to the invention may be produced according to techniques which are known to those skilled in the art. Monoclonal antibodies may be prepared using conventional hybridoma technology as described by Kohler and Milstein (1979). Polyclonal antibodies may also be prepared using conventional technology well known to those skilled in the art, and which comprises inoculating
10 a host animal, such as a mouse, with a protein or epitope according to the invention and recovering the immune serum. The present invention also includes fragments of whole antibodies which maintain their binding activity, such as for example, Fv, F(ab') and F(ab')₂ fragments as well as single chain antibodies.

Antibodies according to the invention may also be used in a method of
15 detecting the presence of a polypeptide according to the invention, which method comprises reacting the antibody with a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

20 The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi such as, but not restricted to, *Candida albicans*, *Aspergillus* spp., *Fusarium* spp., *Botritis*, spp., *Cladosporium*
25 spp.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response.

- 5 The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

Figure 1. *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID Nos 1 to 284)

5 **Figure 2.** *Candida albicans* sequences (SEQ ID Nos 285 to 456).

Figure 3. Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters. The filters are cut in the upper right corner for orientation and the DNA is on the labelled side of the filter. Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.

10 The spots represent the genome wide expression profile without (A) and with (B) *Bax* modulated expression.

Table 1. Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed more than fivefold. The factor by which the transcript level was affected, is expressed as the Qt value. Upregulation or downregulation of a specific mRNA is stated when Qt had a value of at least five or at most 0,21, respectively.

15

20 EXAMPLES

Example 1. Differential gene expression analysis upon *Bax*-induced cell death

Materials and media

Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980)

25 was used for the construction and the amplification of plasmids. Yeast strains were

grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* strain INVSc1 (Invitrogen®) was transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with YlpUTyL or YlpUTYLMuBax, after linearisation in the Ty δ element (Zhu, 1986).

5

Cloning of mouse BAX cDNA

Mouse *Bax* cDNA, encoding the mouse Bax- α protein, was cloned by Pfu DNA polymerase (Stratagene®) chain reaction amplification (PCR) from an EL4/13.18 thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the

10 primers:

5'-ATGGACGGGTCCGGGAGCAG-3' and

5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3'.

The resulting PCR product was cloned in a *HincII*-openend pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).

15

Plasmid constructions

The 2 μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *Clal* and *BglII*. A *BamHI*-*HindIII* GAL1 promoter fragment was ligated into the *BglII*-*HindIII*-opened plasmid.

20 A *XbaI*-*FspI* FLP terminator fragment was inserted into this *XbaI*-*HindIII*(blunted)-opened plasmid so that the plasmid YlpUT was obtained. Insertion of a blunted *EcoRI*-*BsaAI* Ty δ element in the *KpnI*-*AatII*-opened and blunted YlpUT resulted in the plasmid YlpUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *BsaAI*-*BsrGI* fragment, in the *BamHI*-openend and blunted YlpUTy resulted in the

25 plasmid YlpUTyL.

Mouse *Bax* cDNA was excised from pUC19 by digestion with *Xba*I and *Hind*III and subcloned into the *Xba*I-*Hind*III-opened plasmid YIpUTyL, obtaining the final expression plasmid YIpUTyLMuBax.

The plasmid YIpUTyLMuBax has been deposited in the BCCM™/LMBP
5 culture collection as p5CTyGALmBax with accession number 3871 under restricted use.

GeneFilters

The Yeast GeneFilters™ were purchased from Research Genetics Inc.
10 (Huntsville, AL, USA).

The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the
15 filter.

Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3
20 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

The yeast filters consist of over 6000 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer
25 pairs designed to amplify the entire open reading frame. The primers were

generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per 5 microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

10 Results

Induction of Bax-expression in yeast cells

Precultures of yeast strain INVSc1 containing YlpUTyLMuBax, wherein 5 Bax-cassettes under the control of the GAL1 promotor are integrated in the 15 genome near Ty δ elements, were grown overnight in parallel with the yeast strain INVSc1 containing YlpUTyL as a control. The precultures were diluted to an OD₆₀₀ of 0,25 in 100 ml minimal glucose-containing medium and grown for about 8 hours at 30°C until an OD₆₀₀ of 1 to 1,5 was reached. Subsequently, the yeast cells were transferred into minimal galactose-containing medium at an OD₆₀₀ of 1 (Bax- 20 expressing strains) or 0,4 (control strains) and grown for an additional 15 hours period.

RNA isolation

25 Total RNA was isolated using RNeasyTM Reagent (GenHunter Corporation Nashville, TN, USA) according to the GenHunter protocol. 1.5×10^9 cells were

concentrated in a microcentrifuge tube and 1ml RNAPure™ Reagent was added together with 1 g of glass pearls. The yeast cells were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNase digestion. Chloroform (150 µl) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA pellet was resuspended in 50 µl RNase free dH₂O.

10

First strand cDNA synthesis in the presence of α -³³P dCTP

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1YIpUTyLMuBax or INVSc1YIpUTyL yeast cells and incorporation of α -³³P dCTP as follows: 2 µl (1 µg/ml) of Oligo dT was added to 20 µg of total RNA in a maximal volume of 8 µl RNase-free dH₂O and incubated at 70° for 10 min. After cooling down on ice for 1 min, the following components were added:

6 µl 5x concentrated First Strand Buffer (GIBCO-BRL)
1 µl 0,1 M DTT
20 1 µl RNase Block (40 units/µl) (Stratagene)
1,5 µl 20 mM dXTP-solution (X = A, G and T) (Pharmacia)
1,5 µl SuperScript™ Reverse Transcriptase (200 units/µl) (GIBCO-BRL)
10 µl α -³³P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham)
and incubated for 2 h at 37°C during which first strand cDNA synthesis took
25 place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Pharmacia). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was $3,1 \cdot 10^8$ cpm/ μ g and $3 \cdot 10^8$ cpm/ μ g for the INVSc1YipUTyL and the INVSc1YipUTyLMuBax probe, respectively.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

10

Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection

The Yeast GeneFilters™ were successively hybridised with the α - 33 P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during hybridisation. The MicroHyb solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 10 ml MicroHyb™ solution (42°C) containing 5 μ l polydA (0,5 μ g/ml) and incubated for 24 hours at 42°C whilst rotating. After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA probe ($3,1 \cdot 10^8$ cpm/ μ g, $6,5 \cdot 10^7$ cpm) was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third more stringent wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min

at room temperature. The filters were flushed with dH₂O to avoid SDS precipitation. The Yeast GeneFilters™ were placed in a PhosphorImager™ cassette with storage phosphorscreen. After 4 days of development the screen was developed and scanned using the PhosphorImager™ 455 SI from Molecular Dynamics. The results of these can be seen in Figure 3.

In-between the hybridisation experiments, the filters were stripped off by incubation in 500 ml of a 0,5% SDS solution (prewarmed to near boiling temperature) during at least 1 hour at room temperature.

10 **Example 2. Quantification of hybridisation Signals**

Quantification of the hybridisation signals was done using the ImageQuant™ 4.1 software tool from Molecular Dynamics (Sunnyvale, CA). The quantification was performed per grid of the Yeast GeneFilters™, and by drawing a roster of 24 columns and 8 rows onto each grid of each filter. As such, each rectangle of the roster corresponds to a spot on the Yeast GeneFilters™. Subsequently, from each grid a volume-report (quantification) was drawn up and the data were transferred to a Microsoft™ Excel sheet. Also for each grid a correction factor was calculated. Signals neighboring big and dark spots were separately quantified. For each grid, a background level was calculated.

Statistical processing of quantification results

The statistical processing of the results was accomplished in Microsoft™ Excel. For each grid, the following statistical functions were separately defined:

5 1. The frequency of occurrence of the values in a precisely defined intensity range(data range), established between 1000 and 61000, split up in intervals of 5000.

2. The frequency in terms of percentage.

3. The cumulated frequency in terms of percentage.

10 These numeric values were used for the graphical display of the cumulated frequency in terms of percentage.

Subsequently, the results of the two experiments (hybridization with cDNA from YlpUTyL containing INVSc1 cells and hybridization with cDNA from YlpUTyLMuBax containing INVSc1 cells) were integrated by determination of a
15 second range of statistical functions:

1. The average of the values of the two experiments for each spot on the filter.

2. The standard deviation on this average. This is a measure for the distribution of the values around this average.

20 3. The standard deviation in terms of percentage.

The quotient of the values of the second experiment (Bax expression) against the values from the first experiment (control) was determined. This immediately gives the factor by which the expression of a specific gene is changed upon Bax induction.

In order to process all these data and to be able to discriminate between differences in gene expression, a gene showing a standard deviation in terms of percentage of at least 90% and a difference of a factor 5 in expression as a result of Bax induction, was identified as a differentially expressed candidate gene.

5 (Table 1). Requantification of these candidates confirmed their selection.

When the expression pattern of all 6144 genes is compared in the two experiments, it could be concluded that the expression profile of 142 genes (this is 2,3 %) has been changed with at least of factor 5. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 1.

10 The sequences of these genes and the amino acid sequences which they encode are shown in Figure 1.

Example 3 . Search for homologues in *Candida albicans*

Sequence similarity searches against public and commercial sequence
15 databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL
20 (Bairoch and Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).

Sequence similarity searches were performed using the BLAST software
25 package version 2. The identity between 2 sequences was calculated as

percentage identical residues, the similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.

Example 4 . Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans*

The method proposed is based on observations (Sandbaken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to the wild type (WT) cell.

Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to

a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti-sense or strains which carry disruptions in an essential gene. An in silico approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

Example 5. Assay for High Throughput screening for drugs.

35 µl minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems). A 96-channel pipettor (Hydra, Robbins Scientific) transfers 2.5 µl of R-compound at 10^{-3} M in DMSO from a stock plate into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, CAI-4, the medium is always supplemented with 20 µg/ml uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250,000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20,000 to 50,000 cells/ml. Cultures are grown at 30°C while shaking at 250 rpm until a final OD_{600} of 0.24 (+/- 0.04) is reached.

200 μ l of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 μ l total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

Optical densities are measured after 48 hours.

- 5 Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Tabl 1.

ORF	Qt	Sequ nce ID Number
YAR061W	7.80	SEQ ID NO 1
YAR073W	11.19	SEQ ID NO 3
YBL048W	5.07	SEQ ID NO 5
YBL051C	5.22	SEQ ID NO 7
YBL066C	6.04	SEQ ID NO 9
YBL078C	6.94	SEQ ID NO 11
YBR072W	26.56	SEQ ID NO 13
YBR073W	5.46	SEQ ID NO 15
YBR086C	7.14	SEQ ID NO 17
YBR093C	11.05	SEQ ID NO 19
YBR181C	0.15	SEQ ID NO 21
YCL007C	20.99	SEQ ID NO 23
YCL016C	23767.57	SEQ ID NO 25
YCR052W	10.51	SEQ ID NO 27
YCR064C	14.91	SEQ ID NO 29
YCR073WA	5.92	SEQ ID NO 31
YDL010W	5.31	SEQ ID NO 33
YDL036C	5.34	SEQ ID NO 35
YDL083C	0.16	SEQ ID NO 37
YDL125C	6.80	SEQ ID NO 39
YDL133CA	0.21	SEQ ID NO 41
YDL136W	0.20	SEQ ID NO 43
YDL167C	6.37	SEQ ID NO 45
YDL184C	0.21	SEQ ID NO 47
YDL191W	0.17	SEQ ID NO 49
YDR103W	6.26	SEQ ID NO 51
YDR238C	5.75	SEQ ID NO 53
YDR259C	9.68	SEQ ID NO 55
YDR294C	8.38	SEQ ID NO 57
YDR430C	5.66	SEQ ID NO 59
YDR438W	6.47	SEQ ID NO 61
YDR450W	0.16	SEQ ID NO 63
YDR471W	0.11	SEQ ID NO 65
YDR486C	5.27	SEQ ID NO 67
YDR499W	6.14	SEQ ID NO 69
YDR507C	6.34	SEQ ID NO 71
YDR515W	5.42	SEQ ID NO 73
YDR518W	6.15	SEQ ID NO 75
YDR519W	5.57	SEQ ID NO 77
YER102W	0.19	SEQ ID NO 79
YER153C	5.63	SEQ ID NO 83
YFL014W	41.08	SEQ ID NO 85
YFL015C	5.62	SEQ ID NO 87

Tabl 1. - continued -

ORF	Qt	Sequenc ID Num b r
YFR022W	9.44	SEQ ID NO 89
YGL011C	6.14	SEQ ID NO 91
YGL031C	0.11	SEQ ID NO 93
YGL032C	0.14	SEQ ID NO 95
YGL043W	10.74	SEQ ID NO 97
YGL102C	0.15	SEQ ID NO 99
YGL103W	0.17	SEQ ID NO 101
YGL130W	8.35	SEQ ID NO 103
YGL147C	0.08	SEQ ID NO 105
YGL213C	6.02	SEQ ID NO 107
YGL235W	6.23	SEQ ID NO 109
YGL260W	6.61	SEQ ID NO 111
YGR085C	0.16	SEQ ID NO 113
YGR118W	0.17	SEQ ID NO 115
YGR142W	8.91	SEQ ID NO 117
YGR236C	12.72	SEQ ID NO 119
YGR277C	6.27	SEQ ID NO 121
YGR284C	5.95	SEQ ID NO 123
YGR285C	5.84	SEQ ID NO 125
YHR010W	0.20	SEQ ID NO 127
YHR021C	0.16	SEQ ID NO 129
YHR141C	0.10	SEQ ID NO 131
YHR217C	7.6	SEQ ID NO 133
YIL112W	11.15	SEQ ID NO 135
YIL115C	7.67	SEQ ID NO 137
YIL148W	0.13	SEQ ID NO 139
YIL150C	6.83	SEQ ID NO 141
YIL167W	6.66	SEQ ID NO 143
YJL034W	11.61	SEQ ID NO 145
YJL035C	14.48	SEQ ID NO 147
YJL070C	5.29	SEQ ID NO 149
YJL078C	5.16	SEQ ID NO 151
YJL179W	0.19	SEQ ID NO 153
YJL180C	0.14	SEQ ID NO 155
YJL181W	0.21	SEQ ID NO 157
YJL187C	0.17	SEQ ID NO 159
YJL188C	0.1	SEQ ID NO 161
YJL189W	0.08	SEQ ID NO 163
YJL190C	0.09	SEQ ID NO 165
YJL197W	0.13	SEQ ID NO 167
YJL198W	0.2	SEQ ID NO 169
YJR049C	0.17	SEQ ID NO 171
YKR094C	0.14	SEQ ID NO 173

Tabl 1. - continu d -

ORF	Qt	Sequence ID Number
YLR040C	10.13	SEQ ID NO 175
YLR048W	8.55	SEQ ID NO 177
YLR088W	6.09	SEQ ID NO 179
YLR159W	0.18	SEQ ID NO 181
YLR167W	0.06	SEQ ID NO 183
YLR232W	7.4	SEQ ID NO 185
YLR233C	7.63	SEQ ID NO 187
YLR234W	5.68	SEQ ID NO 189
YLR238W	6.74	SEQ ID NO 191
YLR241W	6.48	SEQ ID NO 193
YLR321C	12.17	SEQ ID NO 195
YLR322W	5.54	SEQ ID NO 197
YLR325C	0.06	SEQ ID NO 199
YLR344W	0.12	SEQ ID NO 201
YLR367W	0.19	SEQ ID NO 203
YLR393W	7.05	SEQ ID NO 205
YLR423C	8.61	SEQ ID NO 207
YML026C	0.11	SEQ ID NO 209
YML063W	0.16	SEQ ID NO 211
YML128C	5.1	SEQ ID NO 213
YML130C	5.41	SEQ ID NO 215
YMR022W	6.45	SEQ ID NO 217
YMR118C	5.13	SEQ ID NO 219
YMR143W	0.08	SEQ ID NO 221
YMR174C	6.75	SEQ ID NO 223
YMR191W	9.56	SEQ ID NO 225
YMR230W	0.13	SEQ ID NO 227
YNL054W	5.19	SEQ ID NO 229
YNL067W	0.12	SEQ ID NO 231
YNL075W	0.16	SEQ ID NO 233
YNL096C	0.14	SEQ ID NO 235
YNL162W	0.07	SEQ ID NO 237
YNL178W	0.11	SEQ ID NO 239
YNL182C	0.18	SEQ ID NO 241
YNL190W	0.07	SEQ ID NO 243
YNL208W	5.87	SEQ ID NO 245
YNL210W	0.02	SEQ ID NO 247
YOL031C	5.32	SEQ ID NO 249
YOL048C	14.34	SEQ ID NO 251
YOR010C	7.27	SEQ ID NO 253
YOR019W	5.19	SEQ ID NO 255
YOR027W	6.03	SEQ ID NO 257
YOR031W	5.35	SEQ ID NO 259
YOR096W	0.12	SEQ ID NO 261
YOR248W	0.18	SEQ ID NO 263

Tabl 1. - continu d -

ORF	Qt	Sequence ID Number
YOR293W	0.11	SEQ ID NO 265
YOR312C	0.12	SEQ ID NO 267
YOR369C	0.21	SEQ ID NO 269
YPL047W	5.09	SEQ ID NO 271
YPL090C	0.1	SEQ ID NO 273
YPL137C	10.41	SEQ ID NO 275
YPL159C	5.61	SEQ ID NO 277
YPL175W	5.95	SEQ ID NO 279
YPL180W	7.68	SEQ ID NO 281
YPL218W	6.26	SEQ ID NO 283
YPR102C	0.17	SEQ ID NO 285

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CLAIMS

1. Use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or
5 fungi and which nucleic acid sequence is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98,
10 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238,
15 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378,
20 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid molecule encoding a protein having an amino acid
25 ~~sequence which is more than 70% similar, preferably more than 80%~~

similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456;

(c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106,

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304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330,
332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358,
10 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386,
388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414,
416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442,
444, 446, 448, 450, 452, 454 or 456;

(d) a nucleic acid molecule comprising a sequence as represented in any
15 of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31,
33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69,
71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105,
107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133,
135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161,
20 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189,
191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217,
219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245,
247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273,
275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301,
25 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329,

331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357,
359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385,
387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413,
415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441,
5 443, 445, 447, 449, 451, 453 or 455;

(e) a nucleic acid sequence which is more than 70% identical, preferably
more than 80% identical, more preferably more than 90% identical and
most preferably more than 97% identical to any of the nucleic acid
sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21,
10 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59,
61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97,
99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125,
127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153,
155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181,
15 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209,
211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237,
239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265,
267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293,
295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321,
20 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349,
351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377,
379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405,
407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433,
435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455; and

(f) the complement of any of the nucleic acid sequences as specified in a) to e),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

5

2. Use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

(a) a protein having an amino acid sequence as represented in any of SEQ

10

ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444,

15

20

446, 448, 450, 452, 454 or 456, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16,

18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54,
56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92,
94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122,
124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150,
5 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178,
180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206,
208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234,
236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262,
264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290,
10 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318,
320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346,
348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374,
376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402,
404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430,
15 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454 or 456; and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

20 3. A pharmaceutical or fungicidal composition comprising a nucleic acid molecule as defined in claim 1 or a polypeptide as defined in claim 2 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

4. A vaccine for immunizing a mammal against yeast or fungal
25 infections, comprising at least one nucleic acid molecule as defined in claim 1, or

at least one polypeptide as defined in claim 2, in a pharmaceutically acceptable carrier.

5. A genetically modified yeast or fungus in which modification results
5 in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or the polypeptides as defined in claim 2, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungus.
- 10 6. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:
- 15 (a) contacting a compound to be tested with yeast or fungal cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound,
- 20 (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said

mutated yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

5

7. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

10

15

- (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,

20

- (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

25

- (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the

compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

- 5 (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

8. A method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to
10 programmed cell death of yeast or fungi, which method comprises:

- (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2,
- (b) detecting the complex formed between the compound to be tested and said polypeptide,
- 15 (c) alternatively, examining the diminution of complex formation between said polypeptide and a receptor, caused by the addition of the compound being tested.
- (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

20

9. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

- (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene,
- (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested.

5

10. A method according to any of claims 6 to 9 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

10

11. A compound identifiable according to the method of any of claims 6 to 9.

12. A compound according to claim 11 for use as a medicament.

15

13. Use of a compound according to claim 12 for the preparation of a medicament for treating diseases associated with yeast and fungi.

14. Use of a compound according to claim 12 or a genetically modified organism as defined in claim 5 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

15. Use of a compound according to claim 12 where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*,

25

Coccidioides immitis, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*,
Cryptococcus neoformans, and *Sporothrix schenckii*.

16. A nucleic acid sequence encoding a polypeptide which is involved in
5 a pathway for programmed cell death of yeast or fungi selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as
represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302,
304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338,
342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372,
10 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408,
410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442,
444, 446, 448, 450, 452 or 454, or encoding a functional equivalent,
derivative or bioprecursor of said protein;

(b) a nucleic acid molecule encoding a protein having an amino acid sequence
15 which is more than 70% similar, preferably more than 80% similar, more
preferably more than 90% similar and most preferably more than 97%
similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288,
290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322,
324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360,
20 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392,
394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430,
432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454;

(c) a nucleic acid molecule encoding a protein having an amino acid sequence
which is more than 70% identical, preferably more than 80% identical, more
25 preferably more than 90% identical and most preferably more than 97%

identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454;

(d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451 or 453;

(e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451 or 453; and,

(f) the complement of any of the nucleic acid sequences as specified in a) to e).

17. A nucleic acid according to claim 14, characterized in that it is derived from *Candida albicans*.

5 18. A nucleic acid sequence according to any of claims 14 to 16 which is mRNA

19. A nucleic acid sequence according to any of claims 14 to 16 which is DNA.

10 20. A nucleic acid sequence according to any of claims 14 to 16 which is cDNA.

21. A nucleic acid sequence capable of hybridizing to a nucleic acid
15 according to any of claims 14 to 20 under high stringency conditions, or the complement thereof.

22. An antisense molecule comprising a nucleic acid sequence capable of hybridizing to the nucleic acid sequences according to any of claims 14 to 20.

20 23. An isolated protein which is involved in a pathway for programmed cell death of yeast or fungi selected from:

(a) a protein having an amino acid sequence as represented in any of SEQ ID
NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316,
25 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354,
356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386,
388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424,
426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or

454, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- 5 (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 10 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 or 454;
- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 15 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 20 442, 444, 446, 448, 450, 452 or 454; and,
- (d) a functional fragment of any of said proteins as defined in a) to c)

24. An expression vector comprising a nucleic acid sequence according to any of claims 16 to 22.

25. An expression vector according to claim 24 which comprises an inducible promoter.
26. An expression vector according to any of claims 24 or 25 which
5 comprises a sequence encoding a reporter molecule.
27. A host cell transformed, transfected or infected with the vector of any of claims 24 to 26.
- 10 28. A nucleic acid molecule according to any of claims 16 to 22 for use as a medicament.
29. A polypeptide according to claim 23 for use as a medicament.
- 15 30. An antibody capable of binding to a polypeptide according to claim 23.
31. An antibody according to claim 30 for use as a medicament.
- 20 32. A pharmaceutical composition comprising an antibody according to claim 30.
33. Use of an antibody according to claim 30, or an antibody capable of binding to at least one of the polypeptides as defined in claim 2, for the preparation
25 of a medicament for treating diseases associated with yeast and fungi.
34. Use of an antibody according to claim 33 where the fungus is *Candida albicans*.

35. A nucleic acid probe which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 16 and which hybridises specifically with any of said nucleic acid molecules.
- 5 36. A nucleic acid primer which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 16 and which specifically amplifies any of said nucleic acid molecules.

ABSTRACT

The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a medicament for treating diseases associated with yeast or fungi. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical or fungicidal compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

YAR061W, 704 bp, CDS: 501-704 (SEQ ID NO 1)

AAAATTTGGCACTTCAGAGCTTATCGTATCTTCTCCCGAGTTCTCAAGACTTATACTT
CAGCCCGTTTAGGAATGCATAAAAGCAAATAGGATTCGTTACAACGCTGCAGGACTCTT
TAGGACTGCATCAAGGTAAGCCTCGCTGCACCTAAACGCAAAATGTGGTTGTAACCTTTT
TAATTTTTTCTTGAAGTTGTTGAGTCGTAATAAATCGTTTCTGGGAAGTGAAGGTAAT
AATGTAATGGAATCGGCGTTACTCGCATGTGCAGATATCAGCGACAAAAGTGTGTAGG
GACGTTTCGATACCAAATTTCTAAATACAGCGCAGGAACATCACTACGCTAAACAAAT
CGTAGCGCATACATCTGATCGAAAAAGACAGTTCCCAAAACAATGACATATGAAGAGAC
CAGCATCAAAATTTTCATCATTAACAGCATGGCTAAAAGTTATTGTTTAATATACCCATA
CCTGATTGACGAACCAAGAAATGCCTTATCACTATTTATTTTGGCACTCTTCACCTACC
TGGCCACGTCCAATGTTGTTTCAGGAAGTACACAAGCATGCCTGCCAGTGGGCCCCGAGGA
AAAATGGGATGGAATGTCAACTTTTATAAACTACTCATTACTGGATTCAACAACGTATTCTT
ACCCGCAATATATGACTTCTGGATATGCCTCGAATTGGAATTAG

YAR061W, 67 aa (SEQ ID NO 2)

MPYHYLFALFTYLATSNVVSSTQACLPGPRKNGMNVNFYKYSLLDSTTYSYPQYMTS
GYASNWN

YAR073W, 1712 bp, CDS: 501-1712 (SEQ ID NO 3)

AGTGGCTCATGATCTGTAAATGATCGGTTGACCGCAGTATTATATAATAACATCCGTATA
AGTACATATACTACCATGTCTGTTCTCTACATTGCTTTTTATTCAGATTATTGGTTTTC
CTAACCGCCGCGCGCGCAGGTACCCCGCGCATCTCTTCTCTCGAAGAAAGCGGAAAAA
ACAAAAAAGTATAAATAGTGGAGTCTTTTCCCATTTAACATTTAGAAAAAATTCG
AATGGAAATTTCTTGGCGAACATTTAACCGGAGACCCTTGGCGGCTTTTTCTCAGTTTCG
TGGGCTAGTACATTTTACCTAGTATGCTGGGAACTTTTTTCCGTATTCTATTCTATTCC
TTGCCTTACTTTTCTTATCATTTTTTATATAACCAATTTCAAAAATACTTTTAACTGTC
ATAGACGCATTTTGTATTATACAAATTAAAAGAATCAAATATAATATGTGCAATTAATAA
CTCCACAAGTAGCGAAAGCAATGGCCGCCATTAGAGACTACAAGACCGCACTAGATCTTA
CCAAGAGCCTACCAAGACCGGATGGTTGTGTCAGTGCAGGAAGTATGGACTCCAAGATCA
GAGGTGGGTGGCTTATAACGATTTTTTAATCTTACCAGGTTTAGTCGATTTTGCCTCCT
CTGAAGTTAGCCTACAGACCAAGCTAACCGAATATTACTTTAAACATTCCATTAGTAT
CCTCTCCAATGGACACTGTGACGGAATCTGAAATGGCCACTTTTATGGCTCTGTTGGATG
GTATCGGTTTCATTACCATAACTGTACTCCAGAGGACCAAGCTGACATGGTCAGAAGAG
TCAAGAATCATGAAAATGGGTTTATTAACAACCTTATAGTGATTTCTCCAATACGACCG
TTGGTGAAGCTAAGAGCATGAAGGAAAAGTATGGATTGTCAGGCTTCCCTGTCACGGCAG
ATGGAAAGAGAAATGCAAAGTTGGTGGGTGCCATCACCTCTCGTGATATACAATTCGTTG
AGGACAACCTCTTACTCGTTGAGGATGTCATGACCAAAAACCTGTTACCGGCGCACAAG
GTATCACATTATCAGAAGGTAACGAAATCTAAAGAAAATCAAAAAGGGTAGGCTACTGG
TTGTTGATGAAAAGGGTAACCTTAGTTTCTATGCTTTCCCGAACTGATTTAATGAAAATC
AGAAGTACCCATTAGCGTCCAAATCTGCCAACACCAAGCAACTGTTATGGGGTGCTTCTA
TTGGGACTATGGACGCTGATAAAGAAAAGACTAAGATTATTGGTAAAAGCTGGCTTGGATG
TCGTCATATTGGATTCTCTCAAGGTAACCTATTTTCCAATTGAACATGATCAAATGGA
TTAAAGAACTTTCCAGATTGGAATCATTTGCTGGTAACGTTGTCACCAAGGAACAAG
CTGCCAATTTGATTGCTGCCGGTGCCGACGGTTTGAGAATTGGTATGGGAAGTGGCTCTA
TTTGTATTACCCAAAAGTTATGGCTTGTGGTAGGCCACAAGGTACAGCCGTCTACAACG
TGTGTGAATTTGCTAACCAATTCGGTGTTCATGTATGGCTGATGGTGGTGTTCAAAAAC
ATTGGTCAATTATTACCAAGCTTTGGCTCTTTGGTTCTTCTACTGTTATGATGGGTGGT
ATGTTGGCCGGTACTACCGAATCACCAGGTGA

YAR073W, 403 aa (SEQ ID NO 4)

MAAIRDYKTALDLTKSLPRPDGLSVQELMDSKIRGGLAYNDFLILPGLVDFASSEVSLQT
KLTRNITLNIPLVSSPMDTVTESEMATFMALLDGIGFIHNCPTEDQADMVRRVKNYENG
FINNPIVI SPTTTVGEAKSMKEYGFAGFPVTADGKRNAKLVGAITSRDIQFVEDNSLLV
QDVMTKNPVTGAQGITLSEGNEILKKIKKRLLVDEKGNLVSMLSRTDLMKNQKYPLAS
KSANTKQLLWGASIGTMDADKERLRLLVKAGLDVILDSSQNSIFQLNMIKWIKETFPD
LEIIAGNVVTKQEAANLIAAGADGLRIGMGTSICITQKVMACGRPQGTAVYNVCEFANQ
FGVPCMADGGVQKHWSYYYQSFGSWFFYCYDGWYVGRYYRITR

FIG. 1 - 1

YBL048W, 812 bp, CDS: 501-812 (SEQ ID NO 5)
GGGAGAAGCTTATCTTACTGTAGAAGAAAATGGGATTGCGTTACTCCATATATATTGAAA
ATCCGTTATCTTCCCCATCATCATCGTATAAATCAATAAACGACCCGTTATTCCACTCTC
AGCATCGATCGCAAAAAACGTGAGCTTCATCACCTACGGTTGTAGACATTGCAAGACAC
ATCTTTCCAGTTCCTTCCAGATTATTTCTAGAGATTATAGGGGTAGGACCGGAAGTCTT
ATTTAATGAACAAAGTTGTTAATGTCGTTGAAGGAAAGGTCGAGCAACGAAGAATGTTGA
CTGGCGACTACTTAGTCTGTGATATTTCTTTGTGTCATTGGTGCAAGAGGAACGTAGGTTGGA
AATACTTGCAGAGCAGCAATGATGATCAGCAGTATAAGGAAGGAAAGTTTATCTTAGAGC
TGAAAAACATTTGTAAATGTACTTGATGTCTTCTCTTGTCTGCTATCTAGCACCTCTCGT
CTTTTAGTGCTTTTTAGCGTATGATTCTTTTTAAGAATCTGGTCTTCTCTCCTTCTATTT
TGATTGGGTATATTTCTATTCGTGTTTCATTACTGGTCTGGGTAAATTGGGTTTTGGTTT
GGTCCAGTTGTTTTCAAGTAGCCTTTATTTTTTCATTGTGGTATTTTATCTTATCGATTT
ATACTTTTTTTTATTCAAAGAAAATTAAACAGATAATCTCTTATGAGCCTAGCTACTTTG
TTTTTCTTACAGGGCCATTGACTTATGCCCTGAACGAGTCTTACTTTACTTTTTTTGTAA
TTTTCAATAATGTCGTGTTTCCCATGTTGTAA

YBL048W, 103 aa (SEQ ID NO 6)
MILFKNLVFLPSILIGYISIRVSLLVWVNWVLWSSCFQVAFIFSLWYFILSIYTFYFSK
KIKQIISYEPSYFVFSYRAIDLCPERVLLYFFCIFNNVFPML

YBL051C, 2507 bp, CDS: 501-2507 (SEQ ID NO 7)
GGGAAATATCAATTCCCGTATTTCAATGTTAGTAATTTGCCTTCGTAAATTACGGAATCA
CATAGCTTTTCATTTTGTTCCTTTGATATATTTCCCTACTACATACTCTTTTCAATAACTC
TACAGGGTCTGACATTTTAACTTTCAGGTTAATGATGGTGTCTTACTATATTCTCGAG
TCGTACAGAAGTTAGTTCAGATAAACTGCTTCGGTGCTGCCACTTCTTATCATTACTTC
AACTTTACCTTCCCTATACCTGTGTGCTCTTATTAATTCAAGTTAATCCGAGGTAATAGA
TTAGGGTAACCTTCAATGATGTCACGAAACACGGATGCTGCAACTTTGCGATTTTTTCCT
GGAAAAGAATAACAATTAAAGGCAGCCTTTCAGCTGAGATTACCAGCAGGTCTTTGGAGA
TTAGCGCAAGAAGAAGTGTGATATAGTACTCATAGAGGCAGGCTACAGACTAGGGAAAGC
GTGTTCAACAACAATAAGAAATGGAGAGCAGTTCTTTTGAGAATGCTCCTCTGCAGCCA
TCAATGATGCTCAGGATAATAATATAAATACGGAGACTAATGACCAGGAAACAAATCAGC
AATCTATCGAACTAGAGATGCAATTGACAAAGAAAACGGTGTGCAACGGAAACTGGTG
AGAACTCTGCAAAAAATGCCGAACAAAACGTTTCTTCTACAAATTTGAATAATGCCCCCA
CCAATGGTGCTTTGGACGATGATGTTATCCCAAATGCTATTGTTATTAATAAATCCCGT
TTGCTATTAATAAAGAGCAATTGTTAGACATTATTGAAGAAATGGATCTTCCCTTCTCTT
ATGCCCTTCAATTACCCTTTGATAACGGTATTTTCAGAGGACTAGCCTTTTGCGAATTTCA
CCACTCCTGAAGAACTACTCAAGTGATAACTTCTTTGAATGGAAAGGAAATCAGCGGGA
GGAAATTGAAAGTGGAATATAAAAAATGCTTCCCAAGCTGAAAGAGAAAGAATCGAGA
GGGAGAAGAGAGAGAAAAGAGGACAATTAGAAGACAACACAGATCGTCATCTAATCTTT
CTTTGGATTCTTTATCTAAATGAGTGGAAGCGGAAACAATAATACTTCTAACAATCAAT
TATTCTCGACTCTAATGAACGGCATTAATGCTAATAGCATGATGAACAGTCCAATGAATA
ATACCATTAACAATAACAGTTCTAATAACAACAATAGTGGTAACATCATTCTGAACCAAC
CTTCACTTTCTGCCCAACATACTTCTTTCATCGTTGTACCAACAAACGTTAATAATCAAG
CCAGATGTCCACTGAGAGATTTTATGCGCCTTTACCATCAACTTCCACTTTGCTCTCC
CACCCCAACAACCTGGACTTCAATGACCCTGACACTTTGGAAATTTATTCCCAATTATTGT
TATTTAAGGATAGAGAAAAGTATTATTACGAGTTGGCTTATCCCATGGGTATATCCGCTT
CCCACAAGAGAATTATCAATGTTTGTGCTCGTACTTAGGGCTAGTAGAAGTATATGATC
CAAGATTTATTATTATCAGAAGAAAGATTCTGGATCATGCTAATTTACAATCTCATTTGC
ACAACAAGGTCAAATGACATCTGCTCATCTTTGCAGCCAACTCCACTGGCGGCTCCA
TGAATAGGTCACAATCTTATACAAGTTTGTTACAGGCCCATGCAGCAGTGCAGCGAATA
GTATTAGCAATCAGGCCGTTAACAATTCTTCCAACAGCAATACTATTAAACAGTAATAACG
GTAACGGTAACAATGTCATCATTAATAACAATAGCGCCAGCTCAACACCAAAAAATTTCTT
CACAGGGACAATTCTCCATGCAACCAACACTAACCTCACCTAAAATGAACATACACCATA
GTTCTCAATACAATTCCGCAGACCAACCGCAACAACCTCAACCACAAACACAGCAAAATG
TTCAGTCAGCTGCGCAACAACAATCTTTTTTAAGACAACAAGCTACTTTAACACCAT

FIG. 1 - 2

CCTCAAGAATTCCATCCGGTTATTCTGCCAACCATTATCAAATCAATTCCGTTAATCCCT
TACTGAGAAATTCTCAAATTTACCTCCAAATTCACAAATCCCAATCAACAGCCAAACCC
TATCCCAAGCGCAACCACCAGCACAGTCCCAAACTCAACAACGGGTACCAGTGGCATACC
AAAATGCTTCATTGTCTTCCCAGCAGTTGTACAACCTTAACGGCCCATCTTCAGCAAAT
CACAGTCCCAACTGCTTCCACAGCACACAAATGGCTCAGTACATTCTAATTTCTCATATC
AGTCTTATCACGATGAGTCCATGTTGTCCGCACACAATTTGAATAGTCCGACTTGATCT
ATAAATCTTTGAGTCACTCTGGACTAGATGATGGCTTGGAACAGGGCTTGAATCGTTCTT
TAAGCGGACTGGATTTACAAAACCAAAACAAGAAGAATCTATGGTAA

YBL051C, 668 aa (SEQ ID NO 8)

METSSFENAPPAAINDAQDNNINTETNDQETNQOSIETRDAIDKENGVOETETGENSAKNA
EQNVSSSTNLNAPTNGALDDDVIPNAIVIKNIPFAIKKEQLLDII EEMDLPLPYAFNYHF
DNGIFRGLAFANFTTPEETTQVITSLNGKEISGRKLKVEYKKMLPQAERERIEREKREKR
GQLEEQRHSSSNLSLDSLSKMSGSGNNNTSNNQLFSTLMNGINANSMMNSPMNNTINNNNS
SNNNNSGNIIILNQPSLSAQHTSSSLYQTNVNNQAQMSTERFYAPLPSTSTLPLPPQQLDF
NDPDTLEIYSQLLLFKDREKYYYELAYPMGISASHKRIINVLC SYLGLVEVYDPRFIIIR
RKILDHANLQSHLQQGQMTSAHPLQPNSTGGSMNRSQSYTSLLQAHAAAAANSISNQAV
NNSNSNTINSNNGNNGNVIINNNSASSTPKISSQGQFSMQPTLTSPKMNIHSSQYNSA
DQPQQPQPQTQQNVQSAQQQQSFLRQQATLTSSRIPSGYSANHYQINSVNPLLRNSQI
SPPNSQIPINSQTLQAQPPAQSQQTQQRVPVAYQNASLSSQQLYNLNGPSSANSQSQQLP
QHTNGSVHSNFSYQSYHDESMLSAHNLNSADLIYKSLSHSGLDDGLEQGLNRSLSGLDLQ
NQNKKNLW

YBL066C, 3674 bp, CDS: 501-3674 (SEQ ID NO 9)

ATCCCAAGAAGAAGATTAGACTGATTTTTTACCTACCTTCCACCGTCGGAAGAAACACTT
CTGAAGTGTTAAGGGTAATCGACGCCTTGCAATTGACTGACAAGGAGGGCGTAGTAATC
CAATTAATTGGCAGCCAGCTGACGATGTCATTATTCTCCCTCTGTCTCCAATGATGAGG
CGAAGGCTAAATTTGGTCAATTTAATGAAATTAAACCTATTTAAGATTACCAAGTCGA
AATAAGCTTTGAAATAAACGACTTTACTATATACAGGTATATGAAGTATCTCTAACTAAA
ACTTTTATCTATCTTTTATTCTTATTATATCTCATCTCGTACGAAGGGCCGCTCATTGGA
TCATTTTCTTTTACATACCGTAAAGGAATGGCGTTAAAAATATATATATGAAAAATGCATG
TAATAAACTCTCTGCAGAAACCTTAATGTCAAAGGTCCCGTATACAGATTATATTGGCTC
TGCGTATACGCATTCTCGTCATGGTGAAGGATAATCGAGATTCTGACCAAGACCAAGATT
TTAGTTCTGCTCATATGAAAAGACAACCGGAGCAGCAACAGTTGCAACAGCACCAGTTCC
CAAGTAAGAAACAACGAATATCTCACCATGATGACAGTCATCAAATCAACCATAGACCAG
TTACCTCATGTACACATTGTAGACAGCACAAAATCAAATGCGATGCTAGTCAAAATTTCC
CTCATCTTGTCTCCAGATGCGAAAAAATTTGGTCTCCACTGTGAAATCAATCCTCAATTC
GGCCTAAGAAGGGCTCACAGTTGCAACTACTGAGACAAGATGTGGATGAAATCAAATCTA
AACTCGATACTCTTCTGGCCAATGACAGCGTTTTCTGTTTCTATCTTTTACAACAGATTCCCA
TGGGCAATAGCCTTTTGAATAAGCTCAATCTGCATCCAACCTCCAACCTCCGGGTACTATTA
TCCCTAACCCAGATTCTTCTCCTTCTCAGGTTCTCCAACCTCTTCCGCGGCTCAACGAG
ATTCTAAGGTTTCAGTTCAAACCTTATTTGTCCAGGGAACCCCAACTCTTACAAGCAAATC
AGGGCAGCAATACGAATAAATTTAAAGCAAATAATGAAGCATCTTCTCACATGACGTTGC
GCGCATCTTCTTTAGCGCAAGATTTCGAAAGGCTTGGTTGCAACAGAGCCAAATAAGCTGC
CCCCGCTGCTAAATGACTCAGCATTGCCTAATAATTCAAAGAATCTTTACCTCCTGCTT
TGCAAAATGGCTTTTTTATAAGAACAACCTCTGCAGGTAACACTCCGAACGGCCCCCTTCTCTC
CAATTCAAAAACATATTCCCCTCATACTACGTGACACCGTTACAACGACAACAAATC
AACCACCATTTGCAGCAACAAGCCACGTAGCAACAAATAACAATGCAGATAGGACGAAGA
CGCCGGTAGTAGCCACCACGACTATGCCATTATTGCCCTTCGCCGATGCAATGTAG
ATGAGTTTGTACTGGGCGATATTAGTATTTCCATTGAAAAAGCGAATAGATTACACCATA
TTTTCTGTGACTAGGTATCTGCCGTATTTTCTTATTATGTATTCCAATAACGCCACCGAAT
TATACTCCCAATCTCAGTTGCTTTTTCTGGACCGTGATGTTGACGGCATGTCTGTCTGATC
CTGAACCGACGATGTATTGCAAGCTAAGCTCTTTGATCAAGCAACTTGCCATAGAGACCT
GCTGGATAAGAACACCTAGATCCACACATATTTGCGAAGCTTTGTTAATATTGTGCATTT
GGCCTTTGCCTAACCAAAAAGTCCCTAGATGATTGTTCTTACCGTTTTGTAGGATTAGCAA
AGTCACTGTCTTATCAATTAGGTTTGCACAGAGGTGAATTCATTTCTGAATTCACAAGAA
CTCAAACATCAATGCCAAATGCAGAAAAGTGGAGAACTAGGACTTGGCTGGGAATATTTT
TTGCCGAACCTTTGTTGGGCGAGTATCCTTGGTTTGGCCAACTTCACAGACAGACTATT

FIG. 1 - 3

TATTAGAAAAAGCCTTATCCTGTGGTGACGAAGAATCAGAAGAAGATAACAATGACAGTA
TTGACAATAACAACATGATAAAAGGAACAAGAAAGACGAGCCGCACGTTGAAAGTAAAT
ACAAACTACCGGGCAGTTTTAGAAAGATTGCTCAGCCTGGCGAATTTCCAAGCAAAATTGT
CTCATATCTTGGTTCTTCCACTTCCAGTCTGATGGTTTATTGGAACCAAGTATCGTG
CTGAGACACTGTCCATCTTGGGAAAAGAGTTAGATTTATTAGCAAAAACTTTAAATTTCC
AGAGTGACGATACTGTCAACATTTATTTTCTTTATGTTAAATTAAGTGTCTGTTGTTTTG
CATTCTACCCGAAACACCTCCTACCGATCAAATTCATATGTCACAGAGGCCTATCTAA
CAGCTACTAAAATTGTCACTCTATTGAATAATCTTTTAGAAACACACCAATTAATTGAAC
TGCCTATTTATATTAGACAAAGCTGCTACATTTTCTGCACTGATTCTCTTTAAATTGCAGT
TGACTCCTTTACTTCTTGACAAATATTTTGATTGACGAAGGCAATCCGTGGTCACTATCC
ATAGACTTTTATAGAAATCAGTTAACTGCGTGGGCCACTAGTGTGAGAATGATATTTTCCA
GAAGTGAAGTATGTTAGAAAACCTGAACCTCGTACTGATCATGCATCCGAAGTTTTTG
TGGAAGAAGACGGTATTATTTCTAGGATGAGATCACATTTAACAGGTCTCTATTCTATG
ATTTGGTTTGGTGTGTTACGAGGCGAGAAGAAGGGAAATGGATCCCGAATATAACAAGC
AAGCCTTAGAGAAAGCCGCTAAGAAAAGAAAATTTTCTCAAATGGTATCTACAATGGCA
CTTCGTCTACGGGTGGCATAACGGACAGAAAACCTATATCCATTGCCACTATATAACCATA
TCTCCAGAGATGACTTTGAAACTGTAACAAAAACAACACCAAGTGGAAACCACTGTTACCA
CTTTAGTTCTACTAAGAATGCCTTAAAGCAGGCAGAAAAGCTAGCCAAGACAAAATAACG
GAGATTCTGACGGTTCTATAATGGAGATTACGGGATACCTCTTTCCATGCTCGGGGAAA
CAGGCAGCGTAAAATTTCAAAGTTTATTTCGCTAATACCTCGAATAGTAACGATTATAA
ATAATAGGACGTTATTGGATGCGTCTAATGACATATCAATTCCCTCTAATTCAATTTATC
CAGTGGCTTCTGTCCCCGCTTCGAATAACAATCCACAAAGTACTAAGGTAGACTATTATA
GTAACGGACCTAGTGTAATTCCCTGATCTCTCCATGAAAAGATCAGTAAGCACTCCCGTTA
ATCATTTTCTGCGTCCGTTCCAGGGTTAAGGAACCAACCCCGTTGGCAACTTATCTAATA
ATGTTACATTGGGAATAGACCACCCCTATTCCAAGGGAGCACAGTAATTTACAAAATGTCA
CCATGAATTATAATAATCAATTCAGCAACGCCAACGCGATTGGAAGATCACAAAGTAGTA
TGTCCTTCCATTACCGTACACCTTTGTTTCGGTCAATATATGACAGTTGGATTCCGCGTCCGA
CCCCGGTCTCTAA

YBL066C, 1057 aa (SEQ ID NO 10)

MVKDNRDSDQDQDFSSAHMKRQPEQQQLQHQFPSPKKQRI SHHDDSHQINHRPVTSCTHC
RQHKIKCDASQNFPHPCSRCEKIGLHCEINPQFRPKKGSQQLQLLRQDVDEIKSKLDTLLA
NDSVFVHLLQQIPMGNSLLNKLNLHPTPTPGTIIIPNDSSPSSGSPTSSAAQRDSKVSQ
TYLSREPQLLQANQGSNTNKFKANNEASSHMTLRASSLAQDSKGLVATEPNKLPPLNDS
ALPNNSKESLPPALQMAFYKNNSAGNTPNGPFSPIQKTYSPHTTSTTVTTTTNQPFFAAT
SHVATNNNADRTKTPVVATTTTmplLPSPHANVDEFVLGDISISIEKANRLHHIFVTRYL
PYFPIMYSNNATELYSQSLLFWTVMLTACLSDPEPTMYCKLSSLIKQLAIETCWIRTPR
STHISQALLILCIWPLPNQKVLDDCSYRFVGLAKSLSYQLGLHRGEFISEFTRTQTSMPN
AEKWRTRTWLGIFFAELCWASILGLPPTSQTDYLLEKALSCGDEESEEDNNDSDNNND
KRNKDEPHVESKYKLPGSFRRLLSLANFQAKLSHIIGSSTSSPDGLLEPKYRAETLSIL
GKELDLLAKTLNLFQSDDTVNIYFLYVKLTVCCFAFLPETPPTDQIPYVTEAYLTATKI
LLNNLLETHQLIELPIYIRQAATFSALILFKLQLTPLLDPKYFDSARQSVVTIHRLYRQ
LTAWATSVENDISRTASMLEKLNFLIMHPEVFVEEDGII SRMRSHLTGSLFYDLVWCVH
EARRREMDPEYNKQALEKAACKRFSSNGIYNGTSSTGGITDRKLYPLPLYNHISRDFE
TVTKTTPSGTTVTTLVPTKNALKQAEKLAKTNNGSDSGSIMEINGIPLSMLGETGSVKFQ
SLFANTSNSNDYNNRLLDASNDISIPNSNIYPVASVPASNPNQSTKVDYYSNGPSVI
PDL SMKRSVSTPVNHFPASVPGLRNHPVGNLSNNVTLGIDHPIPREHSNLQNVTMNYYNQ
FSNANAIGRSQSSMSHSRTPLFRSIYDSWIPRPTPVL

YBL078C, 854 bp, CDS: 501-854 (SEQ ID NO 11)

TAGTGGAGTACGAATTAGTTAAAGATACTATCGACTTTGAAGCCATTGTCAAAGAACATT
TTGATATGTTAAGCAAGACCTGTAGATCCGACATTGCCAAATATGACGGCTCAAAGACAG
ACCCAATGTTGATGAAGAACAATCTATTAATGACACCATTTTCAAATAAAAGTGTTCA
AATTATGAAAACAACTCATATAAAATACGTACAAATTTTCTCTACTCGAAGTGATATAGA
TGTATATGTGTAAGTTTACGTTTAAAGTTAGAGTCATGTAATGCTAACTGTCTCCACCGAT
AATGTTGTATAATACCCGTGAAATCATAGCACATGATATATCATCACCCGGAGGCCGGTT
ATTTTCGGCGGGCGGCAAAAATATTTGGTATAATTATGGAATAACAAAAGGGGAACCAT
AAAGGTTGAGGAGGGGATTGATAAGAGAATCTAATAATTGTAAAGTTGAGAAAATCATAA

FIG. 1 - 4

TAAAAATAATTACTAGAGACATGAAGTCTACATTTAAGTCTGAATATCCATTTGAAAAA
GGAAGGCGGAGTCGAGAGGATTGCTGACAGGTTCAAGAATAGGATACCTGTGATTTGCG
AAAAGCTGAAAAGTCAGATATTCCAGAGATTGATAAGCGTAAATATCTAGTTCCTGCTG
ACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAGAGAATTATGCTACCCCTGAGA
AGGCCATCTTCATTTTGTCAATGATACTTTGCCACCTACTGCGGCGTTGATGTCTGCCA
TATATCAAGAACACAAGGATAAGGACGGGTTTTTGTATGTCACCTACTCAGGAGAAAATA
CATTTGGCAGGTAG

YBL078C, 117 aa (SEQ ID NO 12)

MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQF
VYVIRKRIMLPPEKAIFIFVNDLPPPTAALMSAIYQEHKDKDGLYVTYSGENTFGR

YBR072W, 1145 bp, CDS: 501-1145 (SEQ ID NO 13)

GCAGCAGCAACTCCGTGTGTACCCCTAACTCCGTGTGTACCCCTAAAGAACCTTGCTGT
CAAGGTGCATTGTTGGATCGGAATAGTAACCGTCTTTACATGAACATCCACAACCAACGA
AAGTGCTTTTTCAAGCATTGCTTGATTTCTAGAAAGATCGATGGTTATTCCTCCCTCCCTT
ATGCGTCCAAAAATATAGGGTGTCTCGTAACAGTAAGGTATTTCGCACTTAGCGTGTCTGCA
ACACAAAATTAAGTAATATGCGAGTTTTAGATGTCTTGGCGATCTATGCACGTTCTTGA
GTGGTATTTTATAACAACGGTTCCTTTTACCCTTATTCCTAAACATATAAATAGGACCT
CCATTAGTTAGAGATCTGTTTTTAATCCATTACCTTTTCATTCTACTCTTTATACTAAT
AAAACCACCGATAAAGATATATCAGATCTCTATTAACAGGTATCCAAAAAGCAAACA
AACAACTAAACAAATTAACATGTCATTTAACAGTCCATTTTTTGATTTCTTTGACAACA
TCAACAACGAAGTTGATGCCTTTAACAGATTGCTGGGTGAAGGCGGCTTAAGAGGCTACG
CACCAAGACGTCAAGTAGCAAAACACACCGCAAGGATTCTACTGGCAAGGAAGTTGCTA
GACCAATAACTATGCTGGCGCTCTTTATGATCCCAGAGATGAAACCTTAGATGATTGGT
TCGACAATGACTTGTCCCTGTTCCTATCTGGTTTCGGTTTCCTAGAAAGTGTGCGAGTTT
CAGTTGATATTTTTGGACCATGACAACAACACGAGTTGAAAGTCGTGGTTCCCTGGTGTCA
AAAGCAAGAAGGACATTGATATTGAGTACCATCAAAACAAGAACCAATTTTGGTTTCTG
GTGAAATTCCATCTACCTTGAATGAAGAGAGTAAAGACAAGGTCAAGGTCAAGGAGAGCA
GCTCTGGTAAGTTCAAGAGAGTCATCACTTTGCCAGACTACCCAGGTGTGGATGCAGACA
ACATTAAAGCAGACTACGCAAAATGGTGTTTTGACATTAACAGTTCCAAAATTGAAGCCTC
AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA
ACTAA

YBR072W, 214 aa (SEQ ID NO 14)

MSFNSPFFDFFDNINNEVDAFNRLLGEGGLRGYAPRRQLANTPAKDSTGKEVARPNNYAG
ALYDPRDETLDWFDNDLSLFPSPGFPRSVAVPVDILDHDNNYELKVVVPGVKSKKDID
IEYHQNKQILVSGEIPSTLNEESKDKVKVESGSKFKRVITLPDYPGVDADNIKADYA
NGVLTLTPVKLPQKDGKNHVKKIEVSSQESWGN

YBR073W, 3377 bp, CDS: 501-3377 (SEQ ID NO 15)

AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA
ACTAAAGTGACCTGGCTCTATAGTGTGTCCCTCTCGCGAGGACCATTTGTTGCTTGCATA
TGGCTTGAAACATATGTCATCACATCTGAGCGATTTTACCTCTTAGAATTAGTTTAGATA
TATATGAGTTGATGAATAAATAGTTATAAAACTTGCTTTGGCTTCGATATATGACCGTT
ATTTTTGACTAAGTTTTAACGAAGGAATCTAACCTCGTTCTTGTAATTACCAAAATCTTC
AACACGCGCTGTTGGAGGTATCTCTATGGATGTGGCTTGAAATATGGATGTCTTGCCTA
CTTCTACTTCTGGGAAAGGCATTTTTACTCGATCGCGTTAATATATGCATCAAGAAAATA
AAAAATAAAACGCGAAGAGCTAAAAAAGAAAACCTACTATAAATAACCGATTAG
AATCGAGTTTTTGTATTGAAATGGCGGTAAATAGCGTTAAACCTCGACGAAGAGAGAAGA
TCCTACAGGAGGTAAAAAACAGCTCGGTATATCAAACGGTATTTGATTCCGGTACTACTC
AAATGCAGATACCGAAATATGAGAACAAGCCATTCAAGCCTCCAAGAAGGGTTGGATCAA
ATAAGTACACACAACCTCAAACCAACCGCCACTGCAGTCACAACAGCCCCATATCTAAAG
CCAAAGTTACTGTCAACTTGAAAAGAAGCATTTTCGGCGGGACCTACTTTAAATCTTGCCA
AGAAGCCGAATAATCTGTCTCAAATGAAAACACTAGATATTTTACTATCATGTACAGGA
AGCCTACTACCAAAAAGCACAAGACTTGGAGTGGTGTATGGCTACGCTACCTTAAAGCCA
GTAGCGTAAGTTATGCTTTTATAACGAAGCAGGAAATTTCTTGGGTCAAGTATGTAC
CAAGTGATTTCAGATTCTCTCTTCGAACTCTTTTCAAAGCAGGCTCCAATGAAGTACAAT

FIG. 1 - 5

TGGATTACGAATTGAAGGAAAAATGCAGAAATACGTAGCGCCAAAGAAGCCTTATCACAAA
ACATGGGAAATCCCAGCCCACCGACCACAAGCACAACAGAAACAGTGCCTTCTACGAAGA
ATGACGGTGGCAAATACCAAATGCCTCTGTCTCAGCTGTTTCACTAAACACTGTGAAAA
GATTCAAATCAGTAACAAAGCAAAATAATGAACACATGACCACAGTACCTAAACCAGTC
AAAATTCCAAAGCCAAAAATATTATCCAGTATTTGATGTCAACAAAATCGATAATCCCTA
TAGTAATGAACAAAAATGCAGCCGCTGAAGTTGACGTAATTTGTTGATCCATTACTGGGCA
AATTCCTTGCGCCCTCATCAGAGGGAAGGGGTGAAGTTCATGTATGATTGCTTAATGGGCT
TGGCAAGACCAACTATTGAAAATCCGGATATCGATTGTACTACTAAAAGTTTAGTGTTAG
AAAATGACTCAGATATTAGTGGATGCCTTTTGGCTGATGATATGGGTTTAGGTAAAACAC
TAATGAGTATAACTTTGATTGGACATTAATTAGGCAAACTCCTTTTGCATCAAAAGTTT
CATGTTTCGCAATCAGGCATACCATTAACTGGACTTTGTAAGAAGATTTTAGTCGTTTGT
CCGTTACTTTAATAGGAAATTTGAAAAGAGAATTTGAAAATGGTTAAATTTGTCAAGAA
TAGGTGTTTTGACATTAAGCTCAAGGAATTTCTCTGATATGGATAAAATGGCTGTCAGAA
ATTTTTTAAAAGTGCAACGAACCTTATCAAGTCTTGATTATTGGCTACGAAAACTCTTGA
GTGTTTCTGAAGAATTAGAGAAAAATAAACATTTGATTGACATGCTGGTGTGTGACGAAG
GCCATCGACTAAAAACGGGGCTTCTAAAATTTTAAATACGCTGAAGAGTTTAGACATAA
GAAGGAAGCTTTTGCTTACGGGAACCTCTATACAAAATGATCTTAATGAGTTTTTCACTA
TTATAGATTTTCATAAACCCAGGAATCCTTGAAGCTTCGCTTCTTTCAAAAAGAGATTCA
TTATCCCTATAACTAGAGCCAGAGACACTGCAAAACAGATACAACGAAGAATTTGTTGGAA
AGGGGGAAGAAAGGTCAAAAGAGATGATAGAAATTACGAAAAGATTATTTTGAGACGAA
CAAAATGCGATTTTAGAAAAAGTACCTTCTTCCAAAGACGGATATAATTTTATTCTGTAAAC
CATAACGCCAACAGATATTGGCATTCAAAGATATTTTGCAGGGCGCACGTTTAGATTTTG
GACAATTGACGTTTCACTTCTCGCTAGGACTAATAACATTACTGAAAAAGGTTTGTAACT
CTCCTGGATTGGTTGGCTCAGATCCCTATTACAAATCACATATAAAGGATACCCAATCTC
AGGACAGCTATAGTCGTTCTTTGAACCTCTGGTAAGTTAAAGGTATTAATGACATTACTAG
AAGGTATTAGGAAGGGTACCAAGGAGAAGGTCTGCTAGTGTCTAACTACACTCAACAT
TGGATATAATTGAAAATTTGATGAATATGGCTGGGATGTCACATTGCAGACTCGACGGTT
CCATACCTGTCTAAACAAAGGGACTCTATCGTCACATCTTTCAATCGGAATCCAGCCATAT
TTGGATTCTTGTGAGTGCAAAATCGGGAGGTGTAGGATTGAATCTAGTCGGTCGTTTCGC
GACTTATTTTATTTGATAATGATTGGAATCCTTCAGTAGATTTGCAAGCGATGTCACGAA
TTCATAGAGATGGTCAAAAAAGCCGTGCTTCATATATAGACTTGTCACAACTGGGTGTA
TCGATGAGAAAATATTGCAAAGGCAATTAATGAAGAACAGTTTGAGCCAAAAATTTCTAG
GTGACTCGGAGATGAGAAATAAAGAATCTTCTAATGATGATCTTTTCAATAAAGAGGACT
TGAAGGACCTGTTTTCTGTCCATACAGATACCAAGAGTAACACACATGACTTAATTTGTT
CTTGCGATGGTTTAGGTGAGGAAATTGAATATCCTGAAACAAATCAACAGCAGAACACCG
TAGAGCTGAGAAAGCGTAGCACTACGACATGGACAAGTGCCTGGATTACAAAAGAAAA
TGAATGAAGCAGCCACCAACGATGATGCCAAAAAGTCACAATACATTAGGCAATGTCTCG
TTCATTATAAGCATATCGATCCAGCAAGACAAGATGAATTATTTGATGAGGTTATCACAG
ATTCGTTACCGAATTGAAAGATAGTATTACCTTTGCGTTTGTAAAGCCCGCGGAGATAT
GTCTCAGAGAACAAATGA

YBR073W, 958 aa (SEQ ID NO 16)

MAVISVKPRRREKILQEVKNSSVYQTVFDSGTTQMQUIPKYENKPFKPPRRVGSNKYTQLK
PTATAVTTAPISKAKVTVNLKRSISAGPTLNLAKKPNNLSSNENTRYFTIMYRKPTTKKH
KTWSGDGYATLKASSDKLCFYNEAGKFLGSSMLPSDSLSLFTLFKAGSNEVQLDYELKE
NAEIRSAKEALSQNMGNPSPPTTSTTETVPSTKNDGGKYQMPLSQLFSLNTVKRFKSVTK
QTNEHMTTVPKTSQNSKAKKYYPVFDVNKIDNPIVMNKNAAAEVDVIVDPLLKFLRPHQ
REGVKFMYDCLMGLARPTIENPDIDCTTKSLVLENDSDISGCLLADDMGLGKTLMSITLI
WTLIRQTPFASKVSCSQSGIPLTGLCKILVVCPTVLIGNWKREFGKWLNLNRIGVLTLS
SRNSPDMDKMAVRNFLKVQRTYQVLIIGYEKLLSVSEELEKNKHLIDMLVCDGHRKNG
ASKILNLTLSLDIRKLLLTGTPPIQNDLNEFFTIIIDFINPGILGSFASFRRFIIPITRA
RDTANRYNEELLEKEERSKEMIEITKRFILRRTNAILKYLPPKTDIILFCKPYSQQIL
AFKDILQGARLDFGQLTFSSSLGLITLLKKVCNSPGLVGSDPYKSHIKDTSQSDYSRS
LNSGKLKVLMTLLEGIRKGTKEKVVVVSNYQTLDIENLMNMAGMSHCRLDGSIAPQR
DSIVTSFNRNPAIFGFLLSAKSGVGLNLVGRSRLILFDNDWNPSVDLQAMSRIHRDGQK
KPCFIYRLVTTGCIDEKILQRLMKNSLSQKFLGDSEMRNKESNDDL FNKEDLKDLSV
HTDTKSNTHDLICSDGLGEEIEYPETNQQTVELRKRSTTTWTSALDLQKKMNEAATN
DDAKKSQYIRQCLVHYKHIDPARQDELFDDEVITDSFTELKDSITFAFVKPGEICLREQ

FIG. 1 - 6

YBR086C, 3341 bp, CDS: 501-3341 (SEQ ID NO 17)
AGATCCTAAAACAGCACGAAGCATATTATTGCGCATAAATTGTTCTTGTAGGATCTTTTC
TTGACATTTTTTTTCACTCTGCGAGAACTTCTCTTTTTTTTTCCTTCTAGGGACGAAAA
CAAACAAGGGCACTTTTTTTATCTTTTTTTTTTCTCTGTGTTTTCAAACAAGAAAGAT
TCCACCACTACATCAGTGTGAAAGACTGTAAAAGCTTTCTGATAAATAAGCACTTTCCAT
ATTTTTCAACTGAAAAATAGTTTTCTTTTTGCAGCTATTATTGACTTCATTAAGAAATAT
CCCTTTTTTCCCGTTGCAATTATTTCTATAAGGGAAGCTGGAAATAGGGGGCTGGAAAA
GATATTTGAACAGTCGCTCCAATAACCGTTCTCACCATCATTAACATTTTTGAAGGTGAA
TACTGTTTTCGGTGCGATTATGGCTAATTTGTCAAATACATTTGAAAAAGATTAAAAAAG
CACAAGCGGTTGAGCATACTATGTCGAGACAATTACATCTCTAGATCCGAATTGTGTTA
TTGTATTCAATAAACTTCGAGTGCAAAACGAGAAGAGTTTGAATGTCGAATTCAAACGTT
TGAATATACATTCTATTATCGAACCTGGCCATGATCTGCAAACAAGCTATGCGTTTATTA
GAATCCATCAGGATAATGCGAAACCGCTTTTTTCATTTTTGCAGAATCTGGACTTCATTG
AATCCATCATACCATATCATGATACTGAATTGTCCGATGATTTGCATAAACTGATTTCTA
TCAGCAAATCAAAAATACTGGAGGCTCCAAAACAGTATGAGTTGTACAACCTATCGAATT
TGACCAATAATCCCAACAATCCTTATATTTTGCATTCTTACAGAACTATATAAAATGGT
TGATTCCTTCTCCTTTTTTGGATTATCAATTAGATTTTTATCTAATTTTACGTATGAAT
TCAATTCACATACTCGCTGTTCCGCATCCTATGGACATTGTCATTTACAGCCTTTTGGC
TTTATAAATATGAACCATTTTGGTCTGATAGACTGAGTAAATACTCATCATTTTTCTACCA
TTGAGTTTCTTCAAGATAAACAGAAAGCCCAAAAAAAGCTAGTTCCGTTATCATGTTGA
AGAAATGTTGTTTTATTCCTGTGGCTTTGTTGTTTGGCGCAATATTACTATCATTCACAGC
TATATTGTTTTGCGTTGGAAATTTTCTACAAGCAAATTTATAACGGCCCAATGATTTCCA
TCTTGCTTTTTTGCCTACTATACTTATTTGCACGTTTACTCCGGTTTTAACTGTGATTT
ACAACAAATATTTCTGTAAGCAATGACAAAGTGGGAAATCATAGCAGTTGTGTAATG
CAAAGAAATCTAAGAAGCTAAGAAGCTTTGTTATTTATTTTTCTATCCAGTTACGTTCCCC
TATTAATTACACTATTTCTTTATCTGCCAATGGGGCATTTGTTGACCGCAGAAATAAGAA
CTAAGGTTTTCAATGCCTTTTCAATATTGGCCCGTTTACCTACCCATGATTCAGATTTTA
TTATTGATACAAAGCGCTATGAAGATCAATTTTTCTACTTTATTGTTATCAACCAACTGA
TTCAATTTAGCATGGAAAACTTTGTTCGAAGCCTTGTTAGCATTGCTCAGCAGAAAATTA
ATGGACCAATCCTAACTTTGTCAAAGCTGAGAGTGAAATCGGTAAAGCTCAACTCAGCT
CATCAGATATGAAAATTTGGTCAAAGGTTAAGTCTGACCAAACAGACCCCTGGGGAGCAA
CATTTGATTTGGACGCCAATTTCAAAAAGCTTCTTCTACAATTCGGGTATCTTGTATGT
TTTCTACAATTTGGCCACTAGCTCCATTTATCTGTTTGATAGTCAATTTGATTGTTTACC
AAGTCGATTTGAGGAAAGCTGTGCTTTATAGTAAACCTGAGTATTTTCCATTTCCAATCT
ACGATAAGCCATCCTCTGTGTCTAATACCCAAAACTGACGGTTGGTCTATGGAACCTG
TCTTAGTTATGTTCTCCATCTTAGGTTGTGTTATCACTGCTACTTTGACCTATATGTACC
AGAGCTGTAATATACAGGTGTGCGGCTACTACTTCCATCCATACGAATAAAGCTTGGT
ACCTAGCAAATCCAATAAACCACTCGTGGATAAATATTGTACTATATGCTGTTTTTATTG
AGCATGTTAGTGTGCTATTTTTCTTCTTTCTCTAGTATTTTGAAATCTTCCCATGATG
ACGTTGCAAATGGCATTGTGCCAAAGCATGTAGTTAACGTGCAAACCCACCAAAACAAG
AAGTCTTTGAAAAAATCCCTCCCTGAATTTAATTCGAATAACGAAAAAGAACTAGTTC
AAAGAAAAGGGTCTGCGAATGAGAAGTTGCACCAAGAACTCGGTGAGAAACAGCCTGCCT
CTTCTGCCAATGGATATGAGGCACATGCTGCCACTCATGCCAACAATGATCCGCTTCTCT
TATCCTCAGCCTCCTCGCCTTCATTATCTTCTTCTTCTTAGCAGCAAAAACCGGTGTAG
TCAAAGCTGTTGATAACGATACAGCCGATCTGCTGGTAAAAAGCCATTGGCCACAGAAA
GTACTGAAAAAAGAAATCTTTGGTGAAGGTGCCCTACCGTTGGCTCATATGGTGTGCGG
GCGCCACTTTACCAGAAACAATCCAACATCTAAAAATTACTACTTAAGGTTTGATGAGG
ACGTTAAATCCATTAGGGATGCGAAATCCAGTGCAGAACTTCCAACGCCACCAATAACA
ACACCTTAGGCACGGAAGTAAGCTTTTGCCAGATGGTGACGCCGTTGATGCACATAAGTA
GAAAAATTGATCAAATACCCAAAATTGCTGTTACTGGTGGCGAAAATAACGAAAATACCC
AGGCCAAAGACGATGCTGCCACTAAGACTCCACTCATTAAGATGCAAATATTAAGCCTG
TTGTCAACGCAGCTGTTAACGATAACCAATCGAAGGTTTCAGTGGCTACTGAACAAACAA
AAAAGACTGAAGTAAGCACGAAAAATGGCCCATCAAGATCTATTTCCACGAAGGAACTA
AGGATTTCTGCGAGACCATCTAATAACAATACTACTACTACTACTACAGATGCTACTC
AGCCCCACCATCATCATCACCACCACCGCCATCGTGATGCTGGAGTGAAGAATGTCACGA
ACAATTTAAGACAACCGAATCCTCTTCTTCTCATCGCGGCAAGGAAAAACCAAAAC
ATAAAAAGGGGCTATTGCATAAGCTGAAAAAGAAGCTTTAA

FIG. 1 - 7

YBR086C, 946 aa (SEQ ID NO 18)
MSQTITSLDPNCVIVFNKTSSANEKSLNVEFKRLNIHSIIIEPGHDLQTSYAFIRIHQDNA
KPLFSFLQNLDFIESIIPYHDELSDDLHLKLISISKSKILEAPKQYELYNLSNLTNNPKQ
SLYFAFLQNYIKWLIPFSFFGLSIRFLSNFTYEFNSTYSLFAILWTLSTAFWLYKYEPF
WSDRLSKYSSSFSTIEFLQDKQKAQKKASSVIMLKCCFIPVALLFGAILLSFQLYCFALF
IFYKQIYNGPMISILSFLPTILICTFTPVLTVIYNKYFVEPMTKWENHSSSVNNAKKSKEA
KNFVIIIFLSSYPVLLITLFLYLPNGHLLTAEIRTKVFNAFSILARLPHTSDFIIDTKRY
EDQFFYFIVINQLIQFSMENFVPSLVSIAQQKINGPNPNFVKAESEIGKAQLSSSDMKIW
SKVKSQYQTDPWGATFDLDANFKLLQLQFGYLVMFSTIWPLAPFICLIVNLIVYQVDLRKA
VLYSKPEYFPFPIYDKPSSVSNTQKLTVGLWNSVLVMSILGCVITATLTMYQSCNIPG
VGAHTSIHTNKAWYLANPINHSWINIVLYAVFIEHVSVAIFFLFSSILKSSHDDVANGIV
PKHVNVQNPPKQEVFEKIPSPFNSNNEKELVQRKGSANEKLHQELGEKQPASSANGYE
AHAATHANNDPSSLSSASSPSLSSSSSSSKTGVVKAVDNDTAGSAGKKPLATESTEKRN
LVKVPTVGSYGVAGATLPETIPTSKNYLRFDEGKSIRDAKSSAESSNATNNNTLTGES
KLLPDGDAVDALSRKIDQIPKIAVTGGENNENTQAKDDAATKTPLIKDANIKPVVNAAVN
DNQSKVSVATEQTKKTEVSTKNGPSRSISTKETKDSARPSNNNTTTTTTDTATQPHHHH
HHRHRDAGVKNVTNNSKTTESSSSSAAKEKPKHKKGLLHKLKKKL

YBR093C, 1904 bp, CDS: 501-1904 (SEQ ID NO 19)
ACGTATTTGGAAGTCATCTTATGTGCGCTGCTTTAATGTTTTCTCATGTAAGCGGACGTC
GTCTATAAACTTCAAACGAAGGTAAAAGGTTTCATAGCGCTTTTTCTTTGTCTGCACAAAG
AAATATATATTAATTAGCACGTTTTTCGCATAGAACGCAACTGCACAATGCCAAAAAAG
TAAAAGTGATTAAGAGGTTAATTGAATAGGCAATCTCTAAATGAATCGATACAACCTTG
GCACTCACACGTGGGACTAGCACAGACTAAATTTATGATTCTGGTCCCTGTTTTCGAAGA
GATCGCACATGCCAAATTATCAAAATGGTCACTTACTTGGCAAGGCATATACCCATTTG
GGATAAGGGTAAACATCTTTGAATTGTCGAAATGAAACGTATATAAGCGCTGATGTTTTG
CTAAGTCGAGGTTAGTATGGCTTCATCTCTCATGAGAAATAAGAACAACAATAATAGAG
AAGCAAATTCGAGATTACCAATGTTTAAATCTGTTGTTTATTCAATTTTAGCCGCTTCTT
TGGCCAATGCAGGTACCATTCCCTTAGGCAAACTAGCCGATGTCGACAAGATTGGTACCC
AAAAAGATATCTTCCCATTTTTGGGTGGTGCCGGACCATACTACTCTTCCCCTGGCGACT
ATGGTATTTCTCGTGATTTGCCTGAAGGTTGTGAAATGAAGCAACTGCAAATGGTTGGTA
GACATGGTGAAAGATACCCTACTGTCAGTCTGGCTAAGACTATCAAGAGTACATGGTATA
AGTTGAGCAATTACACTCGTCAATTCACGGCTCATTTGTCATTCTTGAACGATGATTACG
AGTTTTTTCATCCGTGATGACGATGATTTGGAAATGGAAACCACTTTTGCCAACCTCGGACG
ATGTTTTTGAACCCATACACTGGTGAAATGAACGCCAAGAGACATGCTCGTGACTTCTTGG
CTCAATACGGTTACATGGTGCAGAAACCAACAGTTTCGCCGTTTTTACCTCTAATTCTA
AGAGATGTCATGACACTGCTCAATATTTTATTGATGGTTTAGGTGACCAATTCAACATCA
CCTTGCAGACTGTCAGTGAAGCTGAATCCGCTGGTGCCAACACTTTTGAGTGCTTTGTAAC
CATGTCCTGCTTGGGACTACGATGCCAATGATGACATTGTAATGAATACGACACAACCT
ACTTGGATGACATTGCCAAGAGATTGAACAAGGAAACAAAGGGTTTGAACCTTGACCTCAA
CTGACGCTAGTACTTTATTCTCGTGGTGTGCATTTGAAGTGAACGCTAAAGGTTACAGTG
ATGTCTGTGATATTTTACCAAGGATGAATTAGTCCATTACTCCTACTACCAAGACTTGC
ACACTTATTACCATGAGGGTCCAGGTTACGACATTATCAAGTCTGTCCGTTCCAACTTGT
TCAATGCCTCAGTCAAATTTATTAAGCAAGTGAGATTCAAGACCAAAAGGTTTGGTTGA
GTTTTACCCACGATACCGATATCCTAAACTTTTTGACCACCGCTGGTATAATTGACGACA
AAAACAACTTAACCTGCCGAATACGTTCCATTTCATGGGCAACACTTTCCACAGATCCTGGT
ACGTTCTTCAAGGTGCTCGTGTCTACACCGAAAAATTTCAATGTTCTAACGACACCTACG
TCAGATACGTCATTAACGATGCTGTTGTTCCAATTGAAACCTGTTCCACTGGTCCAGGGT
TCTCTTGTGAAATCAATGACTTCTACGACTATGCTGAAAAGAGAGTAGCCGGTACTGACT
TCCTAAAGGTCTGTAACGTCAGCAGCGTCAGTAACTCTACTGAATTGACCTTCTACTGGG
ACTGGAACACTACTCATTACAACGCCAGTCTATTGAGACAATAG

YBR093C, 467 aa (SEQ ID NO 20)
MFKSVVYSILAASLANAGTIPLGKLADVQKIGTQKIDIFPFLGGAGPYYSFPGDYGISRDL
PEGCEMKQLQMVGRHGERYPTVSLAKTIKSTWYKLSNYTRQFNGLSFLNDDYEFFIRDD
DDLEMETTFANSDDVLNPYTGMENAKRHARDFLAQYGYMVENQTSFAVFTSNSKRCHDTA
QYFIDGLGQFNITLQTVSEAESAGANTLSACNSCPAWDYDANDDIVNEYDTTYLDDIAK
RLNKENKGLNLTSTDASTLFSWCAFEVNAKGYSVCDIFTKDELVHYSYYQDLHTYYHEG

FIG. 1 - 8

PGYDIKSVGSNLFNASVKLLKQSEIQDQKVWLSFTHDTDILNFLT TAGIIDDKNNLTAE
YVPFMGNTFHRSWYVPOGARVYTEKFQCSNDTYVRYVINDAVVPIETCSTGPGFSCEIND
FYDYAEKRVAGTDFLKVCNVSSVSNSTELTFYWDWNTTHYNASLLRQ

YBR181C, 1563 bp, exon1: 501-506, intron1: 507-858, exon2:
859-1563 (SEQ ID NO 21)

TAACCTCTCAACATAATTATGTAAAAAATTATCTCATTAAAGCCAGATAGCAAATATATCA
CATATTGCATTGATTAATTTGAGAAAAATATACATGTATCTTTTCAGTTAATTTTATTAA
AAATAAATTATTTCTTACTTTTTTTTCTACAGTTTGCACCATTAACCTCTTTTCTTGCA
TCCATACATCTTTGAACTCCATACATCTTATTTTTTTGCTGTTTTTTTCAGTGTCTCGG
GCATACAGGCCGCTTATCTTTCATGCCGCCATCATCCTAGGAAACTCTTTTCGGTATGGG
CCAAGGGCAGGCGAAAATCCTATGTGCGTGGAGCTGATACAATCTCGGCTGGCTTGGTTT
GTAGGGCACGGTCAATGAATGCCTGATGGGAGAAAAATTCATCTTTATGAAAAGTGATCT
TAATTTGAATAGTGTGCCCTTCAAAACATTTGGAAGTCATTAATTGAAACTATCCAGTGT
GAATAGACGACTGAGCCATCATGAAGGTATGTAATATCACCCAAATCCTTAGAATTCTAA
TGAATCAGCACGCGCTAACCGGCTGTTTCTGACTGTTTGATAAACGTATACCCACAAATT
AGTGCATATAATAAAAAATTCTCAAGAACACGTTGTTTAAACGAGATAATTCCTCTCTAA
TATACACGTACCGACACTTAGGAAAAATATCTCGCTAAGTTCAAATTAAGGAATGAAAAAG
GAATTTACGAAAAGGGTTTAGAAATATCAATGAAAAATAAGAAAAACCTGTAACGGAAGAA
AGGACAGCAGGGATTGTTGGAATTTGTCGATATTGGCTTCGGACAACCTTTACTAACAAA
TGGTATTATTTATAACAGTTGAACATTTCTTACCCAGTCAACGGGTCTCAAAGACCTTC
GAAATTGATGATGAACACCGTATTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAGTC
GATGGTGAAGCCGTTGGTGATGAATTCAGGGCTACGTCTTCAAGATCTCTGGTGGTAAC
GACAAACAAGGTTTCCCAATGAAGCAAGGTGTTTTGTTGCCAAGTGAATAGAACTGTTG
TTGACCAAGAACGTTTCTTGTACAGACCAAGACGTGATGGTGAAAGAGAGAAAGTCC
GTCAGAGGTGCCATTGTTGGTCCAGATTTGGCTGTCTTGGCTTTGGTCATTGTCAAGAAG
GGTGAACAAGAATTGGAAGGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAG
AGAGCTAAACAACATCAGAAAGTTCTTCGGTTTTGTCCAAGGAAGATGACGTTTCGTGATTTT
GTCATCAGAAAGAGAAGTCACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAA
AGATTGGTTACTCCTCAAAGATTGCAAAGAAAGAGACACCAAAGAGCTTTGAAGGTGAGA
AACGCTCAAGCTCAAAGAGAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTG
TCTGAAAGAAAAGGCTGAAAAGGCCGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCT
TAA

YBR181C, 236 aa (SEQ ID NO 22)

MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEVDGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAI VGPDLAVLALVIVKKGEQE
LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKEKTYTKAPKIQRLVT
PQRLQRKRHQALKVRNAQAQREAAEYAQLLAKRLSERKAKEAEIRKRRASSLKA

YCL007C, 893 bp, CDS: 501-893 (SEQ ID NO 23)

ATTACTTTAAATTTGTTTGTCTATTCCAACATAATCATTAGCAGCACATGTCGAGCAACAG
ATAAACACAGCAGCGGCACGGTGAACCACATAAGTGTATGTGCACACGCGTGTGTTTGTGC
AGTGTATTACCAACTTGCGCATGCAAGGATATCACACTCCTGTTTCTGCCCTCATGTCTTT
TAAACGCTTCCACGGGACATGGGTTCTAATTATGGAGAAGATCAAGCTTTGAAATGGCC
CGTTTACACATTTTGATACAACCGTAGACGGCGTCTCGTTTCAAAGACCGTGTGGTTGTC
TATCAGTATATACTCATTTGTGTTTTTCAAAAAATCTCTGGGTTGTTTAGATGCCACTATA
TTTCTATTTCGTATTTATTTTTATGTATACTTATTTTGCTTATTTTTCTTATACTCAGGAA
ACGTCACTTGGCTTGATATACTCGACGCTTATTTCTGCAAATTCAGGTCTCAAATCTGAA
CGGCGTGGAGCCACCAAGGGATGGAGCTGGCAAAGGAACGTAATGGCCACATCAAAAAC
ATCATGGCCAATGTCAAATCACTGTACTTCTCCAAACACTGTACGACAAAACAAAACAA
ACAAACTCTTGTTAGTAAAAAAGAAAGGGAACTAGTAATATGGAGACACATCGTAAAAA
AAATGTTGCACATACGCTTGGTTGTTCTTTGGAGCCATTATCCAGAACAGCACGGACATG
GACTAACCCTATGAATACACCAACAACAGTATAGCTAAATTGGACGCGCAGAGAGTTA
GTAGAAGAAGAAGGAAGAAAAGGGAAGCGGAGAGAAGAGATTATGACACATACAAACTAC
TCATTACTCTTTGTTCTTTATTATTTCGTTGGACCTTTGTTTCTTAAAGTATAG

FIG. 1 - 9

YCL007C, 130 aa (SEQ ID NO 24)
MELAKERNGPHQKHGQCQNHCTSPNTVRQNTKNLLLVKKKGKLVWRHIVKKMLHRL
VVLWSHYPEQHGHTNHYEYTNNSIAKLDAQRVSRRRRKREAERRDYDTYKLLITLCSL
LFVGPLFLKV

YCL016C, 1430 bp, CDS: 501-1430 (SEQ ID NO 25)
ACATGACCTAATTTATAGCTTAGGGTTCTTTTTGTCAATTCTATGCGTATGACAAAGA
GCACCACGATGGTGATCGAAATCTCTAGGAGTAGCATACCACAGCGATATTATTTAGTAG
TAGGCGGTTTATTATCTTTGTCCCTTTATACTGTTGTGTTTCTTGCTTATTGCTTCAGTA
GGCAGCGTATAGTATAACCAGAAAAAGTGAAAAATAAACTAAAAAAGCACTATGAGATG
AACGGTAAAAATCCACCAGAGATTTGCTCACTAATAATCCTGTACCATGTCCATCAACCT
ACATTCCGCACCCGAGTATGATCCATCTTATAAGCTGATCCAGTTGACACCAGAGTTACT
GGATATAATACAGGATCCGGTTCAAATCACCAGTTAAGGTTAAGTCATTGGACAAAAGA
CAAGTCTGAAGTTGTACTGTGTTTCGCACGACAAGACTTGGGTGCTGCAAGCAGCGCAAAC
ATTCAAACACAGTTCTACTAATGAGAGAATTTGTTCTGAACAACCTATTACTTTTCGACG
AAACGCTCTTGTGTTGGACTGTCCAAGCCGTACATGGACGTCGTGGGATTCGCCAAGACTG
AATCAGAATTTGAGACCAGAGAGACACATGGCGAATTGAAGTTGAATTCAGTACCAATAT
ACAACGGAGAACTGGATTTCTCCGACAAAATCATGAAGAGGTCATCTACAAAGGTTATCG
GGACCCTGGAAGAACTACTTGAGAACTCACCATGTTCTGCGCTAGAAGGTATATCAAAAT
GGCATAAGATTGGTGGATCTGTGAAAGACGGTGTGTTGTGTATTCTTTCACAAGACTTCC
TTTTCAAAGCACTGCATGTACTACTGTAGAGCGCAATGGCAGAATCACTCGATCTACAGC
ATCTGAATGTTGAGGATACACATCAGCTGTGGGAAGGACATTGAGGACGAGTTCAATC
CATAACAAGAGAAATCATTGAAACAGTGCTGAATAAAATTTGCTGTTCAAGAGCAAGAGG
CTGAAAACAATACGTGGCGCTTGAGAATACCGTTTATAGCTCAGTGGTACGGGATTCAAG
CGCTAAGGAAATATGTTTCTGGAATAAGCATGCCAATTGATGAGTTCCTCATCAAGTGA
AGTCCCTTTTCCCACCTTTCTTCCCATGTGACATTGACATTGACATGCTGCGAGGCTATC
ATTTCAAGCCTACCGATAAGACTGTCCAGTATATAGCGAAAAGCACACTACCAATGGACC
CCAAAGAACGGTTTAAAGTCCTGTTTAGGCTACAGTCACAGTGGGACTTGGAGGATATCA
AGCCTCTAATTGAAGAACTAAATTCAGAGGTATGAAAATAGACAGTTTCATCATGAAGT
ATGCCCGCCGTAAAAGACTGGGCAAAAAGACCGTGGTCACGAGCAGGTAG

YCL016C, 309 aa (SEQ ID NO 26)
MREFVPEQPITFDETLFLGLSKPYMDVVGFAKTESEFETRETHGELNLSVPIYNGELDF
SDKIMKRSSTKVIGTLEELLENSPCSALEGISKWHKIGGSVKDGVLCILSQDFLFKALHV
LLMSAMAESLDLQHLNVEDTHHAVGKDIEDEFNPYTREIETVLNKFVQEQEAENNTWR
LRIPFIAQWYGIQALRKYVSGISMPIDEFLIKWKS LFPFPFPCDIDIDMLRGVHFKPTDK
TVQYIAKSTLPMDPKERFKVLFRLQSQWLEDIKPLIEELNSRGMKIDSFIMKYARRKRL
GKKTVVTSR

YCR052W, 1952 bp, CDS: 501-1952 (SEQ ID NO 27)
GTCATCGACAGCAAATTGCTGGAAGAGTTCAAGGACAACGTGAGATACACCTTGGAATAAT
GACCCGTAGGAAGGAGCCGATGAGGCCACTCTGCAACGCAGGAGGCAGTTGGAACAGATC
ATTACGGGAGACAACGCTGAGGAGGAGTTGGAAGGTACATCCGTGCTATGGTCAGAGAG
CAGATGCTGGGCCAGGGCTCCATGGCGGGTTCCGGGGACGAACCAGATTCCAAGAGAAGA
AAATAACGACCCAGCACAAAGGCTCTTACAGCTTGCTAAAAGAAATTGAACGCGACGCTA
CATGAAGTACTTCTTCTCTTACATAGTCTTTTCCCTTATGTATCTTTTCTGTACATTAA
TAGACGTTCTTACAAGGTAATAATTTACCGCGTTTTTAAATAGAAATGAAAAAACGTTGT
AGAGTGAAAGAAAAGCAACAAATATACAGTTTACAAGGCAGCTTCGTATAGTAATACAGC
ACGAAAAACAGCTCATAGAAATGGTAACACAGACCAATCCGGTCCCTGTTACATATCCAA
CGGATGCTTATATCCCCACGTATCTGCCCGATGATAAGGTCTCCAATCTGGCAGATTTGA
AAAAATTGATAGAAATGGATTCCAGACTAGATTTGTATCTGACAAGAAGGAGGCTGGATA
CGTCCATCAATTTACCTACAAACACCAAGACCAAGGACCATCCCCCAATAAAGAGATGC
TGAGGATTTACGTCTACAACACTACGGAAAGCAGCCCTCGCAGCGATTCTGGCACCCAG
CGGACTCAGGCAAGACTACATGGACACTGAGAATAGAAGGTAAGCTTCTGCACGAGTCCG
CAAACCGGAAAGCACCATTAGTGAGTTTTTGGAAAGGTGTGCGGTCGACTTTAAAGAC
TGAAACCGCTGGGCATGGGCAAGAAGAGGAAACGCGATTTCGTATTGAGCCTTCCTTTGA
ATCTGCAACAACCCGAATACAATGATCAAGATAGCACCATGGGCGATAACGACAACGGCG
AGGATGAGGACAGTGCAGAGGCAGAATCCAGGGAGGAAATTGTAGACGCACTGGAATGGA

FIG. 1 - 10

ACTACGATGAAAACAACGTTGTGGAGTTTGATGGTATCGACATCAAGAGGCAAGGCAAGG
ATAATTTGCGATGCAGTATAACCATCCAGTTGAGGGGTGTCGACGGTGGAAGTACAGT
ACTCGCCCAACTTAGCTACCTTGATAGGTATGCAAACGGGCTCCGTTAATGACGCGGTTT
ATTCGATCTACAAGTACATTTTGATCAACAATCTGTTTGTACGGAACAAACAGAGGCTC
AAGATGGTTCCAACGATGCCGAAGACAGCAGTAACGAGAATAACAATAAAACGGTGCTG
GTGACGATGATGGCGTCGAGGGAAGTACTCCAAGGATAAGCCCGAATTGGGTGAAGTGA
AGCTAGATTCACTCTTACAAAAGGTATTGGATACAAACGCCGCGCACCTCCCCCTTGATGA
ATGTTGTGCAAACCGTGAACAAACTGGTATCACCCCTACCGCCCATCATCCTAGATTATA
CAATTGATCTTTCCAAGATACCACCTATGGTGCTACCACCTTGGATGTAGATGTGTGCGC
ACATTCCTCCACCAGCCTCAACCCAGCCAAATTTACAAAAGAGGAAGAAACAGATGCTG
AAGACACAGCAAACTACGTGAAATCACAAAGCTTGCTTGCAGTTGAACTCTAGTGCTC
AAAAATACCAGTTTTTCCACGAACTGTCTTTCATCCAAGAGAAACGCTGACTCACTACT
TATGGTCTTCCAAGCAAAACGAGCTTGTGCTGCAGGGCGACCAATACTTCAATGAAGATG
CTGCAAGAACGAGTGACATATACAGTAACAACAATGACAGGTCACCTAATGGGCAATA
TCTCACTACTGTACTCCAAGGAAGACTATAA

YCR052W, 483 aa (SEQ ID NO 28)

MVTQTNPVVPTYPTDAYIPTYL PDDKVS NLADLKKLIEMDSRLDLYLTRRLDTSINLPT
NTKTKDHPNKEMLRIYVYNTTESSPRSDSGTPADSGKTTWTLRIEGLLHESANGKHPF
SEFLEGVAVDFKRLKPLGMGKKRKRDSLSLPLNLQPEYNDQDSTMGDNDNGEDED SAE
AESREEIVDALEWNYDENNVVEFDGIDIKRQGKDNLRCSITIQLRGVDGQVQYSPNLAT
LIGMQTGSVNDVYSIYKYLINNLVTEQTEAQDGSNDAEDSSNENNNKNGAGDDDGVE
GSTPKDKPELGEVKLDSLLQKVLDTNAHLPLMNVVQTVNKLVSPLPPIILDYITIDLSKD
TTYGATTLVDVSHILHQPPQPNLQKEEETDAEDTAKLREITKLALQLNSSAQKYQFFH
ELSLHPRETLTHYLWSSKQNELVLQGDQYFNEDAARTSDIYSNNMNDRLMGNISLLYSQ
GRL

YCR064C, 911 bp, CDS: 501-911 (SEQ ID NO 29)

AGGTTTTTAACGCGTTATCTTTGTTCGAAAAAAGGAAAAATATATTTTTTC
GCGTCGCGTTCTCGCGTCTGTTTTGTTTTTCGCGTTCCAATGACCAAAATGGGAAAGTG
GTCGTCFTTGACGAAGGAGACGAAAACCTCTTCTAAAACGTTGGGAGAGAGATAATTACA
TGGCCAGAACAACTACTGCAACGTGCATATAGTCGTTAGTCTGTGCTTGCACATCCACGGC
AGCCGCACTGGACGCACTGATGGAAGGACACCTGTGTGCCCTTTTTCGCTGCTTCTTCTC
CTAACTGTGCACGAGGCACCTGCAGATGCAAGTGCTACCGTTGTTAGTTTCGTTCTTTT
GAATGCAGCGCAGACAGCACAGTTTTTCATACCCGGTTTTTTCGCCATTTGGCAATTAGCA
ATTTATCAGCATACTTTTCTTTATCAACCAATCGTAAAGGTCTTTGGAGATGGCCTTTC
TCTTGTAGTACAGAGTATATATGTATCTAGAGCGCTGGTGGTGGAGTTGCATTATCTCCC
AGAGCTGCTCATTGGACTTTGCTGCGAGCTTAGACGACTTGTCTTTTGGGCATCTCTGA
GTTGGATTTCGAAATCTGTGAGGGTTGGCTTGATTTTTTCGAACCCGTCAGGTGCAGGCT
TGGATCTTCTGGTCTTTATGCGCGGCATGTCGTTTTGTGAGGTGAGCTTTGCTAGTCTTG
ACGGCTGTAGAGGTGTTTACATTGATGATGAGTCCCTAAGAAAATTTTTCTTTTTTTTC
AGTATTTTCACTTTCCGTTGTGAACGACAAATGTACTATGCGTTCAAGAGCCAACGCAGTA
TCATCGTCAAAGTTCCTACCACAACGCGTGTGATTGATCTTGTACTGGTTGTAAATGTGC
TAAGTCTGTGA

YCR064C, 136 aa (SEQ ID NO 30)

MYLERWWWSCIISQSCSLDFAASLDDLFWASLSWISKSVRVGLIFSNPSGAGLDLLVFM
RGMSPCEVSFASLDGCRGVYIDDESLRKFFFFFYFTFR CERQMYAFKSQRSIIIVKVPT
TTRVIDLVLVNVLSL

YCR073W-A, 1448 bp, CDS: 501-1448 (SEQ ID NO 31)

GTTTATGGCTGGAATGACTTGATAATCTCTTCACGAGCTTACTTGAGATGGTATGAGGAG
CCAGAACTCTCCCGCCTTCAGCCGCTTTTGTGTGCTGTGATTTCAGTATATCCATCATCA
TTTTTCACCTACAAGGAACCTTTTATAGCCACCCTAAGTAAAACAACATTAGCTTAGC
ATCCTCAATTCTTATCGTATGTTGTTGCTGCTATTTTTATCCTATTGTTCCCTGGCATCGC
TTTTTTACATAAGGTACCAAGGCAAGAGAAAAGACCCGCGAAATTTTCAATTCGAGACAT
AGGGTTAATACGAAATATGTTAAGGTCTAGTTTCCAAAAATGAAGAAAATGTGATTAGA
CATCCTGGGGAAATTAGGTTTAAATAGGGCGGGCGCTACAGGGGTTTTCTTAACAAATTT

FIG. 1 - 11

CAATGATAATAGTGGCATCATCATCGTCATATCCAGTGTAGGTATGGACTAGAACAGAAA
GCAATTTGCAGCAAGACAATATGACTACGACGGTACCCAAGATATTCGCGTTTCACGAGT
TTTCAGACGTGGCAGAGGCCGTAGCTGACCATGTAGTCCACGCGCAAGACGGTGCATTGG
CTCCAAAGAACGAGAGGAAACACTCTGTTCCCAACATCAGCATGAATGCACCTGGATATGA
CGAGAGAGGCCTCTTGGCAAAGCACAGCATCTGCCGCGGAAGGAAAAGTGGTAGCAGTG
GTAGTGGCAGTGGTAGCAGTAAGCCCCAAAAGGAGAAAACGGTTCAAGATTGCTCTCTCCG
GTGGGTCAATTGATCGAAGTGCTACACGAAGGTCTGCTAAAACGAGACGATGTACGGTGGG
GAGACTGGGACATTTACTTTGCAGACGAGAGACTTGTACCCTTCAGCTCGAATGAAAGCA
ATTATGGATGCGCCAAAAGGAAGATTTTGGACCTGATAGACACGGCGAAGTATGGAAGTC
CGAAGGTGTACCACATTGACGAGTCATTGATTGACGACCCGCAAGAATGCGTTGATAACT
ATGAAAAGGTGCTAATCCGCGGGTTTGGCCGGTAGAGATTCCGTCAAACCTCCGATGTTCC
ACTTGTTCCTTGGTTGTGCCCCGATGGTGCATATCGCATCACTCTTCCCTAATCTCC
AGGACAATCTACGTGAGAACTTGCATGGGTGGTGGCCGTGGAGAACGCTCCTAGTGGGC
CCTCGACCAGAATTTGCTGACTATACCTGTAATCTGCCATTCTCACAGGGTTACTTTTCG
TTGTGCAAGGTGCAACCAAGGCGCCCATCATCAAGACCATTATGGAAGGCCTGAAAAGG
GCCTACCTAGCAGTATTGTCAACGAAGGTGCTGCTGGTTCGTGTATCATGGTTTGTGACG
ACGATGCTCTTACGGACGTCCTCGTCACCAAAAAAAGTATAAATTCACCAAGGTTTGT
CTATTTAA

YCR073W-A, 315 aa (SEQ ID NO 32)

MTTTPVKIFAFHEFSDVAEAVADHVHVAQDGLAPKNERKHSVPNISMNALDMTREASCK
STASAAEGKSGSSGSGSGSSKPKKEKRFKIALSGGSLIEVLHEGLLKRDDVVRWDWDIYF
ADERLVFPFSSNESNYGCAKRKILDLIDTAKYGTPKVYHIDESLIDDPQECVDNYEKLIR
GFAGRDSVKLPMFDLFLGCAPDGHIALSPNFQDNLREKLAWVVPVENAPSGPSTRISL
TIPVICHSHRVTFVVEGATKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWSFVDDALTDV
LVTKKKYKFHQGLSI

YDL010W, 1196 bp, CDS: 501-1196 (SEQ ID NO 33)

TAGTAATTAGTTTCTTATGATGGATTTAATGGCGTAGTTCATCCGCGTTTAATTTAACTA
GAGGATAATCTACTTGCAGCATGAATGAAAATAGTAAGCCAGTAAGGATGCACTGACAGA
CTCAGCTACCGATTAGTGTGTTGACTTTTCCGCAAGATCCTTTTCTCCCTCTTTGGACC
TAGTCAATCCCTCCACACAAGATTTCGCTCTTAAGTAGTGGCGCAGGCTGTTTCGCTTTTAAG
CATAGTGCTTAATGTGCAAGGCTTTATAGATCCCAAATACTACGCCTTGAGAAAATTGAAT
GCACTAGCAGTTAGTTAACTTTCTGGAACGCGCATGACGCGTCCCGGGGCGCCTGAGGCG
GAGCGTTCGCGAAATCGGGAAAACATTATACTGGGAAAGATCACTATCTATTCTCTAAAT
GAACTTTTAAGCAAATTATCGTAAGATAGAAAAGACGAAACCTTAGCAACCTAGCGGTTT
AATATAGAAACAATTTTATTATGATACCTTCCAATAAGAGAAAATGCTAGAATTTTAAGCA
TTACAACGCTATTATTGTTGTTAGTGTTTTTCTGAGCGCAAAATGCGCAACTTCTTGACGG
TAGAGATAAAAAGAGGAAACTTCTAAAGCATTTAGTACTAATATGGACAATTGCGCTGGAG
GATCTTCCAGGGAATATGCTGCTATGCCGACTTCTACCACGAATAAGGGGAGCTCTGAAG
TAGACGAAGAAATTAATGAAATAAAACAGAAGGTGGGACTCCAACAGCCCATAGCATCGG
TTGATGATAGTTTGTGCGCCATTAAAAACGATAAAGGGTTCGCGAATAACCAAAGCTTTTA
ATGTTCAAAAAGAATACTCCCTCATACTAGACTTGTCTCCGATTATAATATTTAGTAAAA
GCACCTGTTTATATAGCAAGGGCATGAAGGAAGTCTTGAAAATGAGTATCAGTTTATCC
CAAACCTACTATATTATAGAAGTTGACAAACATGGACATGGGGAAGAGCTGCAAGAATATA
TCAAGTTGGTGACCGGTAGAGGAACTGTTCCAAACCTTTTGGTTAATGGAGTATCAAGAG
GAGGTAATGAAGAAATCAAGAACTGCACACTCAAGGGAACTTTTAGAATCATTACAAG
TCTGGAGTGATGGTAAATTCTCGGTTGAGCAACGTGAAAACCTTCCAATAATTGA

YDL010W, 231 aa (SEQ ID NO 34)

MIPSNKRNARILSITLLLLLVFFVAQNANFLTVEIKEETSKAFSTNMDNMAGGSSREYA
AMPTSTTNKGSSEVDEEINEIKQKVGLOQPIASVDDSLSAIKNDKGSRITKAFNVQKEYS
LILDLSPIIIFSKSTCSYSKGMKELLENEYQFIPNYIIELDKHGHGEELQEYIKLVTR
GTVPNLLVNGVSRGGNEEIKKLHTQGKLLLESLOVWSDGKFSVEQREKPSNN

YDL036C, 1889 bp, CDS: 501-1889 (SEQ ID NO 35)

TCAAATCCAGCTTCTTTTCAAGCAATATTGTCACAAACGATGATGAGAATAGCATTGAAG
AGGATAAGAATTTACGCTATTACAGATGCTAGTGCATCTGAAAATTATCTGGTCAAGCCCA

FIG. 1 - 12

CAATACCAGGTACGACTCCTGATCCAATAATTGAGGCGCAGAACGATAATGATAGTAGTG
 ATAGTAGCGGCATAGATTTGATAGCCTTCTTAAGAAATGGACCATTATATAAGTTTTTGTA
 TCGCGATGTTTTGAAAATGGAAAGTAAGGAACGTAATACAAATTGACAAGTAGCCGACATG
 AATGACGCTCACTTCTCTTATATATGTTAGGTAGTATATGCATTATAGAATTTATTCATT
 GAAGCAATGTGATTCCTCGATAAGTAAGCTTTTTTCTGTCTGGCGCGAACCATTAGAG
 AACAAAAGACCGAGTTAAGAAAAAGTTCATAAAAAACTTTTGAAAATGGATGAGTGCTCG
 TATAATGGAATAGGAACTTATGCAAAGAAATAATAGGTAAAGAAATTTGTTTACAGTGC
 CAGTAATAATGGCTCGACAACCTCAAAAGGAATGCATTATCTGCAGGTCCTTGCTTTTGCAG
 GTAATGCAACCTCAAATGAGTTTGATGAACATTTGCAAAATGAGGTTGAAAGAGAGAGGG
 AAATTCAAAAGAAAAAAAATAAAGCGAACTCAATCAAAAAATCGCCAGATTTGATTA
 ATAAATCTACTTTTCAATCACGAACGATAGGCAGCAAAAAAGAGAAACATAGACAACCTAG
 ATCCAGAGTATGAAATTGTCATCGATGGCCCTCTAAGGAAAATCAAGCCCTACCATTTTTA
 CGTACAGGACCTTTTGCAAGAGCGTTGGAGAGATAAAAAATGGTTGATGTCTTTATAT
 CTGAATTTTCGAGATCGTGAATCTGAATATTATAAAGAACAATCGAAAACGGGGACGTTT
 ATATAACGATGAACTGCGGACTTATCTACTGTAATTCGCAATGGTGACCTGATTACGC
 ATCAGGTACATAGACATGAACCTCCAGTCACTTCCAGGCCTATCAAAGTTATTTTTGAAG
 ATGATAACATAATGGTTATTGATAAACCGAGCGGTATACCTGTTCACCCAACTGGCCGAT
 ATCGGTTCAATACAATTACGAAAATGCTTCAAAATAATCTCGGATTTGTTGTGAACCCAT
 GTAATAGGTTAGATAGGCTTACAAGTGGATTAAATGTTTTTGGCAAAAACCTCGAAGGGAG
 CCGATAATATCGGCGATCAACTAAAAGCTCGAGAAGTCACTAAGGAATACGTGGCCAAAGG
 TAGTTGGAGAATTTCCAGAAACGGAAGTAATTTGTTGAAAAACCTCTAAAACCTGATCGAGC
 CAAGGCTTGCTCTTAATGCAGTTTGTCAAATGGACGAGAAAGGAGCCAAACATGCAAAAA
 CTGTTTTTAAACAGAATCAGCTACGACGGTAAAACGAGTATTGTAAAGTGCAACCGCTTA
 CCGGGCGATCACATCAAATTAGAGTACATTTACAGTACTTAGGCCACCCAATTGCTAACG
 ATCTTATTTATTCCAATGATGAAGTATGGGGTAACAATCTCGGAAAAGGCGGCCAGGCTG
 ACTTCGATATAGTTATTACTAAGCTAGACGAAATAGGGAAAAGAAAACCTGCTAAAAGTT
 GGTTCATAGTAATGGCGGGTACGGTGAGGTATTAAGGCAAGAAAAATGTTCTATTTGTG
 AATCTGATTTGTATACTGATCCTGGCCCCAATGATCTTGATCTGTGGTTACATGCCTATC
 TATACGAATCAACTGAGACTGAAGAAGGAACCGAAAAGAAAAAGTGGTGCTACAAAACAG
 AGTATCCAGAATGGGCTCTGAGAAGATAG

YDL036C, 462 aa (SEQ ID NO 36)

MQRNRLRLNFTVPVIMARQLKRNALSAGLAFAGNATSNEFDEHLQNEVEREREIQKKK
 IKRTQSKKSPDLINKSTFQSRITIGSKKEKHRQLDPEYEIVIDGFLRKIKPYHFTYRTFCK
 ERWRDKKLVDVFISEFRDRESEYYKRTIENGDVHINDETADLSTVIRNGDLITHQVHRHE
 PPVTSRPKIVIFEDDNIMVIDKPSGIPVHPTGRYRFNTITKMLQNNLGFVVPNCNRLDRL
 TSGLMFLAKTPKGADNIGDQLKAREVTKEYVAKVVEFPETEVIVEKPLKLIERLALNA
 VCQMDEKGAHKAKTVFNRIISYDGKTSIVKCKPLTGRSHQIRVHLQYLGHPIANDPIYSND
 EVWGNLKGKGQADFIDIVITKLDEIGKRKPAKSWFHSNGGYGEVLRQEKCSICESDLYTD
 PGPNDLDLWLHAYLYESTETEEGTEKKKWCYKTEYPEWALRR

YDL083C, 1364 bp, exon1: 501-909, intron1: 910-1341, exon2:
 1342-1364 (SEQ ID NO 37)

TATTCCGACTAGAAAAAATTAAATTTTCTAACTACAAAAAATTGCCTGCATATATGTAA
 GGATGTAACAGGAAATGTATGGGTCACATATTAATAGCTTGTTTTACTCCATAAAAGAGT
 CTGATATTCAGAAAAACACCCATACATGTTGAAAAATAATGCATTGTGAAAAAAGTGG
 TTGAAAAATGTATGCGATCTAGGAAAAACTGAATTTTCTTAGGTTGTGCGCTCCTCCTCT
 AGAAGGATGCTGTGGCCTTTGACCTGGGCGGAAATTTCTCTCTGTTTCCCTCTAGCTGAGG
 GAAACAGAACCTGGTAGCAGTTCTGTTCCGGCCAGGCCGCGTGAGCCTATACCACCGAATAT
 TATCCTAGCGCAGAGAGTAACACTGGCAAAGTCAAAAGTAAATGCCATGTAAAATGTATA
 GGTTACGCAGTAGACTATTTAATATATACCTTTTTATTAGCAGTGTTTCGAAAAATACA
 GCAAGAGAATAAGCAACAAGATGTCTGCCGTCCCAAGTGTCCAAGTATGTTAAATAATTT
 AAACGATGTCACGAATTTGTGAGGGATATTGAAACCATGCAGTGAGATAATTTCAATTTA
 AGAACCATATCACCTGAATAAGACGGGTGGGGCAAGCACTAGATGCGAATCATAGTTTAA
 GAACAACGGATCACCATTTACACGTTAAAGACCGAGTAGAAATAACCAATAAATTTGTGT
 GGGAAAATATTATACTTAATTTCTCTGTGGAGTAAAGTAATGAGCGTCTTTTGGCGTCTT
 ATTTATTCATTCGCTCCCTTGCAATGAATTTTGAACAGAATGCTCCAAAGAGGAAGTGC
 CAGGGTACCTCACTTGTTTACCCCTTTTACACAGTTCATAATATTTTGGAGATTTTGAA

FIG. 1 - 13

TTTCTGTTTTACTAACATGTGACACGAAATGTTTTTCATTTTTGGTTTTATAACAGACTT
TTGGTAAGAAGAAATCAGCTACCGCTGTTGCCCACGTCAAGGCCGGTAAGGGTTTGATTA
AGGTCAACGGTTCTCCAATCACTTTGGTTGAACCAAGAAATCCTAAGATTCAAGGTCTACG
AACCATTATTGTTGGTTGGTTTGGACAAGTTTCTCCAACATCGATATCAGAGTTAGAGTCA
CTGGTGGTGGTCATGTTTCTCAAGTCTACGCCATCAGACAAGCTATTGCTAAGGGTTTAG
TCGCTTACCACCAAAAGTACGTTGACGAACAATCCAAGAACGAATTGAAGAAGGCCTTCA
CCTCTTACGACAGAACTTTGTTGATCGCTGATTCTAGAAGACCAGAACCAAGAAATTCG
GTGGTAAGGGTGCTCGTTCTAGATTCCAAAATCTTACCGTTAA

YDL083C, 143 aa (SEQ ID NO 38)

MSAVPSVQTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKQVYEPDLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIKGLVAYHQKYVDEQSKNELKKAFTSYDRTLIIAD
SRRPEPKKFGGKGARSRFQKSYR

YDL125C, 1088 bp, exon1: 501-597, intron1: 598-708, exon2:
709-1088 (SEQ ID NO 39)

TTCAAAATACGAGTAAAGGAGATCCTAGGTGTGGATTAGTAAGGGGAGTGTGGCAACTTC
CTTTTTCCGGTTAATTCTCCGCGCTTTCGTTAGACTATTTTGCAAGGACCCAAATAGGAG
ACGCTAGGAGGCTTCTACAAAACAGCGTGCCGTTTGTATGGCATGAGCAGGGGGCGCAAA
GGAAACACCGGTAAATCGCGCAAGACCTTGTGGCCACGTAGCCTCAAAGGTTGAATTGA
CACTTGTCTACAGAACTTGAAAAGTACAAAAGGAGGTCACATAAAACAGTAAGCTTGAGA
AGCTTTAAGATATGGTGCGAATCGTTACAGAATATTCCTTGCAGAAATAATGGCGGGTCC
GTTCTCTTCTGAAGAAGTTACCGCCCTACTGAAGCATTGCTGTACGATCGTGTAAATGTGA
TGTGTGTTTCGACTGGAAAGCGGAGAACATTATGAAGTAAAGGACAATCAGCACGCTTC
CAGACTTTTAAGAAACATTGATGGAGCCATTGATATCGGCACCGTACCTAACAACAACAA
AAATGTCTGCTCCTGCTACGCTTGATGCTGCCTGTATTTTTTGCAAGATTATTAAGTA
TGTCACATTACTAATAAAGAGCTTACACTCACACCAATGATGGCGATAGTCTCTATGTAG
TACATATACATAAAGCAGAATACTAACAATCGATCCGCTATGCAACAGGCGAAATTCCAT
CCTTCAAATTGATTGAAACAAAGTACTCGTATGCTTTCTTGGACATCCAACCTACTGCTG
AAGGTCATGCTTTAATCATTCCCTAAGTACCATGGTGCGAAGTTGCATGACATCCCGGACG
AATTCCTTACCGATGCTATGCCGATTGCCAAGAGACTGGCCAAGGCAATGAAGTTGGACA
CTTATAATGTGTTGCAGAATAATGGTAAAATTGCGCATCAAGAAGTCGACCACGTCCACT
TCCATTTGATTCCCTAAGAGAGATGAGAAAAGTGGTTTGATTGTAGGGTGGCCAGCCCAAG
AAACGGACTTCGATAAGTTGGGCAAGCTACACAAGGAATTGCTTGCCAACTAGAAAGCT
CCGATTAG

YDL125C, 158 aa (SEQ ID NO 40)

MEPLISAPYLTTTKMSAPATLDAACIFCKIIKSEIPSFKLIETKYSYAFLDIQPTAEGHA
LIIPKYHGAKLHDI PDEFLT DAMPIAKRLAKAMKLD TYNVLQNNKIAHQEVDHVHFHLI
PKRDEKSGLIVGWPAQETDFDKLGLHKELLAKLEGSD

YDL133C-A, 578 bp, CDS: 501-578 (SEQ ID NO 41)

AAAGGTGGTTGGAGACTTTGTGTTGTAGCTTAGAATTTCTTCCACTATATGAAAGCCAAG
ACCTCTTCTCCTCTTTCGACACTTCGTTTATTTCCACTTTCCTTATTTAGTATTCATCG
TTCAGAATGCTTTCTTTATTTACGACGGTTACCACACCCGTACACCTTATCTCATTTTC
ACCAGTACCTTTCCCTATTAGATTCACTTATTTTATTTTAGGATTTTATAGGTCATTGTA
CGACGCGTGTGCGACCATGGAAAAGGTGTCGACGCTGCGATGCTATCCATTTACCCGTCA
TCATTGCTGGCAGAAATCCCATCTTCTCTGCTGGGGTGATTTATATATATGGAGAGTTA
ACGAATGTAATATTTCTGAATGTTAAATAATTGTTATCCGTCATTATTGTTTCACTTCTC
TCTTTGAAATTTTCGCTTGTTTTCTGTTTTTCATCTTATATTTTACTTCAATCCTAAGATAG
TCATATCGACTTAATTCCAAATGAGAGCTAAGTGGAGAAAAGAAGAGAACTAGAAGACTTA
AGAGAAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL133C-A, 25 aa (SEQ ID NO 42)

MRAKWRKKRTRRLKRKRRKVRARSK

FIG. 1 - 14

YDL136W, 1268 bp, exon1: 501-503, intron1: 504-908, exon2: 909-1268 (SEQ ID NO 43)

CATGCGGACCTTGTGTGTTTGTCTTAGATTGTTTTATTTTTATGATTGTTGAAGATAT
AAACCACTGTATAGTTGTATAAGATAGGATAATGATGCTGCACTGAAAATAAACTTACTA
GCTCTTTAATATTGCAACGGCTTGTAAACGGGCGCCATGATGACATTCAGAATTATACCAC
TACTATATGAAAAATGAAAAAGAGGCCCTGCTTTGAACCCGTACATTTTATTCTATAATA
TTGCATCTGTGGTTTGCCTGACGGCAGCGAGTCCAACACAAAGTCTGGCATATGCTACGA
ATTTTCCACCATGGATTTCAGCACCCAAACATTTGAATTTTTTTTCATGTCGATTGTGAAA
TTTTACTGAAGATGAGGGTAAATAGAGGCCTGCAATCGTCATCATATGAGAAATGGATAT
ATTGAAAAATCTACTCACATCTCTTTTTTGGGGGTTTGGTAGTACAGTGAGAACACGATAA
AGAACCAAATAGGACTAAAAATGGTATGTAGAGATGAATATACATGAAACGGACGTGATA
TAATGTGCTATGGAAGAAAAAGTCTCCTTTAATGTCTGCAGGATAAATAATCAAGTGGT
CTGAAGAAAATTTACAGCTACAGTATTACTGCAACCTTGCAGGCAAATATCAGAGAGAT
CTCACCAGCTACAACCTGGTAACAGAAATTTATAAGTTTATGGCACTTGTAAATTTGTT
TGGAAGTTTTCGAAATTATAATATTGGTCTTCAGAAACCTGGAACCATATGTAACATATT
TTTTTTGGATAATGCATTGCACAGAGCGTATTAGTGTATACGAGAATCTAAAAATTTGAA
ACTGGCTCATAAAAACAGGAACTTTTACTAACAGTTATGATTTTTTGTTCCTTTCTTT
ATCAATAGGCCGGCGTTAAAGCTTACGAACAAAGAACCAATCCAAGGAACAATTAGCTT
CTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGAATTGAAGGTCCAAAGTTGTCCAGAC
CATCTTTGCCAAAGATCAAGACCGTCAGAAAGAGTATCGCCTGTGTCTTGACCGTCATCA
ACGAACAACAAGAGAAGCTGTTAGACAATTATACAAGGGTAAGAAGTACCAACCAAGG
ACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAGAGCTTTGACCAATTCGAAGCTTCCC
AAGTTACCGAAAAGCAAAGAAAGAAGCAAATCGCTTTCCCACAAAGAAAGTACGCTATCA
AGGCTTAA

YDL136W, 120 aa (SEQ ID NO 44)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKLVQKLSRPSLPKIKTVRKSIACVLTVINE
QOREAVRQLYKGKKYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIKA

YDL167C, 2660 bp, CDS: 501-2660 (SEQ ID NO 45)

TGGGTGTCGTCAAACAGGATGCCGTGGAATCATACGAACCGCACATTGTGGTAGAGCTAC
AAAGCGATACGAAAGAAGATATGGTATCTAACGTATCCCGTATTGTTGCTTGGGAAAAGA
TGTGGTTAGAACAACATCCAGATGGAGTCACAAATGAATATCAAGGGCCTCGTAGCGATG
ACGAAGACGATGAAGACAGTGAGTAGGCGTTCCATAACTTTGTGTATCTACATATATACA
TATATAATTGTAAATTAGTAACAGTAGTAATAGTAGTGCCTATTATAAAGGGTTTTCTTT
AAGTAATGTCTACTTGTTTAATGTGACTTTGGTAATATATTTTTTCATTCTCCGATGCC
GATGCCAGTGGAAAAAGTTTAAAGTGAAAAATTTTTCAACACATACAAGTTTAATAAGTT
GGTTTTGATGCAAATAGCATTACTAAAGAAGAGCGCTAGGATAATTGTGCATTGCTATTG
TGATTTTTGATACAGAAATTATGCACTATGTGGTACTAGAGCTGCAAGTTGCGCATTTGC
CAGATACCCCCAAGGATCAATGTGCGATTGCGAATATAGCATTTCAAATTTGTGAATGCTG
AAACATTAGTATGCCATTATGGGACCAATTCCTTTACCGAGCATTGAAGTAAACGGGACGA
CAAAGAGTTTGGAGAGTGCAATGGTGCAATTGGACAAGGATATTCATGACGTTATTGGTA
ACGACGACTTTTGTCTTGTTCCTGTATTCAACATGGCATATCCGTGTTACCTTACCAC
GTCAAGCGAGAGATGATGGGTTTATTCTTACTTCTTATTTACAACATCCGAAAGTATTTG
ACTTATGGAAGGAATTCGATAGATGGTGTGTCAACCATCCGGAGATTTTGGGACAAAAGA
AAGCAATCTCCAACAACAATTGTAATACTAAAAGTATTAGTATTAATGCAGCCAAAAATA
CGAAGGATTTGGACGAAATAGTTAGAATATTGGAAGTTTCAATCCCAACTGAAGAGGCAG
GCTCTGTTCCAGAGATATACTCTCTTTTAAAAAGGACAACGGATATATTAATACAATTGC
ACAAAAAGTGTACTTCCCTGAAGATATGGAATCTGTCTTAACAAAACCATATGACTCAC
ACACCGATATTAGAGCGTTTTTTGCAAGAGAAATCTAAGATTTTGTACATGAACAATTTAC
CGCCCGACACAACCTCAAAGTGAGTTGGAATCATGGTTTACCCAATATGGTGTAGACCAG
TTGGGTTTTTGGACTGTCAAAAACATCGTAGAAGATACGTCTAACGTTAATAATAACTGGA
GTCTAAATAACAGTCCCTATGTGGAAGATCAAGATAGTATCTCAGGATTTGTTGTCTTCC
AAACACATGAAGAAGCAACTGAAGTACTAGCGTTGAATGGGAGATCAATCCTATCTAATC
TGGCAAACACTAAGCAACCAAGGGTGGTGGAACATGTCTTGGAGTTCAACCTTCTTCCA
CCGGAGTACTCGATAAGGCTCAAGAAATTTTATCGCCTTTCCCTCAAAGTAAAAACAAAC
CAAGACCAGTGACTGGAATTGCCCATCTTGTGGTTTTTCAAACCTTTCAAAGACGTACTG
CATGTTTTAGATGTTCTTTTCCGGCACCATCAAATAGTCAAATACATACTGCGAACTCAA

FIG. 1 - 15

ACAATAATGTTAACAGTAGTAGAAATAATTTAAACAATCGCGTGAACCTCGGGATCTTCAA
GCAATATTAGTAACACTGCAGCGAATCACCCCTATGGTGGCCCTGAGTTCAACATGATTG
CTAACACACGCCAGCAGCTTTAACATACAATAGAGCTCATTTTCCTGCAATTACGCCAT
TGTCGCGACAAAATTCATTGAACATGGCACCATCGAACAGTGGGTGCGCGATAATTATAG
CGGATCAATTTTTTCGGGAAATAATAATATAGCCCCAAATTATCGTTATAATAATAATATTA
ACAATAACAACAATAATATTAACAATATGACCAATAATAGATATAACATTAATAACAACA
TCAACGGTAATGGGAATGGTAATGGGAACAACAGTAATAACAATAACAATCATAATAACA
ATCATAATAACAATCATCATAATGGTAGTATCAATAGTAATAGTAATACCAATAATAATA
ATAATAATAACAATGGTAACAATAGTAATAATTGTAATTCCAATATCGGTATGGGAGGAT
GTGGCTCCAACATGCCATTTAGAGCAGGAGATTGGAAGTGTTCCACGTGCACGTATCATA
ACTTTGCTAAAAACGTAGTGTGCTTACGCTGTGGTGGTCCAAAATCAATAAGCGGCGATG
CAAGTGAACCAATCATTACATAGATTCAACATTTGGACCAGCGTCGCGTACTCCCA
GTAATAACAATAATTTCTGTTAATACTAATGGTGGTAGCAATGCTGGTTCGCACCGATGGGA
ACGATAACAAAGGTCTGTGATATTAGTTTGTATGGAATTTATGTCACCACCGTTATCGATGG
CAACAAAGTCAATGAAGGAGGAGATGGGAATGGTAGCTCGTTAACGAGTTCAAAAGTG
ACAAAGCTAACGTTAATTTTTTCCAATGTTGGTGATAATAGCGCTTTCGGTAATGGTTTTA
ATAGTTCAATACGTTGGTAG

YDL167C, 719 aa (SEQ ID NO 46)

MHYVVLELQVAHLPTPKDQCRIANIAFQIVNAETLVCHYGTNSLPSIEVNGTTKSLESA
MVQLDKDIHDVIGNDDFVLVSLYSTWHIRVTLPRQARDDGFILTSYLQHPKVFDLWKEFD
RWCNVNHEILGQKKAISNNCNTKSISINAANKTKDLDEIVRILEVSIPTEEAGSVPEIY
SLLKRTTDILILQHKKCTSPEDMESVLTKPYDSHTDIRAFLQEKSKILYMNLPDPTTQS
ELESWFTQYGVVRPVGFWTVKNIVEDTSNVNNNWSLNNSPYVEDQDSISGFVVVQTHEEAT
EVLALNGRSILSNLANTKQPRVVEHVLELQPSSTGVLDKAQEILSPFPQSKNKPRPGDWN
CPSCGFSNFQRRACFRCSFPAPSNSQIHTANSNNNVNSSRNNLNRRVNSGSSSNISNTA
ANHYPYGAPEFNMIANNTPAALTYNRAHFPAITPLSRQNSLNMAPSNSGSPIIIDHFSGN
NNIAPNYRYNNNNNNNNNNNNNNNNMTNRYNINNNINGNGNGNGNNSNNNNNNHNNNNHH
NGSINSNSNTNNNNNNNNNGNNSNNCNSNIGMGGCGSNMPFRAGDWKCSTCTYHNFKNVV
CLRCGGPKSISGDASETNHYIDSSTFGPASRTPSNNNISVNTNGGSNAGRTDGNNDKGRD
ISLMEFMSPLSMATKSMKEGDGNGSSFNEFKSDKANVNFNVGDNSAFNGNFNSSIRW

YDL184C, 578 bp, CDS: 501-578 (SEQ ID NO 47)

AACAAGAAAACCCTTCCGTTGATCTTAGATTTCTTAGAGGTTTCATGAAGTAGAAAGCGAC
TTGAACAAAGTCATCCTTCAAGAATCGAAATCTCAAGAGAAAAACAAAATTTAATGTAGA
TTGTCCACTATCTCATGTAAATATACATAACAGGTATTCCTGAGCGTTCGAAAATTAGAC
TGTAATTTTCTGATGCGCTCCCGTACACCTTTGACATATACAAACATCCGCACATTTTAT
AGCTTTCTTTCTAGAATTTTTTCCACGCGCTCTCGATCAATGAACCTCTTAAAAGTAAGTG
ACCCCTAACTTTTTCCAGGCAAGGCTGGCCTCATTACCTTACCCGAAAGTTTCACTTTA
CCCCATGGCAGATGGACGATATTTTAACAAGACGAAACTGACCTCGTCTTCTATAAAACT
GGACTTCTAAGCAACTCTCATTTATCTTATATCCGTTCCATTTTGTACTAAAAGAACCAG
ACCACATCGATTCAATCGAAATGAGAGCCAAGTGGAGAAAGAAGAGAACTAGAAGACTTA
AGAGAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL184C, 25 aa (SEQ ID NO 48)

MRAKWRKKRTRRLKRRKVRARSK

YDL191W, 1354 bp, exon1: 501-503, intron1: 504-994, exon2:
995-1354 (SEQ ID NO 49)

TATTGACGTTTTGCTCTCAGGTCCACCGTGTCTCAAAAAGATACTTTTAAAACCTAAAAC
ACACGAAATCATATTATGATAATTCAGAAATGATAGTGTGGTACTGTGTCAATTGACTGTT
CAAGACTGAAGAGGATCTTTGATTTGTTGTTACTCAACAAATAATCTTCACGAAAACCTTT
CTCAATCTGGGGACTGTATTAATCTCAGACCCATACATATCTACACCCATAACTTTTTTAC
ATTTAATTTTTTATCACATAATAGGTAGCTTAAATTGTAAAGTCGCAAAAAAATAATGGCA
GCGCAGCCTCTCCGGGTGAACCCACGACAACCTTACCTGGCACTCCATGCACCTAACGGGC
GGGTTTGGGCAGGATTCAGCATCAATTTTGCAAAATTCACACCTGAGTAATTCATATAT
GTAATATAATGTTAAGCATACGCTGTGATGACTATTATTGACCGTAGAATAGGTAC
AGTGAGACAGTATATTCGAAATGGTATGTTTGAGATGAACAAAATAATAAAGACTGACAA

FIG. 1 - 16

CTGCAGAACAGAGAGGATCATAGCAACCTAGTGCAAGAAAGAGCCTCGAAGCGTTAAACT
TTTGGAACGTAATTCATCCGTTGGCTATGTCTATTCAATACAGTTAGAATACGAAAGCTG
TAATCAAGTATATCGGATTATTCGCAAGCAAAGAATCAAGGAAAAGAAAGTGAAATAGC
ATACATCTTTAAATTCAGAGGTTTTGCTGAATTTTAATAGGGAAGTTTACGTTATGATTG
TTGGCCGTAGATCGCCTAGCGTTTGACCAAATTTAATTCCTCAATTTTTTTATTGTAAA
AAAGCCTTCCAACGAAATAAATTAGTTATTGGTTTTTTTTCTCTGTACGAGGGATATAT
GATGCTGTGCTTGTAGTTCATTATAAGTGCTAATAAAATACTAACGTTAATAAAAAAT
TGGAATATTATTCATTTTTTATCCTATTAATAGGCCGGTGTAAAGCTTACGAACTAAG
AACCAAATCCAAGGAACAATTGGCTTCTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGA
ATTGAAGGTCCAAAAGTTGTCCAGACCATCTTTGCCAAAGATCAAGACCGTCAGAAAGAG
TATCGCCTGTGTCTTGACCGTCATCAACGAACAACAAAGAGAAGCTGTAGACAATTATA
CAAGGGTAAGAAGTACCAACCAAGGACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAG
AGCTTTGACCAAATTCGAAGCTTCCCAAGTTACCGAAAAGCAAAGAAAGCAAATCGC
TTTCCACAAAGAAAGTACGCTATTAAGGCTTAA

YDL191W, 120 aa (SEQ ID NO 50)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKLVQKLSRPSLPKIKTVRKSIACVLTVINE
QQREAVRQLYKGKKYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIKA

YDR103W, 3254 bp, CDS: 501-3254 (SEQ ID NO 51)

ATCAAGTTTCCTTTAAAGGGATATATAACAGATTCTAAACTGACAGAAATATTTTCGAGT
GAAGAAGAAGCGTTAAATATTGGATCTTTCCGCAAGTTCTACTCTGATACATTTTGAAGT
AGGAGAGTCAATTTAGAAGGCGTATTGCTCAATAGTAGAAAGCAGGCCTGTGCACATGAAT
TAATTAATAAATAATAAAGCTAGTGATTAGACGACACATGTCCATAGGTAACCTGTCTATA
TTTTGAACAATTTCCCTTCTTTTCTTTTTTTTTTTTTTGGGTGCGGCGATATGTAGCTTGT
AATTTACACATCATGTACTTTTCTGCATCAAAATATGAAAGGCGATAGTAGCTAAAGAAA
ATACCGAGAATTTCTCGAAAAGTTGACGACAAAAGAAAGGCATAAAAAAGTAATTTGAA
AATATTTTAAACTGTTTAAACCATCTAGCATCCGCGCTAAAAAAGGAAGATACAGGAT
ACAGCGGAAACAACCTTTTAAATGATGGAACCTCTACAGACAATATAGTTTCCCTTTTTC
ACAAATTTGGTAGCTCGACACAATATAGTGGTACCTTGTTCGAGAACTCCCAACCAAATAA
TAGAGCTTAGAGAAGCCCAGTACTCTATCCCCATTGTCAAGAGGAAAAAATGGACGGAAA
AGTTAGCCAGGTTCCAAAGAAGTAGTGCTAAAAAGAAAAGATTCTCACCTTCTCCTATTT
CCTCCTCTACATTTTCGTTCTCACCCAAATCTAGGGTCACTTCTTCAAACCTTCTTGGCA
ATGAAGACGGTAACCTAATGAATACACCTTCTACGGTTTCCACTGATTATTTGCCACAAC
ACCTTCACAGAACATCGTCTTTGCCAAGACCTAATCCAATCTCTTTCACGCAAGTAATA
GTAACCTATCCCGAGCAAATGAGCCCCCAAGGGCCGAAAATTTATCAGATAAATATACCAC
CCAAGGTCGCTCCATTTGGCTATCCAATACAAAGAACCTCTATTAAAAAATCCTTTTGA
ATGCTTCTTGACGTTATGTGACGAGCCTATTTCTAACAGAAGAAAGGGAGAGAAAATTA
TAGAGCTTGCGATGTGGCCACTTAAGTCAACCAAGAATGTCTTATTATCTCTTTTGGCACC
CTTCAAAGGCAGACGTTCTGTCGCTATTTCCCTTTTTGTACCAAATGTAAAAAAGATACTA
ACAAAGCCGTTCAATGCAATTCAGAAAATGATGAATAAAGGATATTCTAATTTCTGATT
TTTTGATTTCATAAGATTCTGATTCTGAGTTATCAATCACACCTCAGTCCCGCTTTCCTC
CTTATTCACCACTCTTGCCCTCCTTTTGGGTTATCCTATACACCTGTTGAAAGACAAACGA
TATATTCTCAAGCTCCAAGTCTAAACCCAAATCTCATATTGGCTGCACCCCCCAAGGAAA
GAAACCAAATTCACAAAAAATCAAACTATACATTTTTACATTCACCCCTGGGGCACA
GAAGAATTCCGTCCGGAGCAAATCTATCTTAGCAGACACCTCTGTAGCGTTGTCAGCTA
ATGATTCTATTTCTGCTGTTTCCAATTCGTAAGAGCAAAGGATGACGAAACCAAAACAA
CGTTGCCGCTGTTAAGGTCATATTTTATTCAAATCTTTTGAACAATTTCCAGGAAGAAT
TGCAGGATTGGAGAATAGACGGGGACTATGGATTACTAAGGTTGGTAGACAAATTGATGA
TTTCCAAAGATGGTCAGAGATATATACAATGCTGGTGTCTTATTGTAAGACGCATTTG
TAATAGCAGAAGTGGATAACGATGTTGATGTTTTTGAAATTAGACTAAAGAATTTAGAAG
TATTTACACCTATTGCCAATTTGAGAATGACTACACTCGAAGCTTCAGTACTCAAATGCA
CCTTAAATAAACAACATTGCGCCGATTATCAGATCTTTACATTGTTTCAGAAATATAAAT
CTGACGAAAGCACAACTGTACAGAAATGGATATCAGGTATATTGAATCAGGATTTTGTAT
TCAATGAGGACAATATCACTTCGACCCCTGCCATTCTTCCCATTATAAAGAACCTTTTCAA
AAGATGTTGGTAATGGTAGGCACGAGCAGTACCTTTCTAGGTTTAAATCAATCCTAACA
AAGTTTGAAGTTGGAAATGTGCACGATAATGATACTGTAATCATAAGGAGGGGATTCA
CCTTAAATTCAGGAGAATGTTCTAGGCAGAGTACTGTGACAGTATACAATCTGTTCTAA

FIG. 1 - 17

CCACGATAAGCTCAATTCTTTCCCTTAAACGAGAAAAACCTGATAATTTGGCAATAATCT
TACAGATCGATTTTACGAAATTGAAGGAAGAAGACAGTTTAAATTGTTGTTTATAACAGTC
TAAAAGCTTTAACCATTAAATTTGCGCGTTTGCAGTTTGTTCGTTGATCGAAATAATT
ATGTTCTGGACTATGGATCGGTATTACACAAGATAGATTCACTAGATTCCATCTCAAATC
TCAAATCAAAGAGTTCCCTCGACACAATTTTCACCTATTTGGTTGAAAAATACTCTATATC
CCGAAAATATTCATGAACATTTGGGTATTGTTGCTGTATCAAATAGTAATATGGAAGCAA
AAAAATCCATACTATTTCAAGATTACAGATGCTTTACAAGTTTGGGAAGAAGAAGGCCCA
ATGAATTGAAGATTAAGGTGGGCTATTTGAACGTTGACTACAGTGATAAAATTGATGAAC
TAGTCGAGGCCAGCTCCTGGACTTTTGTTTTAGAACTCTTTGCTACAGTTTCGGTCTAA
GTTTGTGATGAACATGATGACGATGACGAAGAGGATAATGATGATTGACCCGATAATGAAC
TTGATAATTAGTTCAGGATCACTGTCCGATGCTGAATCTACAACACTATTTCATATTGATT
CTCCATTGTGATAATGAAAATGCTACCGCAAATATGGTGAATGACAGAAACCTTCTCACTG
AGGGTGAACATAGCAATATAGAAAACTTGAAACTGTGCTTCTTCAGTACAGCCAGCTC
TGATTCTAATATTAGATTTTCACTTCATTCTGAGGAGGAAGGTACTAATGAAAATGAAA
ATGAAAATGATATGCCAGTATTATTACTTAGTGATATGGATAAAGGAATCGATGGCATAA
CCAGACGCAGTTCATTCTCGAGTCTTATAGAGAGCGGTAATAACAACCTGTCCCCTCCATA
TGGATTATATATAG

YDR103W, 917 aa (SEQ ID NO 52)

MMETPTDNIVSPFHNFGSSTQYSGTLSRTPNQIIIELEKPSTLSPLSRGKKWTEKLARFOR
SSAKKKRFSPPISSTFSFSPKSRVTSSNSSGNEGNLMNTPSTVSTDYLPQHPHRTSS
LPRPNSNLFHASNSNLSRANEPRAENLSDNIPKVPFGYPIQRTSIKKSFLNASCTLC
DEPISNRRKGEKIIELACGHLHQECLIIISFGTTSKADVRLFPFCTKCKKDTNKAVQCI
PENDELKDILISDFLIHKIPDSELSITPQSRFPYSPLLPPFGLSYTFVERQTIYSQAPS
LNPNLILAAPPKERNQIPQKKNYTFHLSPLGHRRIPSGANSILADTSVALSANDSISAV
SNSVRAKDDETKTTLPLLRSYFIQILLNNFQEELQDWRIDGDYGLLRVLVDKLMISKDQGR
YIQWCFLFEDAFVIAEVDNDVDVLEIRLKNLEVFTPIANLRMTTLEASVLKCTLNKQHC
ADLSLDYIVQNINSDESTTVQKWISGILNQDFVFNEDNITSTLPILPIIKNFSKDVGNR
HETSTFLGLINPNKVVEVGNVHDNDTVIIRRGFTLNSGECRQSTVDSIQSVLTTISSIL
SLKREKPDNLAILQIDFTKLKEEDSLIVVYNSLKALTIKFARLQFCFVDRNNYVLDYGS
VLHKIDSLDSISNLKSKSSSTQFSPIWLKNTLYPENIHEHLGIVAVSNSNMEAKKSILFQ
DYRCFTSFGRRRPNELKIKVGYLNVDSYSDKIDELVEASSWTFVLETLCYSFGLSFDEHDD
DDEEDNDSDNELDNNSSGSLSDAESTTTIHIDSPFDNENATANMVNDRNLLTEGEHSNI
ENLETVASSVQPALIPNIRFSLHSEEGTNENENENDMPVLLLSMDMDKIDGITRRSSF
SLIESGNNNCPLHMDYI

YDR238C, 3422 bp, CDS: 501-3422 (SEQ ID NO 53)

CCGTGTCAAGATCTAACACGGTAGTCAGCTACTACACAAGGTCTCAGAACAGAATGAGAA
GTGGAACACTGGATAATGATTACGTGAACAGACAAAAGCTTCCTACACATATCTCTCTTC
AAGATTATCGTGATGCTAATGCTAGAAGTAATATATCGCGTCAGGACTCTGTCTCCACAA
CGAACTCTGATGTGGTAGACCTCAGCTATTCTCTGGGGCATGGCTTGCGTGTGGCAAACC
CTGATTACAGACCCAGAATGATATCCTTCTCTGTAGTTTTGTAGATGTCATATATGTACGT
TTATGGAACAGCATTTTAGAAAAGTATTACCCAGCTTATCACTTCGTTTTTTTTTTCTTT
CCGTGTACTCGCTACACGTAGAAAGAAATCAGAAAACAACAGCTCGACAAGTGAAATTTG
ACGTTCAATTAAGACTCAGTTAAGATTGCCTTGAGAATAAACAAAAGTAATCACAGTTAAC
TATTGAACAAGAGTGCACCTATGACTTCACTTTCTTCACAGCCAGCGTACACGTTGGTTT
TCGATCCTTCTCCGAGTATGGAGACTTACTCGAGTACCGATTTTTCAGAAAGCTCTTGAAA
AGGGATCTGATGAACAAAAAATTGACACGATGAAATCAATTTTAGTTACAATGCTGGAAG
GAAATCCAATGCCTGAATTGTTGATGCACATAATAAGATTTGTATGCCTTCTAAAAATA
AGGAATTAAAAAAGCTTTTGTACTTCTACTGGGAAATGTTCCCAAACCTAGCTGAAGATG
GAAATTGAGACATGAAATGATTCTTGTCTGTAATGCCATTCAACACGATTTGCAACATC
CTAATGAATATATTAGAGGTAACACATTAAGGTTTTTAACGAAATTGAGAGAGGCCGAAC
TCTTAGAACAGATGGTTCCCTCTGTCTTAGCGTGCTTGGAATACCGTCATGCATATGTTT
GTAAGTATGCAATCCTAGCAGTTTCTCCATTTTCAAGGTCAGCGAACATTTACTTCCCG
ATGCTAAAGAAATCATCAATTCGTTCATAGTAGCTGAACTGATCCAATATGTAAAGAA
ATGCATTTATTGGGTTAGCTGAATTAGATCGTGAAATGCCTTACACTATTTAGAGAACA
ATATTGCTGATATAGAAAACCTAGACCCTTTATTACAAGCTGTCTTTGTTCAATTTATCA
GACAAGATGCAACAGGACCCCTGCTTTGAAAGCCCAATATATCGAATTATTGATGGAAC

FIG. 1 - 18

TGCTTTTCGACCACGACTTCCGATGAAGTCATCTTCGAGACCGCATTAGCCCTAACTGTGT
TGTCTGCCAATCCAAATGTCTTGGTTCCTGCGGTTAACAAATTGATTGACTTGGCCGTC
AGGTTTCTGATAATAACATTAAGTTAATTGTTCTAGACCGTATTCAAGACATCAATGCTA
ATAACGTAGGTGCTTTGGAAGAGTTAACCTGGATATTTTGAGAGTCTTGAATGCAGAAG
ATTTAGACGTTCTGTTCAAAGGCGCTTGATATTTCAATGGACTTGGCCACATCCAGAAATG
CTGAAGATGTTGTTTCAAGCTTTTGAAGAAAGAGCTGCAAACAACCGTAAATAACCCAGATC
AAGACAAGGCAATGCAGTACAGACAATTGTTAATAAAAACTATTTCGTACCGTGGCTGTAA
ACTTTGTAGAAATGGCAGCAAGTGTGTTTCGCTATTATTAGATTTTCATCGGTGATTTAA
ACTCGGTTGCGGCCAGTGGTATCATTTGCCTTTATCAAAGAAGTGATCGAAAAATACCCAC
AACTTAGAGCCAATATCCTTGAAAACATGGTTCAAACGCTAGACAAAGTGAGATCTGCTA
AAGCTTACCGCGGTGCATTATGGATTATGGGTGAGTATGCTGAAGGAGAAAGTGAGATAC
AACATTGTTGGAAGCACATTTCGTAACAGCGTAGGTGAAGTTCCTATCCTTCAATCAGAAA
TCAAAAAGTTAACACAAAACCAAGAACACACCGAAGAAAATGAGGTGACGCTACCGCCA
AGCCAAGTGGTCCAGTTATTCTACCAGACGGTACGTATGCCACTGAAAGCGCTTTCGATG
TGAAGACTTCTCAAAGTCAGTTACCGATGAAGAACGTGATTCTAGACCTCCAATTCGCC
GGTTTGTGTTTAAAGTGGTGATTTCTACACAGCTGCCATTCTGGCCAACACCATCATTAAC
TTGTTTTTAAATTCGAAAACGTTTCCAAGAACAAAACGTGCATCAATGCTCTAAAGGCGG
AAGCTTTACTAATTTTAGTTAGTATTGTAAGAGTGGGTCAAAGCTCTTTGGTGGAGAAAA
AAATTGATGAAGATTCTTTAGAGAGAGTTATGACATCTATTTCTATTTTATTGGATGAAG
TTAATCCTGAGGAAAAGAAGGAAGAAGTTAAACTTCTGGAGGTTGCATTCTGGACACCA
CCAAATCCTCATTCAAGAGACAAATTGAAATTGCAAAGAAGAACAAGCATACAGAGCAT
TAAAGACAGTTGCAAAAACATCGAACCATTGATACGCCGATTCTCTTACGGCAATTG
CTGGTGTGGATTCTACTAATGTGCAAAAAGATAGTATTGAAGAAGATTTACAACCTGGCAA
TGAAAGGAGATGCAATCCACGCTACTAGCAGCTCTAGTATTTGGAAGCTGAAGAAGATAG
TACCTTTATGTGGCTTTTCTGATCCAGTTTACGCCGAGGCTTGTATTACAAACAATCAAT
TTGACGTCGTATTAGATGTTCTTCTTGTAAATCAAACGAAAGAAAACATTGAAAAACCTAC
ATGTGCAATTTGCAACTCTTGGTGATTTGAAGATTATTGACACACCACAGAAGACCAACG
TGATTCCTCATGGCTTCCACAAATTCAGTGTACTGTCAAAGTTCTCTGCTGACACAG
GTGTCAATTTTCGGTAATATTATTTATGATGGTGGCGCATGGTGAAGATGCTCGTTATGTTA
TTTTAAACGACGTTTATGTTGACATTATGGATTATATCAAACCAGCCACTGCTGACGATG
AACATTTCCGTACCATGTGGAATGCATTTGAGTGGGAGAACAAAATATCGGTCAAATCAC
AACTACCAACATTGCATGCTTATTTGAGAGAACTGGTCAAGGGAACTAATATGGGTATTC
TAACACCATCAGAGTCGTTGGGAGAAGATGATTGTAGGTTCTTAAGTTGTAATCTGTATG
CGAAGTCGTCCTTTGGTGAAGATGCCCTAGCCAACTTGTGTATCGAAAAGGATTCCAAA
CCAATGATGTCATAGGTTATGTTTCGTATCCGATCAAAGGGACAAGGTTTGGCTCTGTCCC
TAGGTGACAGAGTGGCATTGATTGCTAAGAAGACCAATAAACTTGCTCTCACTCATGTTT
GA

YDR238C, 973 aa (SEQ ID NO 54)

MTSLSSQPAYTLVFDPSMETYSSTDFQKALEKGSDEQKIDTMKSILVTMLEGNPMPPEL
LMHIIRFVMPSPKNKELKKLLFYWEIVPKLAEDGKLRHEMILVCNAIQHDLQHPNEYIRG
NTRLRFLTKLREAELLEQMVPVSLACLEVRHAYVRKYAILAVFSIFKVSEHLLPDAKEIIN
SFIVAETDPICKRNAFIGLAELDRENALHYLENNIADIENLDPLLQAVFVQFIRQDANRT
PALKAQYIELLMELLSTTTSDEVIFETALALTVLSANPNVLVPAVNKLIDLAVKVSNNI
KLIVLDRIQDINANNVGALEELTLDILRVLNAEDLDVRSKALDISMDLATSRNAEDVVQL
LKKELQTTVNNPDQDKAMQYRQLLIKTIRTVAVNFVEMAASVVSLLDFIGDLNSVAASG
IIAFIKEYIEKYPQLRANILENMVQTLDKVRSAYRGALWIMGEYAEGESEIQHCWKHI
RNSVGEVPILQSEIKKLTQNEHETEENEVDATAKPTGPVILPDGTYATESAFDVKTSQKS
VTDEERDSRPPIRRFLVSGDFYTAAILANTI IKLVLFENVSKNKTVINALKAEALLILV
SIVRVGQSSSLVEKKIDEDSLERVMTSISILLDEVNPEEKKEEVKLEVAFLDITKSSFKR
QIEIAKKNKHKRALDKSCKNIEPIDTPI SFQFAGVDSTNVQKDSIEEDLQLAMKGDAIH
ATSSSSISKLKKIVPLCGFSDPVYAEACITNNQFDVLDVLLVNQTKETLKNLHVQFATL
GDLKI IDTPQKTNPVPHGFHKFTVTVKVSSADTGVIFGNIIYDGAHGEDARYVILNDVHV
DIMDYIKPATADDEHFRMTMNAFEWENKISVKSQPLTLHAYLRELVKGTNMGILTPESEL
GEDDCRFLSCNLYAKSSFGEALANLCIEKDSKTNDVIGYVRI RSKGQGLALSLGDRVAL
IAKKTNKLALTHV

FIG. 1 - 19

YDR259C, 1652 bp, CDS: 501-1652 (SEQ ID NO 55)

AAACTTTTGTTCAGATTATGCTTTCTTTGTAAATTTTAAACATAGTCTTGCACCTTATTTTT
ACTGCATGTGGATAAAAGTTTTCGAATCGTTTGCAGGCAAATGTAACTATTACTTTTT
AATGATTCTTGATACTCTTTGATTCCATTCTGTCTACTTTTTCTGCATTGTGAAACGCT
AATTAAGTATTTCTTGGCCCTGCTTCTTTTCCCTTTTGATTCTTTTTTTTATTCTCAAGTT
TTTAATTTCTGGAGAATCTTTTTTTTGTATTGTTAACACAGTTAGTGGAGCCTTG
TAGTATCGAGAGTAGACTATCTTTGGAAGCAATGCGAGTTGAGAGATTGTGGAGTGAC
TACAGAACCAATATTAAACACAATCTTTCCTCAAACCTGTAACACCGAGTTTTTTTCCCA
CCAATCGTGAATCCGATAGCATATACTTTTGTCTAGAAATTTCAATAAACAACAGAATAA
CGAAGAGTGCTAAGGGACAAATGCAAAACCCTCCGTTGATTCTCGTCCCGATATGTATAATC
AGGGAAGCAGCTCAATGGCTACTTATAATGCCTCTGAGAAGAATCTAAATGAGCATCCTT
CTCCGCAAATTGCACAGCCCAGCACGTCCCAAAAGTTACCTTATAGAATAAATCCTACAA
CCACTAATGGGGACACCGACATATCTGTTAACAGCAATCCTATCCAGCCTCCTTTGCCAA
ACTTGATGCATCTATCTGGTCCGTCTGACTATAGATCGATGCATCAAAGTCTTATACATC
CATCTTATATCATCCCTCCGCATTCAAATGAAAGAAAACAATCAGCTTCTTACAACAGAC
CTCAAATGCTCATGTTAGTATTCAACCTTCCGTGGTATTCCCCCTAAAAGTTATTCCA
TATCTTATGCACCTTATCAAATAAATCCCCCTTTACCAAATGGACTTCCGAACCAGAGCA
TATCTTTGAATAAGGAGTATATTGCAGAGGAGCAACTATCAACCCTCCCATCTCGCAATA
CCAGTGTTACTACTGCACCTCCTTCTTTTCAAACAGTGCTGATACCGCTAAAAATTCAG
CTGATAATAATGATAATAATGATAATGTAACCAACCTGTTCTTGATAAAGACACCCA
TCATAAGTAGTTTCAGGCAAACTTTAAGAAATACTAGAAGAGCTGCTCAAAATAGAACCG
CTCAAAGGCATTTAGACAAAGGAAAAGAAAATACATCAAGAATCTCGAACAAAATCAA
AGATATTTGACGATTTACTAGCAGAAAATAATAACTTCAAATCATTAAACGATTCAATTA
GAAATGACAACAACATTTTAAATAGCTCAGCATGAAGCTATAAGGAATGCAATTACTATGT
TAAGAAGTGAGTATGATGTCTTATGTAACGAAAACAACATGTTGAAGAATGAGAATAGTA
TAATAAAAAATGAACACAACATGTCAAGAAATGAAAATGAAAACCTAAAACCTTGAGAATA
AACGCTTCCACGCTGAATATATACGAATGATCGAGGATATTGAAAATACTAAAAGAAAGG
AACAAGAACAACGAGATGAAATAGAGCAACTAAAAAAAATAAGATCCCTGGAGGAAA
TAGTAGGGAGACACTCGGATAGTGCCACGTAA

YDR259C, 383 aa (SEQ ID NO 56)

MQNPLIRPDMYNQSSSMATYNASEKNLNEHPSPOIAQPSTSQKLPYRINPTTTNGDTD
ISVNSNPIQPPLPNLMHLSGSPDYRSMHQSPIHPHYIIPHSNERKQASYNRPQNAHVS
IQPSVVFPPKSYISYAPYQINPPLPNGLPNQSI SLNKEYIAEEQLSTLPSRNTSVTTAP
PSFQNSADTAKNSADNNDNNDNVTKPVPDKDTQLISSSGKTLRNRRAAQNRTAQKAFRQ
RKEYIKNLEQKSKIFDDLAEENNFKSLNDSLNDNNDNLIQAHEAIRNAITMLRSEYDV
LCNENNMLKNENSIIKNEHNMSRNEENENLKENKRFHAEYIRMIEDIENTKRKEQEQRDE
IEQLKKKIRSLEEIVGRHSDSAT

YDR294C, 2270 bp, CDS: 501-2270 (SEQ ID NO 57)

CCGACAGTACGACTTAAAAAACAACCAACGTCCAGGTGGAAAAAGCTGCCGCAATATGG
TACACGGTTTAGATCAACAAGATCCAATACCCCTAATTACACATGAATGTGACGTTTCCT
AAAAGAAGTAGCCTGTATAATATAGAGAGATTTTATATACTTTCTTAATGAATTAGACTG
TTTCTACAAGTATTTGACACTGGAAAAAAGAGAAAGTACATAGAGATTGGCCAAATATT
TAAATCTACACAGTTGCCTATCGTPTTATCGCCTTATTTCTTCAGAAACATTTTCATCAACTA
CTCTGGTGCATTATTTTCATGTTAGTTACCATATATACCGGCCGGCCGCATCGGGGTTTTT
TGATTGAAAAAATGGTATATTTTCAGTACACATATAAATAAAACCCTCAATTTGCCCTCT
CCAACCGTTATAACTATTCCAGATCCTCTTTACCGAGCAAGTAGGCTAGCTTCTGTAAAG
GGATTTTTCCATCTAATAACAATGAGTGGAGTATCAAATAAAACAGTATCAATTAATGGTT
GGTATGGCATGCCAATTCATTTACTAAGGGAAGAAGGCGACTTTGCCAGTTTATGATTC
TAACCATCAACGAATTAATAATAGCCATACATGGTTACCTCAGAAATACCCCATGGTACA
ACATGTTGAAGGATTATTTGTTTGTGATCTTTTGTTCAGCTAATAAGTAATTTTTTTT
ATCTGTTGAAAGTTTATGGGCCGGTGAGGTTAGCAGTGAGAACATACGAGCATAGTTCCA
GAAGATTGTTTCGTTGGTTATTGGACTACCATTTTGGAGGGGTACCGTAGAAAAGGAAG
TCACAAAGGTCACCAATCGATCGAAGACGAACCTAATTAGATCGGACTCTCAGTTAATGA
ATTTCCACAGTTGCCATCCAATGGGATACCTCAGGATGATGTTATTGAAGAGCTAAATA
AATTGAACGACTTGATACCACATACCCAATGGAAGGAAGGAAGGTCTCTGGTGCCGTTT
ACCACGGTGGTGTGATGATTTGATCCACTTACAAACAATCGCATACGAAAAATATTGCGTTG

FIG. 1 - 20

CCAATCAATTACATCCCGATGTCTTTTCCTGCCGTACGTAAATGGAATCCGAAGTGGTTT
CTATGGTTTTAAGAAATGTTAATGCCCCCTCTGATACAGGTTGTGGTACCACAACCTCAG
GTGGTACAGAATCCTTGCTTTTAGCATGTCTGAGCGCTAAATGTATGCCCTTCATCATC
GTGGAATCACCGAACCAGAAATAATTGCTCCCGTAACTGCACATGCTGGGTTTGACAAAG
CTGCTTATTACTTTGGCATGAAGCTACGCCACGTGGAGCTAGATCCAACGACATATCAAG
TGGACCTGGGAAAAGTGAAAAATTCATCAATAAGAACACAATTTTACTGGTCCGTTCCG
CTCCAAACTTTCTCATGGTATTGCCGATGATATTGAAGGATTGGGTAAAATAGCACAAA
AATATAAACTTCTTTACACGTCGACAGTTGTCTAGGTTCTTTATTGTTTCATTTATGG
AAAAGGCTGGTTACAAAAATCTGCCATTACTTGACTTTAGAGTCCCGGGAGTCACCTCAA
TATCATGTGACACTCATAAATATGGATTTCACCAAAAAGGCTCGTCAGTTATAATGTATA
GAAACAGCGACTTACGAATGCATCAGTATTACGTAAATCTGCTTGGACTGGCGGGTTAT
ATGGCTCTCTTACATTAGCAGGGTCCAGGCCTGGTGCTATTGTCTGAGGTTGTGGGCCA
CTATGGTCAACATGGGTGAAAATGGGTACATTGAGTCGTGCCAAGAAATAGTCGGTGCAG
CAATGAAGTTTAAAAAATACATCCAGGAAAACATTCCAGACCTGAATATAATGGGCAACC
CTAGATATTCAGTCATTTCAATTTCTTCAAAGACCTTGAACATACACGAACCTATCTGACA
GGTTGTCCAAGAAAGGCTGGCATTTCAATGCCCTACAAAAGCCGGTTGCACTACACATGG
CCTTACAGGATTGAGCGCTCATGTTGTGGATGAGATCTGCGACATTTTACGTACTACCG
TGCAAGAGTTGAAGAGCGAATCAAATCTAAACCATCCCAGACGGAAGTACGCGCTCTAT
ATGGTGTGCGCGGAGCGTTAAACTGCTGGCGTTGCAGACAAATTGATTGTGGGATTCC
TAGACGCATTATACAAGTTGGGTCCAGGAGAGGATACCGCCACCAAGTAG

YDR294C, 589 aa (SEQ ID NO 58)

MSGVSNKTVSINGWYGMPIHLLREEGDFAQFMILTINELKIAIHGYLRNTPWYNMLKDYL
FVIFCYKLISNFFYLLKVYGPVRLAVRTYEHSSRRLFRWLLDSPFLRGTVKEVTKVKQS
IEDELIRSDSQLMNFQPLPSNGIPQDDVIEELNKLNDLI PHTQWKEGKVS GAVYHGGDDL
IHLQTIAYEKYCVANQLHPDVFPVRKMESEVVSMVLRMFNAPSDTGCGTTTSGGTESLL
LACLSAKMYALHHRGITEPEI IAPVTAHAGFDKAAAYFGMKLRHVELDPTTYQVDLGKVK
KFINKNTILLVGSAPNFPFGIADDIEGLGKIAQKYKLP LHVDSCLGSFIVSFMEKAGYKN
LPLLDLFRVPGVTSISCDTHKYGFAPKGSSVIMYRNSDLRMHQYVNPWATGGLYGSPTLA
GSRPGAIVVGWATMVNMGENGYIESCQEIVGAAMKFKKYIQENIPDLNIMGNPRYSVIS
FSSKTLNIHELSDRLSKKGWHFNALQKPVALHMAFTRL SAHVVD EICDILRTTVQELKSE
SNSKPSPDGTSALYGVAGSVKTAGVADKLIVGFLDALYKLGPGEDTATK

YDR430C, 3470 bp, CDS: 501-3470 (SEQ ID NO 59)

ACGTCATTTTGTCTTGTGGAGCTGGTGGTTCTTGTGGAGCAGATTCTGTGGAGCAGAT
TCCTGTGGAACCTGTGGTTCTTGTGGAGCATCTGGAGCCTGTGGTGGTTCTTGGTGCTGT
TCTTCGACTGGGGCATCGACAACAGATTCTGGTAGTTGCTCTACGTGAGTTTCTTGAGCT
TCAGACATTATCCTTATGGTTTTAGCGTAATTGCTTAATTTTGATTCTTCAAAGTATA
TATATTTAGAAGAGAGGAAATTATTTTCTCATGTCCTTTTTAAATCCCTTTGGGTGGCG
AAAAAAAGAATGTAAAAAATTTTGCCCTTCGTTTACAGTGATAAAATATACGGAGGGGCT
CTATGATAAAGGTAGTAGTAATCATTGAATTGTTGAACAAGCATTGACAGATATGATAA
CAAGCAATTGTAATCAATAAGCCACCAATTAGAAGGCTACTCAAAAGAATAAAGTTACTA
TAAAATATACTGCGGTATATATGTTGCGGTTTCAGCGATTTCGCTCCTCGTATGCCCAAG
CACAGGCCGTTAGAAAATATCCAGTTGGAGGTATATCCATGGTTATGAAGTGAGAAGAA
TTCTACCGGTTCCGGAGCTGAGACTCACTGCGGTAGATTTGGTGCACCTCCAGACAGGAG
CCGAGCATTTCATATTGATAGAGACGACAAGATAATGTGTTTCAGCATTGCTTTTAAAA
CCAACCCTCCAGATTCCACTGGGGTCCCTCATATTCCTAGAGCATACAACGTTGTGTGGGT
CTGTTAAATATCCAGTTAGGGACCTTTTTTCAAATGCTAAATAAATCTCTAGCTAATT
TCATGAACGCTATGACAGGTCCAGATTATACATTTTTTCCCTTTTCCACTACGAACCTC
AAGATTTTCGCTAATTTAAGAGGTGTTTATTTAGACTCCACCTTGAATCCGCTACTTAAAC
AAGAAGATTTTGATCAGGAGGGTTGGAGGTTGGAGCATAAAAACATCACAGACCCGGAGA
GTAACATTGTTTTCAAAGGTGTTGTCTATAACGAAATGAAAGGTCAAATATCAAATGCCA
ATTACTATTTCTGGAGTAAATTTCAACAGTCTATTTATCCTTCCCTGAATAACTCCGGCG
GAGATCCTATGAAAATTACAGACTTGAGATACGGCGATCTCTTGGATTTCCATCACAAAA
ATTACCATCCCTCCAATGCAAAAACCTTCACGTACGGTAACTTGCCATTGGTGGATACGT
TAAAGCAATTAAATGAGCAGTTTCAGTGGTTACGGGAAGAGAGCTCGAAAGGATAAGTTGT
TAATGCCATTGATTATAAAAAAGACATAGATGTCAAGTTACTGGGTCAAATAGATACTA
TGCTTCCACCGGAGAAGCAGACAAAAGCCTCAATGACGTGGATTGTGGAGCGCCACAGG

FIG. 1 - 21

ACACATATGATACCTTTTTGTTAAAGTACTGGGGAATTTATTAATGGATGGCCATTCTT
CTGTAATGTATCAAAAATTAATAGAATCAGGAATTGGTTTGGAGTTCTCCGTAAATTCAG
GTGTTGAACCAACTACAGCAGTAAATTTGCTAACTGTTGGTATACAGGGCGTGAGTGATA
TTGAAATATTTAAAGACACTGTAAATAATTTTTTCAAAACCTGTTGGAAACAGAACATC
CTTTTGACCGCAAGCGTATCGATGCCATAATTGAACAATTGGAATTATCTAAGAAGGATC
AAAAGGCTGACTTTGGACTTCAATTACTCTATTCTATACTACCTGGTTGGACAAACAAAA
TCGATCCTTTTGAGAGCTTGTGTTTGGAGACGTTTGCAGAAAGATTTAGAGGTGACTTAG
AAACGAAAGGTGATACCTTTATTCCAAGATTTAATCCGTAAATATATCGTTCATAAACCTT
GTTTCACGTTTTCCATTACAGGGATCTGAAGAGTTCTCTAAATCTTTGGATGATGAAGAAC
AAACAAGACTGAGAGAAAAAATTACTGCCCTTGGATGAACAAGACAAGAAAAACATCTTTA
AACGTGGTATACTGTTACAGGAGAAAAAAAATGAAAAAGAAGATTTATCCTGTTTACCTA
CCTTACAAATAAAAAGACATCCCAAGAGCTGGTGATAAATATTCATCGAACAGAAGAATA
ATACAATGTCTAGGATTACTGATACCAATGGTATCACATATGTCAGAGGTAAACGTTTAC
TAAATGACATAATACCCCTTTGAACTCTTCCCATACTTACCTTTATTTGCTGAATCGTTAA
CTAACCTAGGGACAACAACAGAATCCTTCAGTGAAATAGAAGATCAGATAAAAATTACATA
CGGGTGGTATATCAACACATGTAGAGGTTACATCTGACCCTAACACCACAGAGCCTCGCC
TGATTTTCGGGTTTGACGGATGGTCTTTAAATTCGAAGACCGACCACATTTTGAATTC
GGTCTAAGACTCTTACTAGAACTGATTTCCATAAAAAACAGCGATAAAATTGAAAGTTCTTA
TCCGCTTATTAGCATCTTCAAACACATCTTCTGTAGCAGATGCCGGTCATGCATTTGCAA
GGGGCTATTCTGCCGCACATTATAGATCAAGTGGAGCTATAAATGAGACCCTCAATGGTA
TTGAGCAACTACAATTTATAAATAGATTGCACAGCTTGTAGACAATGAAGAACTTTCC
AAAGAGAAGTTGTGACAAAGCTAACTGAATTGCAAAAGTACATTGTTGATACCAATAACA
TGAATTTTTTTATCACCTCAGACTCTGATGTTCAAGCGAAAAACAGTAGAAAGCCAAATTT
CAAAATTCATGGAGAGATTACCTCATGGCAGCTGCTTGCCCAATGGACCAAGACTTCAG
ATTATCCTCTTATTGGATCCAAATGTAAACATACTTTGATAAAATTTCCCTTTCCAGGTCC
ATTACACATCCCAAGCTTTATTGGGTGTGCCGTATACACATAAGGATGGCTCTGCACCTC
AAGTTATGTCAAATATGCTAACATTCAAACATTTGCACAGAGAAGTCAGAGAAAAGGGTG
GTGCTTATGGTGGTGGTGTCTTATAGCGCCTTAGCGGGTATTTTCAGTTTCTATTCCCT
ATAGGGATCCTCAGCCTTTGAAGAGTTTAGAAACCTTCAAGAATAGCGGGCGTTATATAC
TGAACGATGCCAAGTGGGGCGTCACAGACCTTGATGAAGCTAAATTGACAATATTTCAAC
AAGTAGACGCACCTAAAGTCCCAAGGAGAAGGCGTGACGTATTTTCATGACGGGTGTTA
CAGACGATATGAAACAAGCAAGAAGGGAACAACACTCTTAGACGTATCTCTCCTGGACGTTT
ATAGAGTCGCCGAAAAATATCTACTAAACAAGAAGGGGTGAGTACGGTCATTGGACCTG
GAATCGAGGGGAAGACTGTTTCACCAAAATGGGAGGTGAAGGAAGTGTAG

YDR430C, 989 aa (SEQ ID NO 60)

MLRFQRFASSYAQAQAVRKYPVGGIFHGYEVRRILPVPELRLTAVDLVHSQTGAEHLHID
RDDKNVFSIAFKTNPPDSTGVPHILEHTTLCGSVKYPVRDPFFKMLNKSANFMNAMTG
PDYTFPPFSTTNPQDFANLRGVYLDSTLNPLLKQEDFDQEGWRLEHKNITDPESNIVFKG
VVYNEMKGQISNANYFWSKFQQSIYPSLNNSGGDPMKITDLRYGDLDFHHKNYHPSNA
KTFTYGNLPLVDTLKQLNEQFSYGKRARKDKLLMPIDLKKDIDVKLLGQIDTMLPPEKQ
TKASMTWICGAPQDFTYDTFLLKVLGNLLMDGHSSVMYQKLIIESGIGLEFSVNSGVEPTTA
VNLLTVGIQGVSDIEIFKDTVNNIFQNLLETEHPFDRKRIDAIIEQLELSKKDQKADFGL
QLLYSILPGWTNKIDPFESLLFEDVLQRFGRDLETGKDTLFDLIRKYIVHKPCFTFSIQ
GSEEFKSLDDEEQTRLREKITALDEQDKKNIFKRGILLQEKQNEKEDLSCLPTLQIKDI
PRAGDKYSIEQKNNTMSRITDTNGITYVRGRLLNDIIPFELFPYLPLFAESLTNLGTTT
ESFSEIEDQIKLHTGGISTHVEVTSDPNTEPRLIFGFDGWSLNSKTDHIFEVWSKILLE
TDFHKNSDKLKVLIIRLLASSNTSSVADAGHAFARGYSAAHYRSSGAINETLNGIEQLQFI
NRLHSLLDNEETFQREVVDKLTQLKYIVDTNNMNFITSDSDVQAKTVESQISKFMERL
PHGSCLPNGPKTSDYPLIGSKCKHTLIKFPFQVHYTSQALLGVPHYTHKDGSAALQVMSNML
TFKHLHREVREKGGAYGGGASYSALAGIFSFSYRDPQPLKSLETFKNSGRYILNDAKWG
VTDLDEAKLTIFQQVDAPKSPKGEVTVYFMSGVTTDDMKQARREQLLDVSLLDVHRVAEKY
LLNKEGVSTVIGPGIEGKTVSPNWEVKEL

YDR438W, 1613 bp, CDS: 501-1613 (SEQ ID NO 61)

CTTTTCTCAGCACCTGTCCAGAGACATAACATCACATCGCCCCAGTAAATGCA
TACGCAAGATAAGATACAACTGGCTACGGGAACACTACGCCAACGTGATTGGCAATTGT
GCTCTAATAGTTACTCTATTATTGCTGTTAATTGACAATGTTTAGTCACGTGCAACACAA

FIG. 1 - 22

TTCAAGTCACGTGGAAAGGCCTTCACATGGTGATCCATCTTCTACATCTTCATCGGTCCT
GCATAAAGTCATAATATGGGGCTACTGGAATGTATGCACTTAACAGTACTATTATATGGT
GAGGCTGTAATGCTTACCGTTTTGTGGCTATTCTCGTATTCTGTAGGCCCCCATAACAC
ATTTTTCGGTAACGCGCATATAGATGAAAGTTGAAATGAATATTCAAAGAATATATA
TAATAATGCAGGAGATCAAGGAAGAATTAGATATGTATAAGAGTGATGGTAGAGGCAAAA
AATAAAAAGTAAGCAGGAGAATGAATCGTGTGGTATAGACGTAGATCATATGATAGGGG
TCCTGCTTCTGGCCGTAGTGGTGGTGTGGTGGGCTTCGTGTTTGACTAATGAAT
TGCTCGAGACAAACGCGTACAATAAACCTTTCTCTCTTACTTATCTAAACATATCATCGT
TTGCTCTTTATTTGACGCCAGATCTATGGAGGATAATCCAATCAAGAAGGAAGAGCTTGC
AGGAACGGACAGAACGAACATTACCTATTACACACAAGAATCTTTTTTCAGAGTTCCTAC
CTTTACTATCTTCAACTCCTTCTACTTCTTCAAATTTGTCTTCGATAGCGGACACGAAAG
TGAAGGATACAATGAGGTGAGTCTGCTATTTTTCGTCTTGTGGTTCGTGGCAAATTTGG
CGGCTAACGCTGCTTTGTGCTATACCACAGTGGCTTCGTCAACAATCTTTTCATCGACAT
CCTCATTTTTTACCTTATTTCTTGGCACTAGTCTAGGAATAGAACTTTTTCGACAAAAA
AACTGCTGGGGTTATTTGTGCTTTTGTGGAATTATCTTAATTGTGATGCCATCCTCGA
AGCAACAGGATTCTGTGAGTGTCTTCTCTCTTTTGGTAGGTAACACTTTAGCACTGCTGG
GGCATTGGGTTACAGTGTCTATACAACCCTTTTGAATAACGAAATATCATCAAAGGTC
TCAGACTAGACATTAGATGTTTCTTGGTTATGTTGGTATCTTCACGTTTCTGTTGTTTT
GGCCAATTTTAATAATCCTGGATATAACACATATGGAACTTTTGAACCTACCAAGTAAT
TCCACATTTCTTTTCTTGTCTATGTTAAATTGTATCATTTATCTTTGTTAGTGACTATTTT
GGGTAAAGCCCTCATTTTGCATCACCTTGGTGGTTACCGTTGCCTTAACCTTTTACTA
TCCCGTTAGCCATGTTTCGTGATTTTGTATGGCGAGAGGCATTTTTTACGCTTGGTATA
TCATTGGTGTATTTTTCATTTTGTGTTTCTTCTTAGTTAACCATCGGGGAGAATCTG
CTGTTGAAAAGGACTGTGCTGCGGTTGAAAAGGACCTATCTTGGATGCCTAA

YDR438W, 370 aa (SEQ ID NO 62)

MNRVGIDVDHMIQVLLAVVVFVWVGASCLTNELLEYNAYNKPFFLTYNLISFALYLTP
DLWRIIQSRKSLQERTERTLPINHTQESFSEFLPLSSSTPSTSSNLSSIADTKVKDTMRL
SLLFVCLWFVANLAANAALSYTTVASSTILSSTSSFFTLFLATSLGIETFTSKLLGLFV
SLFGIILVMQSSKQDSVSASSFLVGNLTALLGSLGYSVYTTLLKYEISSKGLRLDIQM
FLGYVGIFTLLFWPILILDIHMETFELPSNFHISFLVMLNCIIIFVSDYFWCKALIL
TSPLVVTVALFTIPLAMFADFVWREAFPTWYIIGVIFIVSFFLVNHRGESAVEKDCA
AVEKGPILDA

YDR450W, 1376 bp, exon1: 501-547, intron1: 548-982, exon2:
983-1376 (SEQ ID NO 63)

CGGCCCATGAGCATAAATTGAGAACGATATTATTAATTCTAGTATATTTTAGGAACAGCA
GGCCATTATATCCAAACTTTTTTAAATAGCATCCACATCACTTACTGGCGTACAGTTT
CGTGTCTGGCAACAAAAAGTACATTTAATTTCATGATTAAAAAGACATTAAACATCCG
TACATTACGCACCCATGCATGCTATCTGAAAAATTTCTACATGCTGCTTTTAGAAATTTG
AAGCGGCATATGGTGTTCCTTGGCGAGACGCGCGCTCAGGGGAACGCGATTCCGAAAG
ATGCCTTTCCAGTCCCATATGCCCATCCCAAGATCATGCCCGGAGAGCAAATGTCGCC
CCAGCCAGGTCCGACACATCTGTCAATTCGACCACTAAGTATTGTCAAAGCTAGGGTTAAT
TGAAGATAGCTCTACATGTTATTAGTAGAGTTTTTAAACGTTGAGATACTAGTGAACGTA
TACACAAGAGCGGATAAAAGATGTCTTTAGTTGTCCAAGAACAAGGTTCTTCCAACACA
TTTTACGGTATGTTTATTATTACTAGTGAGCTATGACAAAATCGGCTAAAAACTTAAAA
TATGACAGACAAGAAAGGAATTCATTACCTCTTTAATCGTGGCGATTATTTCGCTAACG
ACGTGATTAAATATAATAATGATGTTCCCGGGCTGGACTAAGAACGTAATAATAAGGCTG
ATGAACAAATTTATGGTTTATGCATCAAAAAGGAACATGAATTTGGCATAAGCGCACATA
ATTACGGAACATTGCAATAGCGGTGCGAGGTAAAGTACCGGGAATGCTTTACAATGAATC
AGCTATTGGCGGATATTGACCAACCAACACTAAAATTTTATATCCTGCTCCGATTTTTGT
CTTGGCCGTGAAATCCATTATGCACATTTTTTACTAACGTTTATCAATAAGTTCCGTTTC
CCGTCTAAATTTTTTTACGCAGTTTGTGTAACACTAACGTTGACGGTAACATTAAGATCG
TTTACGCTTTGACCACTATCAAGGGTGTGGTTCGTCTGTTACTCCAACCTGGTCTGTAAGA
AGGCTGATGTTGATTTACACAAGAGAGCTGGTGAATTGACCCAAGAAGAATTGGAAAGAA
TTGTTCAAATTATGCAAAACCAACTCACTACAAAATCCCAGCTTGGTTCTTGAACCGTC
AAAATGACATCACTGATGGTAAGGACTACCACACTTTGGCTAACACGTCGAATCCAAAT

FIG. 1 - 23

TGAGAGATGACTTGGAAAAGATTAAAGAAAATCAGAGCTCATCGTGGTATCAGACACTTCT
GGGTTTTCGGTGTAGAGGTCAACACACCAAGACCACTGGTAGAAGAAGAGCTTAA

YDR450W, 146 aa (SEQ ID NO 64)

MSLVVQEQGSFQHILRLNNTNVDGNIKIVYALTTIKVGRRYSNLVCKKADVDLHKRAGE
LTQEELERIVQIMQNPHTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDDLERLKKIR
AHRGIRHFWGLRVRGQHTKTTGRRRA

YDR486C, 1289 bp, CDS: 501-1289 (SEQ ID NO 65)

ACTGCATACACAATAAAGTGTAGATGTAGCCCAAGGCACTACCACAGGTATTTCTGCTCAC
GACAGGTTCGATGACTTGTAGGGCTCTTGCAGACTCTTCTCTACGCCAAAATCATTTTAA
AAACCAGGGCACATCTGTCCCTTGAGAGCCGCTGATGGCGGTGTTTTGCAGAGAAGAGGC
CACACTGAGGCCGGTGTGCGATTGTGTAAACTAAGTGGACTAAGTCCCGTCGCTGTTTAT
GGCGAATTGGTTAACGATGACGAACAAGGAATATGATGAGATTAAATGACTGCCAAGCG
TTTGGTAAGAAACATGGCATTCTTTGATCTCCATCGAAGAATTGGCCCAATATTTGAAG
AAATAATCTGGTGAACATTTCTCCATTCTATCACAACAGACTCACACATATATAC
ATGTATATATTTGTAACCTTTGTATATATCTTTTGTTTTTTGACCTTTTCTTCTCTATG
TTTTTCAGCCATACAAAATATGGGATTTTAGCAAGAGAAAAAGTACATCTAAAAAAG
TAGTAATAGGAGGAAGCCAAGATTGGTTGAAACACAGTTATAAACTCTTCAAGGCAATTA
TGAACAGGATTTTCGGATATGGGAACAAAAAGAGCCATGATCAGCTCTTACAAGAGTCA
ATCAGTCCATGAATCAGGCCCAACAATCACTATCGAACAGAATATCCCAGTTAGATACTC
AAATCGCCCAGTTAACTTCCAGCTGCAAAATATTCAAAAGAATTTGCAAAGATCAAAACA
ACAAGCAACCCCTCGTTAAGAAAACAGGCTTTGAAGATTTTAAATAAACGTAAACAGTTAG
AAAATATGAAGGATTCTTTAGATTCTCAATCCTGGTCCATGACGCAAGCCCAGTTAACAA
ATGATAACTTACAGAACACAATGATCACTATAAACGCCTAAAGCAAACAAACAATGCCA
TGAAGGCTCAATACGGCAAGATAAATATCGACAAACTACAGGACATGCAGGATGAGATGC
TGGATTTAATAGAACAAGGGGATGAGCTGCAAGAAGTCTTGGCAATGAATAATAACAGTG
GCGAGCTCGACGACATTAGTGATGCAGAGCTGGATGCAGAGCTGGATGCTCTGGCACAAG
AGGATTTCACTTTGCCAACCAGCGAAACTCATTAGGTAACGATATGCCCAGTTACTTAC
TAGGTGCGAATGCGCCACCGCTTTTATTGATGAAGAGCCAACTTAGATACTGAAGACA
AAAATAAAGCTTTAGAAAGCGCTCAGTGA

YDR486C, 262 aa (SEQ ID NO 66)

MGFLAREKVHLKKVVIGGSQDWLKHYSYKLFKAIMNRIFGYGNKKSHDQLLQESNQSMNQA
QQSLSNRISQLDTQIAQLNQLQNIQKNLQRSNNKQPSLRKQALKILNKRKQLENMKDSL
DSQSWSMTQAQLTNDNLQNTMITINALKQTNAMKAQYGKINIDKLQDMQDEMLDLIEQG
DELQEVLAMNNNSGELDDISDAELDAELDALAQEDFTLPTSENSLGNDMPSYLLGANAPP
AFIDEEPNLDTEDKNKALESAQ

YDR471W, 1295 bp, exon1: 501-531, intron1: 532-915, exon2:
916-1295 (SEQ ID NO 67)

GGCAAATCAATTAAAATTCCTTTTCTCTCTACCTTTTGCTAATATTA AAAAACCATAGTTGT
AAAGGGTACTTAATGCTATATTCTGTGTTAAGTTTCCTATTTTACCTTGTTTTTCCAATT
CTTACCAATTTGAAGACTATGTTTTTAAACACCCAATCATTTTCCACCCACACATATATT
ACCTTTTTTTTTGGGTGAAGAGAAGTAGTATTTTGTTTTTTCATGGGAGTGGAAGTCCTTTC
AAAATAATCCGAGCAGTAGTGCTGTCTAGGCGGAGATTATTGAAAGTCGGCATTGGCTG
CAGCTAGCGTTTTTGTTTTTGGTACTACCTGTCAAACCCGGCGTCTGCCTAGATTGCGCGG
AGGGTACGTTGAAACTTTTGCCTTTCCACGTCAGTTTATAATATCAAAAGCAGCAATATA
CACATTTAATGGTTTGCCCTTAGTGACTATTAGGGCGTTTTGGTGAAAAGAAAGAGTCGC
TCAAAGAAATCAATATAACCATGGCTAAATTTTTTGAAGCAGGTAAAGTTGGTACGTAAA
TTTAACAGAGCAAACGCTCTAATTAAGATATCGAATAAAAGGGGACTTTTCAAGGTGCATAA
GATGGGAAATTGTACAATCTGAGGGACAAACAATATGGAAAGCAGTACATGATTGTATTG
TCATTGTAGGAGGTACCAATTGTGCCAGTAAAAAGAGAGGGCCCGGGGAGCACCACATT
CACGACCAATCGTGTGATCTGCAAAAAAGGCACATGGAAAAATGTAATTTATCAGTGTTT
AACACTGAGTTGAACAGATAGCTATCTAATCAATGTTAACTTTCCAGGGAAACAAAAAGCT
AAATCCACTTCTCTTTTATTTCAAAATATCATTAGAAATAGAAAAATTTACTAACAAATT
TTCGTATTATCGTAGCTGTGCTGTTGCTGGTGGTACGCTGGTAAGAAGGTTGTGATCG
TTAAGCCACACGATGAGGGTTCTAAATCTCATCCATTCCGGTCACGCTTTGGTTGCCGGTA

FIG. 1 - 24

TTGAAAGGTACCCATCAAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTCGCTAAGAGAA
CTAAATCAAGCCATTCATCAAAGTCGTCAACTACAACCACTTATTGCCAACAGATACA
CCTTGATGTTGAAGCTTTCAGAGCGTTGTATCTACAGAGACTTTTGAACAACCATCCC
AACGTGAAGAAGCCAAGAAGGTTGTAAAGAAGGCATTTGAAGAAAGACATCAAGCTGGTA
AAAACCAATGGTTCTTCTCCAAGTTGAGATTCTAA

YDR471W, 136 aa (SEQ ID NO 68)

MAKFLKAGKVAVVVVRGRYAGKKVVIVKPHDEGSKSHPFHALVAGIERYPKSVTKKHGAK
KVAKRTRKIPFIKVVNYNHLLPTRYTLTDLVEAFKSVVSTETFEQPSQREEAKKVVKKAFEE
RHQAGKNQWFFSKLRF

YDR499W, 2744 bp, CDS: 501-2744 (SEQ ID NO 69)

TAACAATAGAAAAAATACACACACATTAGATTGGAATTAGAGCTTAAGTGGTACAACT
AGGGCTAATAAAGAGGTAACGGTTCGGTCTCTACTAAGGTTTCGTATTGTGTGGCACCAGT
GTTAAGCACTTTTAAAGCGAATAAAGTCGAGTGGAAATTTTATGTTTAGTTAGGTTTACC
TTGAATTTTTTAAAAAAGAGTCAGACAGGCTCGCTCTTCTACTAAATATTAGG
AGCAAAGCAGTAAAAAGTCTCTGAATAAGGATAGTAACCTGTAGTAAGTCCAAATTTAT
CTTACAAAGAGCTATTAGTATCTTGGTCTTCTATTTTCTTCGATTATTGGTGATTTC
CCGCTCTAGCCAAATCCGAGCGTTCATCGATTTTTTGGGGAAAACAGCACATGCAATA
AAATAAAAAGCAAACAAATACGCGATAGTGCACGAAACGTCAACACAATCATCAAACTCT
TTTGCATATTTCTATTATAGATGAGACGAGAAACGGTGGGTGAATTTCTTCAGATGACG
ATGATGATATTTCTTTTGAATTAGGCACCAAGGCTCCAAAGGTTTACTCAAATACCGCCAT
CATCAGCAGCATTACAAACACAAATTTCCCACTACTTTGGAGGTTACAACGACCACATTAA
ACAATAAACAGAGTAAAAATGATAACCAACTGGTTAACCAACTGAATAAAGCTCAAGGTG
AAGCAAGCATGCTTCGTGATAAAATAAACTTTTGAACATTGAAAGGGAAAAGGAAAAGA
ATATTCAAGCCGTCAAAGTTAATGAATTGCAAGTCAAGCATCTTCAAGAGTTGGCTAAAT
TAAAAACAAGATTACAGAACTGGAAGATGAGAAGAAGTTCTTACAGATGGAAGCGAGAG
GAAAATCGAAAAGGGAAGTTATTACGAATGTAAAACCAAGTCAACAACATTATCAACAA
ACACAAACACTATAACGCCAGATTTCGTCTCAGTTGCAATCGAAGCAAAACCTCAATCAC
CACAATCAAAAAACGTAAGATAAGTGATAATTTACTGAAAAAATATGGTTCCCCTAA
ACCCAAATAGGATTATTCCCAGTGAACGAGTTTATTTCTAGAGTCAATATTACTTCATC
AAATAATAGGCGCTGACCTGAGCACAATAGAAATATTAAATAGATTGAAGCTTGACTACA
TCACAGAGTTTAAATTTAAGAATTTTCGTATTGCTAAAGGAGCCCCCATAGGGAAGTCCA
TAGTTTCTCTACTTTTTCGATGTAAAAAGACGTTGACCCTCGACAGGTTTCATAGATCTT
TGCTAGAGGATATAGCTGTTTGTATCAAGGAAATATCAGTTTCATCCAAATGAATCGAAAT
TAGCTGTCCCATTTCTCGTTGCATTGATGTATCAGATTGTACAATTTTCGTCTAGTGCCA
CTCATAATTTAGCACTGAAGGATTGTTTTCTTTTATTTGCGATTTAATAAGAATCTATC
ATCATGTATTGAAAGTACCGATACATGAATCAAATATGAATTTGCATGTAGAACCTCAGA
TTTTCCAATATGAACTGATAGACTATTTGATAATTTTCGTATTCTTTGATCTCTAGAA
GTATATTAAGGGTACTGCAGTCGCATCCTAAGCAAACCTTATATGGAATTTTTTGATGAAA
ATATTCTAAAATCATTGAAATTTGTCTACAACTAGCACTAACCAATTTTCATACAAGCCAA
TGGTAAATGTAATATTTAGTGCAGTCGAGGTCGTTAATATTATCACTAGTATAATATTAA
ATATGGACAATTCCTCAGATCTGAAATCCTTGATAAGCGGTAGTTGGTGGAGAGATTGTA
TTACAAGATTATACGCTCTTTTGGAAAAGGAAATTAAGAGTGGCGACGTATATAATGAAA
ATGTGGATACTACAACCTCTTCATATGTGCAAGTACCATGACTTTTTTGGGTTAATCCGAA
ATATAGGTGATAATGAATTGGGAGGATTGATATCAAAGCTGATTTATACTGACCGATTGC
AAAGTGTCCCAAGGGTAATTTCTAAAGAGGATATTGGGATGGATAGCGACAAATTCAGT
CCCCATAATAGGTTACAAGATGGAAAAATGGCTTTTGAAGTTAAAAGATGAAGTTTTAA
ATATTTTGAATAATTTATTAATGATCTATGGAGACGATGCGACCATAGTAAATGGAGAAA
TGCTCATCCACTCCTCTAAATTCCTATCCAGGGAGCAAGCGTTAATGATAGAAAGGTACG
TGGGACAAGACTCCCCGAACCTTGGACCTCAGATGCCATCTTATTGAACATACTTTAACCA
TAATATATAGGCTATGGAAAGACCATTTCAAACAATTTGCGTGAAGAACAAATCAAGCAGG
TAGAAAGCCAATTGATTATGTCACTATGGAGGTTTCTCGTATGCCAAACCGAAACTGTGA
CAGCAAACGAAAGAGAAATGAGAGATCATGCACACCTTGTAGATAGTTTGCATGATCTGA
CGATAAAGGATCAAGCCTCTTATTACGAAGATGCCCTTTGAGGATTTACCAAGATATATCG
AAGAAGAATTGAAGATGCAATTGAATAAAAAGAACGGGGAGAATAATGCAAGTAAAGTACG
ATGAGAAATTTCAAGAAATGGCAAGAATATCTTGTAGTCAAAATCATTTCGATCTAACCA
CACTAGAGGAGGCCGATTATTATATATCTCAATGGGACTGTAA

FIG. 1 - 25

YDR499W, 747 aa (SEQ ID NO 70)
MRRETVGEFSSDDDDILLELGTTRPPRFQTQIPSSAALQTQIPTTLEVTTTTTLNNKQSKN
DNQLVNLQNKQAQGEASMLRDKINFLNIEREKEKNIQAVKVNELQVKHLOELAKLKQELQK
LEDEKFLQMEARGKSKREVITNVKPPSTLTSTNTNTITPDSSSVAIEAKPQSPQSKRK
ISDNLLKKNMVPLNPNRIIPDETSLFLESILLHQIIGADLSTIEILNRLKLDYITEFKFK
NFVIAKGAPIGKSIVSLLLRCKKTLTLDRFIDTLLEDIAVLKEISVHPNESKLAVPFLV
ALMYQIVQFRPSATHNLALKDCFLFICDLIRIYHHVLKVP IHESNMNLHVEPQIFQYELI
DYLIISYSFDLLEGILRVLQSHPKQTYMEFFDENILKSFEFVYKLALTI SYKPMVNVIFS
AVEVVNIITSIIILNMDNSDLKSLISGSWWRDCITRLYALLEKEIKSGDVYNENVDTTTL
HMSKYHDFGLIRNIGDNELGGLISKLIYTDRLQSVPRVISKEDIGMDSDKFTAPIIGYK
MEKWLLKLKDEVLNIFENLLMIYGGDATIVNGEMLIHSSKFLSREQALMIERYVGQDSPN
LDLRLKLTIEHTLTIIYRLWKDHFQQLREEQIKQVESQLIMSLWRFLVCQTETVTANEREM
RDHRHLVDSLHDLTIKDAQSYEDAFEDLPEYIEEELKMQLNKRTGRIMQVKYDEKFQEM
ARTILESXSFDLTTLEEADSLYISMGL

YDR507C, 3929 bp, CDS: 501-3929 (SEQ ID NO 71)
CTCTTTAAATATTCTATGTACTTTGTGCAAACATCATTGTGCATCACATAAATGCATTCCCT
ACTATTACTAAGTGAAGTTCACCTTCACTGGAAGAACTGGGTATTCAAGGTAAAGAAAT
CATTTGTTTTGCGCAAGTTTCGTCTGACAAGAAATTTTTTATTATTATTTCCCACTTTTC
ATCGAAGGAAACGCGTCAAATCCATTCTGTTACTACGCGCAATCTGCGTTATTTCCTTTTT
CGGCATACCATCGCGAAATATCAACGGCCACACCATAGATTCCTTTTGATGTTAAATTA
AAGCGACTGAATGAAGTGCACACATTTTTTATTCTTCTTGATTTTCTTTCTATTTTGT
TTTGCTTTCTCTTCTGTGCGACAACGTCTCAACTGTACTCACCATTAGTATTCTCGAAGGC
TTTAGCAGACTTGTGAATAATTAATTGCCACTTTGATCAAGAAAGATATTTCGCAGCACA
ATACAATAATAACATTCAAATGGCAATCAATGGTAACAGTATTCCTGCCATAAAGGATA
ATACCATCGGTCCATGGAACCTAGGTGAACTCTCGGTCTAGGGAGCACTGGTAAAGTCC
AGCTTGCTCGTAATGGATCCACAGGACAAGAGCGGAGTTAAGGTAATATCAAAAGCAG
TATTCAATACCGGTAATGTCAGCGGTACTTCGATTGTTGGCTCCACCACCCAGATGCTC
TACCATATGGTATAGAACGCGAAATAATCATTATGAAGTTGTTAAACCACCCAAATGTGT
TACGTTTATATGATGTCTGGGAAACAAATACAGATTTATACCTTGTTTTAGAAATACGCGG
AGAAAGGTGAGTTGTTCAACTTATTGGTTGAGAGAGGTCTCTGCCAGAGCATGAAGCTA
TCAGGTTTTTTAGACAAATTTATTATTGGTGTGTCGTACTGTGCATGCGTTGGGTATTGTCC
ATCGTGATCTAAACCGGAAATCTATTATTAGATCATAAATATAACATCAAGATTGCAG
ATTTTGGTATGGCTGCTTTGGAACTGAAAGGAAAGCTACTGGAGACGTCGTGCGGATCAC
CACATTATGCTGCACCAGAAATGTATCTGGTATACCGTATCAAGGTTTCGCAAGTGATG
TGTGGTCATGCGGTGTGATCCTATTGCGCCTTCTTACTGGTGGTTACCTTTGACGAGG
AAGATGGAAATATAAGAACACTATTACTTAAAGTTCAAAAAGGTGAGTTGCAAATGCCTT
CTGATGATGAAATTCGCGTGAAGCTCAGGATTTGATTAGAAAAATCTTAACCGTTGATC
CTGAAAGAAGAAATCAAGACCAGAGATATACTCAAACATCCGCTATTACAAAAATATCCAA
GTATAAGAGATTCTAAAGTATTAGAGGCTTACCAAGAGAAGACACATATCTCACGCCAT
TATCAGAAAGTAATCTTCTATTGACGCTACGATTTTGCAAAATTTAGTAATATTATGGC
ATGGAAGAGATCCTGAAGGAATTAAGGAAAACTAAGAGAACCCTGGCGCTAATGCAGAAA
AGACATTATATGCACTACTGTATAGATTTAAGTGTGACACTCAAAAAGAGCTTATTAAGC
AACAGCAAGTTAAGAAGAGGCGAGTCAATTAGTAGCGTTTCTGTTTCCCATCTAAAAAG
TATCGACAACCTCCACAACGCGAGAAGAAATAGAGAATCTTTAATTAGTGTAACATCTTCTC
GTAAAAAGCCAATATCCTTCAACAAATCTACTGCCCTCCAGTGCCTCCTCCAGCAATCTAA
CTACACCGGTTCTTCAAAACGCTTTCAAAAACTTCTCTTCAAGAAGAAATATCTA
CAATCGTTAACCAATCTTCTCCAACACCAGCATCACGTAATAAAAGAGCTTCGGTTATAA
ATGTGGAAAAGAATCAAAAAAGAGCCTCTATCTTTTCTACTACCAAGAAGAACAAAAGAT
CTTCTAGATCTATCAAGAGAATGTCATTGATACCAAGCATGAAACGTGAATCGGTGACAA
CAAAATTAATGTCAACATATGCGAAATTTGGCAGAGGATGACGATTGGGAATACATTGAGA
AGGAAACAAAGAGAACGAGCTCAAATTTTGCACTTTGATAGATGAAATTTTGGAGTACG
AAAAGTACGAACAAATAAGGAAAGAGAAGGAAGAGCTAGAACGTAAAGTGAGAGAAGCAA
AAGCACGTGAAGAGCTGGAACGTAGAAGACGTAAACAAGAAGAAAAAGAACGTGCAAGAA
AATTACTAGAAAAGGAAGATCTGAAAAGAAAACAGGAGGAACTCAAGAAGCAAATTGAAA
TTGATATAAGTGATCTAGAGCAAGAGCTGTCCAAACACAAAGAGGAAAAACTGGATGGTA
ATATTAGATCTATCTCTGCTCCTATGGAAAATGAAGAGAAAAATATCAATCATTGGAGG
TTGATATTGACAATATTCTCCGTCGCCGCACTTTTCTTTTACAACTAGACCTGTGTCAA

FIG. 1 - 26

GGCTTGATCCGGGTATAATGTTCTCCAGTCCAACTGAGGAAGTAAGTCCAGTGGAAACCAA
AGAGAACAGAAAATGAAAGACTTCAACAGAAAAGAAAATTTTAGAAACTATCAGAAGAT
CAAAATTCCTTGGGTTTCATCTTTAATATCGATAAAGAGTTGAAATTGTCATAAATGGAAT
ATCCAAGTATAATTGCACCACAAAGATTGTCAGAGGAGCGAGTGGTGTCTAGATTCTAATG
ATGGATATGAATCTTTGATCCTCCCGAAGGATGGGAATGGCGTATCTCAATTAAAGGATA
GTACCGCAACAACTGCTCCCGTCTCTGATGGTAGGTTGAGGAAGATCTCTGAAATTAGAG
TACCACAATTTTACTAGAAAATCAAGGCATTTTAGTGAGTCCAATAAAAAGGCTATCTGTCC
TGTCGATGTACTCTACCAAGGAGTCGTTTACCAACTTGGTTGATATTTTGAACAAACGGTA
ACCTTGATGTCAATAACCAACAAAGCCAAAGAATTCACACCAAGAAGTGGCGATGATT
CAGAATTTCTTTTGAACCTGTCAACGAAGAAGCTGAATATACAGGAAATAGTTCGAACG
ATGAGAGATTGTACGATGTCCGTGATTCCACTATCAAAGACAAATCCGCGTTAAAGCTGA
ACTTTGCAGATCGTTTAAATGGATCGAACGAAGCGAAACAACTGATACTTACATCTTC
CGATCCTTCCCTCCGCTTAATGGTGACAATGAATTGCGTAAACAGAATAGCCAAGAGGGTG
ACCAGGCACATCCAAAGATTAAATCGATGATACCAAGATCAGGCTCTTCTTCACATACTG
AAAAGGAAGAAGAAAATGAGGAAAAGGAAGAGAAAAGCCAGAACACACAAACAAGAAG
AGGATCAAGAAAAAGAGAGAAAGTAGTAGATGATATGGAGCCACCATTGAACAAATCTG
TGCAAAAAATTAGGGAAGAAAATGCTGGCTCGCAGGCAAAGGATCATTCAAAGATCACT
TAAAAGAGCATAAGCAGGATAAAAATACAGCAATTGGAAATGGTTCCTTCTTTAGAAAAT
TCTCAAATCTTTCGACAAAACAATGGAATTGTATGCCAAGATTTCTGCAAAACAATTGT
TTAATGGTTTGAAGAGCTGTTGCGTGGTTGGACTCAGTATGGTTTAAAAAATATAAAT
CGCACCCCAACAATCTGACCTTAACGGGTAAACTATCGAGTGATAATATTTCTCACTAC
GTTCAACACTCTTTGAGGTTAATATTTATCCGAGAGGTAAGATGAGCGTTGTGCAGTTCA
AGAAAGTTTCTGGTTTCAATCAAAGCTGTCAAAAAGTTGGTCAATGAAGTTGAGAACGTCC
TGAATAAGGAAGGCGTTCTACAAAATAG

YDR507C, 1142 aa (SEQ ID NO 72)

MAINGN SIPAIKDN TIGPWKLGETLGLGSTGKVQLARNGSTGQEA AVKVISKAVFNTGNV
SGTSIVGSTTPDALPYGIEREIIIMKLLNHPNVLRLYDVWETNTDLYLVLEYAEKGELFN
LLVERGPLPEHEAIRFFRQIIIGVSYCHALGIVHRDLKPENLLLDHKYNIKIADFGMAAL
ETEGKLLTSCGSPHYAAPEIVSGIPYQGFASDVWSCGVILFALLTGRLPFDEEDGNIRT
LLLKVQKGEFEMPSDDEISREAQDLIRKILTVDPERRIKTRDILKHPLQKYP SIRD SKS
IRGLPREDTYLTPLSESNSSIDATILQNLVILWHGRDPEGIKEKLREP GANA EKTLYALL
YRFKCDTQKELIKQQQVKRQSISSSVSVSPSKKVSTTPQRRRNRESLISVTS SRK KPI SF
NKFTASSASSNLTPGSSKRLSKNFSKKKLSTIVNQSSPTPASRNKRASVINVEKNQK
RASIFSTTKNKRSSRSIKRMSLIPSMKRESVTKLMSTYAKLAEDDDWEYIEKETKRTS
SNFATLIDEIFEYKEYEQIRKEKEELERKVREAKAREELERRRRKQEEKERARKLLEKED
LKRKQEEELKKQIEIDISDLEQELSKHKEEKLDGNIRSISAPMENEKNINHLEVDIDNIL
RRRNFSLQTRPVSRLDPGIMFSSPTEEVSPVEPKRTENERLTTEKKILETIRRSKFLGSS
FNIDKELKLSKMEYPSIIAPQRLSEERVVSDSNDGYESLILPKDGNVSQLKDSTATTAP
VSDGRLRKISEIRVPQFTRKSRHFSSENKRLSVLSMYSTKESFTNLVDILKNGNLDVNNQ
QSQRIPTRPSADDSEFLFETVNEEA EYTGNSNNDERLYDVGDSTIKDKSALKLNFA DRFN
GSNEAKQTDNLHLPILPPLNGDNELRKQNSQEGDQAHPKIKSMIPESGSSSHTEKEEENE
EKEEKKPEQHKQEEDQEKREKVDDMEPPLNKS VQKIREKNAGSQAKDHSKDHLKEHKQD
KNTAIGNGSFFRKFSKSSDKTMELYAKISAKQLFNGLEKLLRGWTQYGLKNIKSHPNNL T
LTGKLSSDNIFSLRSTLFEVNIYPRGKMSVVQFKKVS GSFKAVKKLVNEVENVLNKEGVL
QK

YDR515W, 1844 bp, CDS: 501-1844 (SEQ ID NO 73)

GAGTTGAATCTATGCGTAACCATTTTGACTACCGCTTCGTATGCTTTCTTGCACTTTGTG
GAGCTACTCATAACAATAGCTTATAATCTGTGTAGTCAAACATATACTAGGCAAATTACT
AGTAAATGCAGTATTCATATGTCCTCAAACCGTTTTTTGCACTATGTTATTGATCCATCG
AATCAAAATTTTTCACCGCCAAGAGAAAAAAGATCTTACTATTTTGTGCTTATGAAAAAA
TTAGTAAAAGTAAAGCTGGAAGCACATACAAGCGCAGCTGAATCACAAAGGAAAAATTGGC
ACATCCTTGGTTGACACTTGTCTATTTATTA AAAAGGTTTAAAAAGTAGTGTTCAGCAGT
TCTATCATATTTTATTTTAAAAAAAATACTGAGAGGAAGCGTATTGTTAAGACACAA
TTTAGGGTGGCGTTAAATAAACGAGAGAGCCCCAAAAATATAACCAAGATAAAGAAAATCA
ATCATAAAGTGAATTCAAAAATGTCATCGCAAACCTCAATGATAATCCAAAAAATACAT
CCTCAGCAGCTGAAGATAAGAAGAAACAACTTCATCCTTAAAGTTGGCACCAATACCAA

FIG. 1 - 27

CCACATCGCCATGGAAATCATCTTCGCCAGATAGCAATACAGTAATTCCTGTAGAGGAAC
TAAGAGATATATCAAAGACTGCAAAGCCAAGTAAAAATGGTTCGGGGTCAATTAAATTAA
CAAGCAATACCAAATGGACTCCAATTACGCCGTCTGTTATAATCTCAGGTTCAGGACA
CAAAATTCAAAGTCAGGAAAGAACTCTAAAAATCTAAGACTAATAAAAAAATGAAAAAGC
GTGGCAAATATAATAACGATATCAATAAAAAGGACTTTAACGGTCAAACCAACAGTACAT
CGGAAATAAGTAACGTTTCCAATCTTGAATCCAAACCTTTAGATGCTAACGCTAAAGTAA
ACATACATTCAAGCTCAGGAGCAACTGCCAATGGGAATATAAAGAGGATAACAAACAACA
ACAAATTCACCAACGGTAGACAATCAAGAAATTATCAAAACAGGAATGGCAAACAAGAT
ACAACAACAATAGTAGACACAGTCAGGCGGCTAATAATGCCATCTCCTTCCCAATAATT
ATCAGGCTAGACCTGAATATATTCCCAATGCCAGCCACTGGTTGAACAACAATTCAAGAA
ATAGCTATAAACAACCTGTCATACTTCCGTCAACAGCAGTATTATAATAACATCAACTATC
AACAACAATTGCAAAACACCATATTATTACTCAATGGAACCTATTTTTTAAATCTATCGAAA
GTATCAAAAACCAAATTGAATTCTATTTTAGTGAAGAGAACTTGAAAACAGATGAATTTT
TAAGATCTAAATTCAAAAAAGCCAATGACGGATTTATCCCATGAGTTTGATAGGGAAAT
TTTACCGTATGGTTAATTTATCTCTTGGTGGAGACCCAAATTTAATTTTGGCATCTATGA
GAGAAGTTTTTACAACATAAAGAAACAAACCATTTGGAAATTGCCCTTGGAAGCATAGAAG
GTGCTCAGAAGAACATGGCAGATGATTTCAATCCATTGGAAAACCTATTTTATTAGGCGCG
AAAATTGGGCTGAATACGCTATGGAAAGTAATTTTGATGAAAATGATGACGAAACTGAAA
AATACAACATTGAGAACTATTGGGACCGAACGATTTAGACAATTATTCTTATATGGGCT
ATCCAAACTTCTTTCCAGTAATGAAAAATGGGAAAAAGAGTCAGAGCTATGACCAAGGTG
AAATTAGCAGGCAGTTTGAACAAAACCTTACAAATAAATGATTAA

YDR515W, 447 aa (SEQ ID NO 74)

MSSQNLDNPNKNTSSAAEDKKKQTSLLKLAPIPTTSPWKSSSPDSNTVIPVEELRDISKT
AKPSKNGSGSIKLTSTNKTWPITPSVVISGSKDTSKSGKNSKNSKTNKKMKRGRKYND
INKKDFNGQTNSTSEISNVSNLESKPLDANAKVNIHSSSGATANGNIKRIITNNNNSTNGR
QSRNYQNRNGKTRYNNNSRHSQAANNAISFPNNYQARPEYIPNASHWLNNSRNSYKQLS
YFRQQQYNNINYYQQQLQTPYYYSMEPIFKSIESIKNQIEFYFSEENLKTDEFLRSKFKK
ANDGFIPMSLIGKFYRMVNLSLGGDPNLILASMREVLQHKETNHLEIALGSIEGAQKNMA
DDFNPLENYFIRRENWAEYAMESNFDENDDETEKYNIEKLLGPNLDLDNYSYMGYPNFFPS
NENGKKSQSYDQGEISRQFEQNLQIND

YDR518W, 2054 bp, CDS: 501-2054 (SEQ ID NO 75)

GCAGCAGGGGCAAGATGACAACCCTGTTCCCTGTTCCCTGTTCCAGTAGAATCTGAGACGGC
TTTTGTGCCATCAGCATTCACAGCACCACCGGTGCCAACAAGAAGAAATCAAAAAATAA
AAAGGGTACCCAGCCATTGGCAATGGATGACTATTTTAATGAAGGCAGAGATAAGTCATC
TACCGCTGCGAAGTCAGCAGAATCTGACATCCTCGCCCCACCACCACAAAAACAGTCATC
CTCTGATTAACCTTTCCTGGTTAGTCTTTTGGTTTTGTTTCATAGCAAAATTAATATATA
TATAAAGCTTGCTTTCCCTTCAAAACACGTAAACGATAGTTGGCAATGTACGAAAAGTA
CCGAGACTTTTTTTCAAAGGCACGCGTGCTCTTTTTTGTTAAGACAATAGATATTTTAGC
ATTCAGAAAGTTTCAATTTCCAAGACTTGACGTTTCAATTATATGGCAATCTCCCAACAA
GCACCCGCTCATATAATACCATGCAAGTGACCACAAGATTTATATCTGCGATAGTCTCGT
TTTGCTGTTTGTCTTCTTTCACGTTGGCTGAAAACAGCGCAAGAGCTACGCCGGGATCAG
ATTTACTCGTTCTAACAGAGAAGAAATTTAAATCATTTCATCGAATCTCATCCGTTAGTCC
TCGTCGAGTTTTTTGCTCCATGGTGTGTCATTCTCAGATCTTACGCCCTCACTTAGAAG
AGGCCGCCTCTATTTTAAAGGAGCATAACGTCCAGTTGTTCAAATTGATTGTGAGGCTA
ACAGTATGGTTTGCCTGCAACAACTATAAATACCTACCCAACCTTGAAAACTTTTAAAA
ATGGTCGTATTTTTGATGGTCAAGTCTATCGCGGTGTCAAGATCACCGATGAAATCACTC
AGTACATGATTTCAGCTATACGAGGCTTCTGTCAATTTATTTAAATTCCGAAGATGAAATCC
AACCATACTTGAAAAATGCAACTTTACCAGTAGTAATAAACAGAGGCTTGACAGGCTTGA
ATGAAACGTATCAAGAAGTCGCACTGGACCTTGCTGAGGATTACGTCTTTTATCCCTTC
TAGATTGAGAAGATAAGTCATTATCAATCCACTTGCCAAACACTACAGAACCAATTCTGT
TTGATGGAATGTAGACTCTTTGGTCGGAAATTCGTTGCTCTAACTCAGTGGTTAAAAAG
TGGAATTTTACCTTACTTTACCGACATCGAACCTGATCTCTTCCCCAAGTACATTTCTA
GCAATTTGCCGTTGGCTTACTTCTTTTATACTTCTGAGGAAGAATTGGAAGATTACACTG
ATCTTTTACGCAGTTAGGTAAGGAAAATCGTGGCCAAATAAATTTTATTGCATTAAACT
CTACAATGTTCCACACCACGTTAGATTCCATAAATATGAGAGAACAGTTCCCATTTATTG
CTATCCATAATATGATCAATAATCTGAAATATGGTTTACCACAACCTACCAGAAGAAGAGT

FIG. 1 - 28

ACGCGAAATTAGAAAAACCACAACCACTAGACAGAGATATGATCGTTCAGTTGGTAAAAAG
ATTACCGTGAAGGTACTGCCAAGCCAATTGTTAAGTCAGAAGAGATTCCAAAAGAACAAA
AGTCCAATGTTTATAAAATAGTTGGGAAGACACATGACGACATTGTTTCATGATGATGACA
AGGATGTCCTTGTCAAATATTACGCGACATGGTGTATTTCATAGTAAAAGGTTTGCGCCCTA
TTTACGAAGAAATTGCAAATGTCTTAGCATCTGATGAATCTGTTTCGCGATAAAATCTTGA
TCGCCGAAGTAGATTTCAGGGGCAAATGATATCTTAAGTTTCTCTGTGACAGGATATCCAA
CCATTGCTTTGTATCCTGCCGGAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAA
ATTTGGAAGATGTTTTCGAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGG
CAATTTATGATAAATTGCACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTAC
ATGATGAATTATAA

YDR518W, 517 aa (SEQ ID NO 76)

MQVTTTRFISAIVSFCLFASF TLAENSARATPGSDLLVLTEKKFKSFIESHPLVLVEFFAP
WCLHSQILRPHLEEAASILKEHNPVQIDCEANSMVCLQQTINTYPTLKIKNRIFDG
QVYRGVKITDEITQYMIQLYEASVIYLNSEDEIQPYLENATLPVVINRGLTGLNETYQEV
ALDLAEDYVFLSLDSEDKSLSIHLNPTTILFDGNVDSL VGNSVALTQWLKVVLVLPYF
TDIEPDLFPKYISSNLPLAYFFYTSEEELEDYTDLFTQLGKENRGQINFIALNSTMFPHH
VRFLNMREQFLFAIHNMINNLKYGLPQLPEEEYAKLEKQPLDRDMIVQLVKDYREGTA
KPIVKSEEIPKEQKSNVYKIVGKTHDDIVHDDDKDVLVKYYATWC IHSKRFAPIYEEIAN
VLASDESVRDKILIAEVDSGANDILSFPVTGYPTIALYPAGNNSKPIIFNKIRNLEDVFE
FIKESGTHHIDGQAIYDKLHQAKDSEVSTEDTVHDEL

YDR519W, 908 bp, CDS: 501-908 (SEQ ID NO 77)

GGGGCAAATGATATCTTAAGTTTCTCTGTGACAGGATATCCAACCATGCTTTGTATCCT
GCCGGAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAAATTTGGAAGATGTTTTTC
GAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGGCAATTTATGATAAATTG
CACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTACATGATGAATTATAATCA
ATAAATAAGCATATATAATGCACATTTTAAACATCTGATTACTCGCATCGTTTCTGGAA
GAAATAGCTAATATTTCGTTATTTATGGCATCACGATTATTCTCACCAGTTACCCGTTTA
TGCTCTTGAAGAGATTTAGCATTACTGCCAGCGCATCTTCAAATACAGGTTTATATGAGA
CCCATTACTATAACCCTAAGAAGAGAAAAAGGAGTGCTTTTCGTTTCAATCACATTCTAG
TTTACAGTAATTGAGTCTCGATGATGTTAATATTTACCTTTTCGTCACTTTTTTTTCCA
CCATTCTTGCAGGTTCCCTGTCAGATTGGAAATCGGTATTATCAAGAGAATACCGGTAG
AAGATTGCTTAATTAAGGCAATGCCAGGTGATAAAGTTAAGGTTCAATTATACAGGATCTT
TATTAGAATCGGGAAGTGTATTTGACTCAAGTTATTCAAGAGGCTCTCCTATCGCTTTTG
AACTTGGCGTTGGCAGAGTAATTAAGGTTGGGATCAAGGTGTTGCCGGCATGTGCGTTG
GCGAAAAAAGAAAGCTGCAAATTCAGTTCTTTGGCCTACGGAGAAAGAGGTGTCCAG
GCGTCATTCTCCAAGTGCTGATTTGGTGTGTTGATGTCAATTGGTAGACGTGAAATCAG
CCGCCTAG

YDR519W, 136 aa (SEQ ID NO 78)

MMFNIYLFVTFSTILAGSLSDLEIGI IKRIPVEDCLIKAMPGDKVKVHYTGSLLES GTV
FDSSYSRGSPIAFELGVGRVIKGDQGVAGMCVGEKRKLQIPSSLAYGERGVPGVIPPSA
DLVFDVELVDVKSAA

YER102W, 1103 bp, CDS: 501-1103 (SEQ ID NO 79)

CGAGCTTGCCAGCATTCCAATGCCCATCGTATTGTACTCAATGGTGAAACTTACCACCAT
ATTGTTAAAAGCTATTATTTATGATTTTTACTTACCAAACATTGAAAGGAGACTGAACAC
ACCACGATAAAACGTATGTTCTGATACCCAGCAAATGAGAAAGTAGAAGGAGAAACCTAA
AAACCTGTGGCGGTCAAGACTGCTAGCAAGATGGATATTTAGATCATAAATTTCTAACGCA
TGCATCCTGAGCAATGAAATCATGCAACCTAACATTTGAGGTTAATATATGAGAATTAAC
TAGCGTTGAGGAGGTACTGCAATTTAAAAGACCGAAGAATTATCGATGCAAGGAAAAATG
GGTCTAGGATGAATACGAGCAATTGAAATACATTTGGAATACCTTGTGAAAATATCACAT
ACTTTCGCCTTCTATCTCGATGCGTTATTACAAGAAAATAGTTTACTAACAAATTAACA
AAAATTAAAATAGTGTA AAAATGGGTATTTCTCGTGATTCTCGTCACAAAAGATCAGCCA
CTGGTGCTAAACGTGCTCAATTCAGAAAGAGAGAAAGTTTGAATTAGGTCGTCAACCAG
CCAACACAAAAATTGGTGCTAAGAGAATCCACTCTGTCAAGACTAGAGGTGGTAACAAGA
AATACAGAGCTCTAAGAATTGAAACCGGTAACTTTTCTTGGGCTTCTGAAGGTATCTCCA

FIG. 1 - 29

AGAAGACCAGAATTGCTGGTGGTGTGTTTACCATCCATCCAACAATGAATTGGTTAGAACTA
ACACTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTCAGACAATGGTTCG
AAGCTCACTACGGTCAAACCTTGGGTAAGAAGAAGAACGTC AAGGAAGAAGAACTGTTG
CCAAGAGCAAGAACGCTGAAAGAAAGTGGGCTGCTAGAGCTGCTTCTGCCAAGATCGAAT
CTTCCGTTGAATCTCAATTACAGCGCCGGTAGATTATACGCTTGTATCTCTTCCAGACCAG
GTCAATCCGGTAGATGTGATGGTTACATCTTGAAGGTGAAGAATTAGCTTTCTACCTAA
GAAGATTGACTGCTAAGAAATAG

YER102W, 200 aa (SEQ ID NO 80)

MGISRDSRHKRSATGAKRAQFRKKRFELGRQPANTKIGAKRIHSVRTRGGNKKYRALRI
ETGNFSWASEGISKKTRIAGVVYHPSNNELVRTNTLTKAAIVQIDATPFRQWFEAHYQG
LGKKKNVKEEETVAKSKNAERKWAARAASAKIESSVESQFSAGRLYACISSRPGQSGRCD
GYILEGEELAFYLRRLTAKK

YER153C, 1265 bp, CDS: 501-1265 (SEQ ID NO 81)

ACCCTATATGGGAGGACAACCTCGCCCACTGTTTGGGTCGTGTTAGCGATAAGGTCCGAAG
TAGAAGCGGAAAGAGAAGGAGCTGAAGAGGTTAATTCATCGATGGAAGGCAACTGGGT
GGATTTCCGAGACATCGTTGGCATTTGGGCCCCGTCGAATTAATCTTTTGGCCTGAAAAG
AGATCCATGACGGATGGGGCCGGGCAATACTATGGTTCGAGCGGTGGCCAGTCTGGAAG
AGGCAGCAAACCTTGACGTGACGAGTCGAGAGGTGAGTTTGAACATCGTCGGGGAGGTTA
TTCTGTGGCTCCGCTTGTACGTGAACAGATACGTATAGAGGGCGAGCCACTGGTTAAATT
TTTCATGGCTCGGATTACTTCCGTACTGCTGGCTAAAATCGAAATCTCGGCCTGCTGAGA
GTGTTTTGAGCAATCAAGGGAACATCTGAACGTGGAAGAGCAGACGAGGCATTAGCTCGA
ACATAAGAACCGGAACACGTCATGTTGACTATCACGAAAAGACTGGTGACCACCGATGTGC
GGTCGCGAATACTGTTAAGCAGTTTAAACGGGAAAATGTCCGATGCACTGGCGCTGCTGC
GTACGACGACGAGACGCGTGGATGTGGAGCTGCTGCACACGATGCTAGCGCGAGCCG
CTGCGCTTGCCCATGCCGACACTATAGCATACTGTGGTATCAGCATGTGATGCCACGCC
GGTTGCCAGTAGAGGGCCGCTGCTATGTGAATGGCTGGCGTAGCATTTGTACCAGGACA
GGCTCTTCTTACCCGCGCAGTTCCTCCAGCACTACCAGGCGATGAATCGCGATCGTCGCA
CCAGCCCAGAAAGATGAACTGATTGAGTATGAGCTTAGACGGATTAAAGTCGAAGCGTTTG
CGCGTGGCACAATGCACTCCACGGCGCTCAGGGAAAAGTGAAGGTATTCCTGAGGAGA
TGGATACGCTACCAGGGCAGCCGCCATTAAGGCTGCGGACTTCCCGCAAATGACCAAGG
CTATGGGCATAGCATTGATGCAGCAAGATGGAGCAAGCAGCTGCCCTGGCGTTGTTTGGAC
GACAGCCCCTAGTGATAAAGAACGAATGGTCACTACCGCTACTACTGGCTGGTGTCTTT
GGCATGTTCCCGGCCAGCGCAGGCGGACGTGTGCTGGCGGAGTTCCGTCAAAGTTATC
GCGGGCTGCCGCTGCTGGATGCCGAAC TAGTGATAAAGAGAAGAGGATTTGAAATCAACA
CATAA

YER153C, 254 aa (SEQ ID NO 82)

MLTITKRLVTTDVRSRILLSSLNGKMSDALALLRQQOOTSVDVELLHTMLARAAALAHAD
TIAYMWYQHVMPPRLPVEGRLLCEMAGVALYQDRLFLPAQFLQHYQAMNRDRRTSPEDEL
IEYELRRIKVEAFARGTMHSTALREKWKVFLQEMDTLPGQPPLRLRDFPQMTKAMGIALM
QQDEQAAALALFGRQPLVIKNEWSLPLLLAGVLWHVPQAPARRVLAEFRQSYRGLPLLD
AELVIKRRGFEINT

YFL014W, 830 bp, CDS: 501-830 (SEQ ID NO 83)

GGACTAGAAGCCAAAAGCCAGAGCGGTAAAAATAGCAAGACTAGAATATTGCTGGCATC
TGTTAAGGGGATATGTTGCAACTTGCAGGGGGCGGCACAAAATAACATAGAAACGTAGTA
AAGAGGGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAAACCATTGACGTAGAAAT
TGAAAGAAGGAAAAGGTATACGCAAGCATTAATACAACCCACAAACACAGACCAGAAAGCAC
TCTAGACGGAGAGTAAGTAGATCTACAGCCCCTGGAAAATCGTTTGGTCAACTTTGAGGT
TCCGGTCGTCCTCCCTCTTGATCTGAAAGGCTTTTCTCTAAATCTATATTTAAACGTATAA
ATAGGACGGTGAATTGCGTTCTACTTCTCTCAATTGCGTTTGATCTTATTTAATCTCTCTC
TAATATATAGAAAAAAAACCATCTGATTATTTCGATAATCTCAAACAAACAACTCAAAAC
AAAAAAACTAAATACAACAATGTCTGACGCAGGTAGAAAAGGATTCGGTGAAAAAGCTT
CTGAAGCTTTGAAGCCAGACTCTCAAAGTCATACGCTGAACAAGGTAAGGAATACATCA
CTGACAAGGCCGACAAGGTGCGTGGTAAGGTTCAACCAGAAGACAACAAGGGTGTCTTCC

FIG. 1 - 30

AAGGTGTCCACGACTCTGCCGAAAAAGGCAAGGATAACGCTGAAGGTCAAGGTGAATCTT
TGGCAGACCAAGCTAGAGATTACATGGGAGCCGCCAAGTCCAAGTTGAACGATGCCGTGC
AATATGTTTTCCGGTCGTGTCCACGGTGAAGAAGACCCAACCAAGAAGTAA

YFL014W, 109 aa (SEQ ID NO 84)

MSDAGRKGFGKASEALKPDSQKSYAEQKEYITDKADKVAGKVQPEDNKGVFQGVHDSA
EKGKDNAEQGESLADQARDYMGAAKSKLNDAVEYVSGRVHGEEDPTKK

YFL015C, 995 bp, CDS: 501-995 (SEQ ID NO 85)

GACCTTCAGCGTTATCCTTGCCTTTTTTCGGCAGAGTCGTGGACACCTTGGAAAGACACCCT
TGTTGTCTTCTGGTTGAACCTTACCAGCGACCTTGTTCGGCTTGTTCAGTGATGATTTCCT
TACCTTGTTTCAGCGTATGACTTTTGAGAGTCTGGCTTCAAAGCTTCAGAAGCTTTTTTCAC
CGAATCCTTTTTCTACCTGCGTCAGACATTGTTGTATTTAGTTTTTTTTTGTGTTTGTGAGTTGT
TTGTTTGTGAGATTATCGAATAATCAGATGGTTTTTTTTTCTATATATTAGAGAGAGATTAA
ATAAGATCAAACGCAATTGAGGAAGTAGAACGCAATTCACCGTCCTATTTATACGTTTTTA
ATATAGATTTAGAGAAAGACCTTTCAGATCAAGAGGGGGACGACCGGAACCTCAAAGTTG
ACCAAACGATTTTCCAGGGGCTGTAGATCTAGTTACTCTCCGTCTAGAGTGCTTCTGGTC
TGTGTTTGTGGGTTGTATTAATGCTTGGCTATACCTTTCCTTCTTTCAATTTCTACGTCA
ATGGGTTTTTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
ATGTTATTTTTGTGCCGCCCCCTGCAAGTTGCAACATATCCCCTTAACAGATGCCAGCAAT
ATTCAGTCTTGCTATTTTTACCGCCTCTGGCTTTTGGCTTCTAGTCCTTGTCCTCAAGAG
CCAAGGGCCCGTCAACACGTCGTCATTGCTACCGCCAGCTGGCACCCACACATCACCGAC
CCTTTTTTTTCCATTTTCGGCTGGGCCGTTAGTGGGATCCGCCCGCTCCCGGAGATTTTCA
CTTGGATTGTGCGCGTCCCCCTTTTTTTTCTTCTTCTGACTCCCCCTACCTTCTCCCACT
TTTCTGTGTATCAAGAGGAAAAGAAGGAGAAAAAGGAGAACTCCGAAAAATACCGAACAAG
AGGGTAACAGAATGTGCATTTGGATGAGCGGGTAA

YFL015C, 164 aa (SEQ ID NO 86)

MLAYTFPSFNFYVNGFFSFLFLFLFLFPSLLRFYVILCRPLQVATYPLNRCQQYSSLAIF
TASGFWLLVLVPRAKGPFSTRRHCRYQLAPTHHRPFPSIFGWAVSGIRPLPEIFTWICASP
FFLHSLTPPTFSHFVYQEEKKEKRRTPKNTEQEGNRMCIWMSG

YFR022W, 2702 bp, CDS: 501-2702 (SEQ ID NO 87)

CTGCCCTCCGTACGTCAACGCATACACAATATAGTTTATATAAACTCCTGCGTATAAT
CTATCCTTTTGCATAATATTTTCGTCACCATTATCTTGTGCGGTGTTTTATTTAAAC
AATAGAACTCGCCTAAAGGGGAAATTTTCGATATAAAAATTCAAAAAAATGGCTTTTCATG
GATCGAGTATTTGTTTGTGCGAAAAAGGATCACTGGAGTGACGTTACTACGCTACGAAGCC
TCCTTCCGGCTTAGCCCTGTTGATTACGAATTTGGATCAGTTGGTATTTGATTCTCTCGGA
AGAGTTAACTTCACGCGGGTAAATCACTTGTGATGCGGTATATTCTCTATACGGCTAATA
GATGAATCAGGGTGTTTTAAAGTGCGTATAAACCCCTTTTGCTATTTTCGTTTATATAATT
GGCGTTGATAAAGAGCCAATATCTATTGTTGCTACATAGAGGCAGCTCTCTTAGCAAAAT
AAAAATACAAAAGTTTCGACATGGGCTTCAGTAGCGGTAAATCAACTAAGAAAAAGCCTC
TGCTTTTTCGATATCAGACTTAAAAATGTTGACAACGATGTAATACTCCTCAAAGGTCTC
CAAACGAGGCCCTCGGTGCTTTTATCTGGTTGCATCGTTTTTATCGATTAAACGAACCCA
TGCAGATCAAAAGCATATCATTGAGACTTTATGGGAAGATACAAATAGACGTACCATTAG
AGAGGCCCCAGGACGCTAGTTCTTCGTCGTTGTCTTCATCGCCGCCAAAGATCAGAAAGT
ACAACAAAGTTTTTTATAATTACGCATGGGATAATGTTAACCTCAAGGAGTATCTGAGTG
GTTTAAAGAGGGCAATCTGGCCTTGCGGGCAGTAGCTCATCAAGTAATATCTTGGGCACTC
GCCAAAGAGCTCAGTCCACAAGTTCTTGAAGCTTTTAAAGGGGTCTCTCACCCCTCTT
CATGTACTTTAGATAAGGGCAACTACGATTTTCCCTTTAGTGCTATTTTGGCTGGTTTCGT
TACCAGAGAGCGTAGAATCTTTGCCAAATTGCTTCGTGACATATAGCATGGAATCCGTTA
TTGAACGCAGCAAAAATTATAGTGATTTGATCTGTAGGAAAAATATTAGAGTTCTGAGAA
CCATTTACCCCGCAGCAGTGGAGTTATCAGAAACTGTTTGTGTAGATAACTCATGGCCCG
ACAAAGTGGATTATTCTATTTTCAGTACCCAACAAAGCCGTAGCTATTGGTTTCAGCCACCC
CTATAAATATTTCCATTGTACCTCTTTCGAAAGGTTTGAAATTGGGCTCAATCAAAGTCG
TATTATTGTGAAATTATCAATATTGTGACCCCTTCCCTCCAGTAATTTCTGAAAAATAGGC
AAGTGACAGAACTAAATCTTGAAGATCCCTTGAACGAGTCATCTGGAGAATTTAATGGTA
ATGGTTGCTTTGTAAATAACCCCTTTTTTTCAGCCTGATCATTCAATCCAAGACAAGTGGG

FIG. 1 - 31

AGATTGATACCATCCTGCAAATCCCGAACAGCTTATCAAACCTGTGTGCAAGATTGTGATG
TCCGCTCTAACATTAAGGTTTCGCCATAAGCTCAAATTTTTCATCATCCTAATTAACCCAG
ATGGTCATAAATCTGAGTTAAGAGCGTCCTTACCGATTCAACTTTTTTATTTACCATTTG
TGGCACTTTCAATAAAACCATTTGTCATCCTCGAATTTGTATTTCGCTTTTTTAGCACCCTA
ACCAGAAAGACGAAACTCATCACAAGAAGAGGAAGAGGAATATCTGTTTTCTAGATCAG
CATCAGTCACAGGGTTGGAATTATTAGCGGATATGCGTAGCGGTGGCTCTGTTCTTACCA
TTTCAGACTTGATGACGCCCCCAAATTATGAAATGCACGTATATGATCGTCTTTATAGCG
GTTCTTTCACTCGCACGGCTGTGGAACGCTCTGGAACATGTACTCCTTTGGGAAGCGAAT
GTTGACTGTGAGGATCAGCAACAGGATTTAGAAGATTTACGTATACGGTTGACAAAAA
TTAGAAATCAACGTGACAATCTAGGGCTACCACCGTCTGCCTCGTCTGCTGCCGCTTCCA
GATCGCTATCTCCATTACTAAACGTTCCAGCACAGGATGGCAGGAGAGAAATCTTAC
CTCAGAGTGCTCTTGGTCCCAATAGTGGCTCTGTGCCAGGAGTACATAGTAACGTATCAC
CTGTTTTACTTTCAAGATCCCCAGCCCCAAGCGTGTGAGCCCATGAAGTGTTACCAAGTGC
CCTCGGGCTTAAATTATCCAGAGACTCAAACCTGAACAAGGTTCCATCGTATGGCAAGG
CAATGAAATATGATATCATTTGGTGAGGACCTTCCTCCTTCTACCCTTGTGCGATACAAA
ATGTGCAACCAAGAAAACCCAGTAGGGTACATTCAGGAACTCTTCGACAACATTTGTCAT
CTTCTATACCAACTAGCTTTTCATTCCTCTAGTTTTATGAGTAGCACTGCTTCCCCTATTT
CCATAATATGGCTCTAGAAGTAGTTCTAGTGGGGTATCTCTTAATACACTAATGAGT
TAACTTCGAAAACCTTCGAATAACCCATCCAGTAATAGTATGAAAAGGTCACCAACAAGAC
GGAGGGCTACTTCTTTAGCTGGGTTTATGGGAGGTTTTCTATCAAAGGGTAACAAACGAT
AG

YFR022W, 733 aa (SEQ ID NO 88)

MGFSSGKSTKKKPLLFDIRLKNVDNDVILLKGPPNEAPSVLLSGCIVLSINEPMQIKSIS
LRLYGKIQIDVPLERPQDASSSSLSPPKIRKYNKVFNYNWADNVNLKEYLSGLRGQS
LAGSSSSSNILGTRQRAQSTSSSLKSLKGSSSPSSCTLDKGNDFPFSAILPGSLPESVES
LPNCFVTYSMESVIERSKNYSDLICRKNIRVLRITISPAAVELSETVCVDNSWPKVDYSI
SVPNKAVAIGSATPINISIVPLSKGLKLSIKVVLFFENYQYCDFFPPVISENRQVTELNL
EDPLNESSGEFNGNGCFVNNPFFQPDHSPQDKWEIDTILQIPNSLSNCVQDCDVRNLIK
RHKLKFFIILINPDGHKSELRLPIQLFISPFVALSIKPLSSSNLYSLFSTTNQKDENS
SQEEEEYYLFSRSASVTGLELLADMRSRSGSVPTISDLMTPPNYEMHVDRLYSGSFTRTA
VETSGTCTPLGSECTVEDQQDLEDLRIRLTKIRNQRDNLGLPPSASSAAASRSLSPLL
NVPAPEDGTERILPQSALGPNSGSVPGVHSNVSPLLSRSPAPSVSAHEVLPVPSGLNYP
ETQNLNKVPSYGKAMKYDIIGEDLPPSYPCAIONVQPRKPSRVHSRNSSTLSSSIPTSF
HSSSFMSSTASPIIINGSRSSSSGVSLNTLNELTSKTSNNPSSNSMKRSPTRRRATSLA
GFMGGFLSKGNKR

YGL011C, 1259 bp, CDS: 501-1259 (SEQ ID NO 89)

AGACAATAAAATATGGAAAATAAAACGCTTAGCACAGCAGTCAATGAAATACTCTGATAT
ATTTTGACTCTGTGGAGCATACAGCTACCACTAAATAGGATTGTGGGGACAAATATGGAA
TGGATCAAAACGTTCTTAGGATTGTGGTGGTAAACTTGTAATCCAAAGCTGAGATCTT
AAATCCAGCAAACCTTCGCCCATATTTATCTTTTATAACAGAAGAAGAGACTATATTCT
CAAAACCTCGTATATTTATATACATATCCTCCAAACAACTCCCAAGTTTCACTTTCTTG
GATTTACCTTGGCATTCTTTTCCCCATCCTCTTATAATGGTAATCGCGATCCTTAATTA
TGATATCACAAATAGACGAAGGGCACACACCAATTTGCCACCGTAAGGATAGAGTAAGTTA
AATGGCTAACTCATTATAATCTTCATGCTAAATCATATAAGGGCAGAGACGAAGCAAAGC
GAAAAAACATATTACAATCATGTGCGGGTCTGCTGCTGCATCTGCTGCTGGTTATGACA
GGCACATCACTATCTTTTCCCCGAGGGTCTGTTTATATCAAGTAGAATATGCCTTTAAAG
CGACTAATCAAACATAAACTCACTAGCGGTCAGAGGTAAAGATTGTACAGTGGTGA
TAAGTCAGAAAAAGGTCCCTGATAAACTGTTGGATCCAACTACTGTTTCGTATATTTTTT
GTATTTCAAGAACAAATTGGTATGGTAGTGAACGGACCAATACCGGATGCAAGAAATGCGG
CCCTAAGAGCCAAGGCTGAGGCTGCAGAAATCCGTTATAAATATGGTTATGATATGCCAT
GCGATGTATTGGCTAAGAGAAATGGCTAACCTTTCCCAAATCTATACTCAAAGAGCATATA
TGAGACCATTAGGTGTTATACTCACATTTGTTTCGGTAGATGAAGAATTGGGTCCCTCCA
TTTACAAAACCTGACCCTGCAGGTTATTACGTTGGCTACAAAGCTACTGCGACAGGACCAA
AACAAACAGGAGATCAACAACAACTTAGAAAACCATTTCAAAAAGAGTAAATCGACCATA

FIG. 1 - 32

TTAATGAAGAATCATGGGAGAAGGTGGTAGAATTTGCTATTACTCATATGATTGACGCAC
TGGGTACCGAATTTTCAAAGAATGACTTGGAGTCGGTGTGCTACAAAGGACAAATTC
TTACCTTGAGTGCTGAGAACATCGAAGAAAGGCTAGTAGCAATTGCTGAACAAGATTAA

YGL011C, 252 aa (SEQ ID NO 90)

MSGAAAAAAGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDCTVVVISQKKVP
DKLLDPTTVSYIFCISRTIGMVVNGPIPDARNAALRAKAEAAEFYKYGYDMPCDVLAKR
MANLSQIYTQRAYMRPLGVILTFVSVDEELGPSIYKTDPAGYVVGKATATGPKQOEITT
NLENHFKKSKIDHINEESWEKVVEFAITHMIDALGTEFSKNDLEVG VATKDKFFTLAEN
IEERLVAIAEQD

YGL031C, 968 bp, CDS: 501-968 (SEQ ID NO 91)

CCAAGTTAAGCAAGACACCAAGACAATAACTTGAGAGGTATGTCCCTATATGATGATGAT
TCATAATTAATGGCGACCGAGGGCAGCGTTGTGCTAGAAAGCAATGTATTAATATATGAG
AGAGCTTCAGATAGCCAATACACCGGAATTTAGACTTTGACAGGATTGTGGCTTGTTC
GTATAACTTATAATATATGTCAACCTTTGAGCAGGAAACCCAATGAAAATGCTTCATTAC
ATATATACGATATGGAGAAGCATGAAAAATAACAGCGTGAGATGTTATCCATGTTGCAAG
AACCTAGTAAAATGAATCTGAATTTGCAAAAAGTCCATATTTCCACGTTCTCCTCTTCC
TACAATTTTGCGAACGCCTGAACAACCATGCGGATTACCATTATTTATATTGACAAGATG
GCTACCTATGAAAAGCATAGACTTACTAACATTTTCTTTTCAAATATGTTTGAAAAACG
TGGATTAATATAGTGATAAAATGAAGGTTGAAATCGATTCTTTTTCAGGTGCCAAAATCT
ACCCAGGCAGAGGTACCTTGTGTTGTCGGTGGTACTCCAAAATCTTCAGATTCCAAA
CTCAAATCTGCCTCTTTTGTCAAGCAAAGAAAGAACCCAAGAAGAATCGCTTGGACTGTCT
TATTCAGAAAGCATCACAAGAAGGGTATCACCGAAGAGTTGCTAAGAAGAGATCTAGAA
AAACCGTTAAGGCCCAAAGACCAATTACCGGTGCTTCTTTGGACTTGATCAAGGAAAGAA
GATCTTTGAAGCCAGAAGTTAGAAAGGCTAACAGAGAAGAAAAATTGAAGGCCAACAAAG
AAAAGAAGAAAGGCTGAAAAGGCTGTAGAAAGGCTGAAAAGGCTAAGTCTGCTGGTACTC
AAAGTTCTAAGTTCTCCAAGCAACAAGCTAAGGGTGCTTTCCAAAAGGTTGCTGCTACTT
CTCGTTAA

YGL031C, 155 aa (SEQ ID NO 92)

MKVEIDSFSGAKIYPGRGTLFVRGDSKIFRFQNSKSASLQKQKRNPRRIAWTVLFRKHHK
KGITEEVAKKRSRKTVKAQRPI TGASLDLIKERRSLKPEVRKANREEKLKANKEKKKAEK
AARKAEKAKSAGTQSSKFSKQQAQKGAQKVAATSR

YGL032C, 764 bp, CDS: 501-764 (SEQ ID NO 93)

CTCCCATATTTTATTACAGGCTAGACAATGGTAATGGTGCTTTAGATGATTTTCAGT
GGATTACATTCGCACAATAGAATAAATGACTAATTTCAAGAATTTGTTTCAACCTGCCG
GCATTTCAGTTATTATAAGTTATTGTTTGTAGTGGTAAACTTCGCCATCACCGGTGCTGCG
TTTATTGCAAAATTACTGAAACCATGTAATTTCCGAATACGGTAATTACACGCAGTTTGA
AATTTGACATGCAAGTTTAACAAAAAACTTCTGTCCGCATCTAAAGCTTAATTAAGGGA
CTGTTTCATACCTTCAGATCCAATATACTGAATATCAGGCAATTGATTTCCCTTGTAAT
ATACAATATAAATAGTTGTAAGAAGAGGTGATATGTTAAGTTTCCATTTTGACGTATTC
TCATTCTAGAATGATTGTAAGCTCTCAACAGTCACTTGTGTGCCAAAATATTATACCTAC
TTCATACATTTTCAATTAAGATGCAGTTACTTCGCTGTTTTCATATTTTCTGTTATTG
CTTCAGTTTTCAGCACAGGAAGTGAACAATATATGCGAGCAAATCCCCTCACCAACTTTAG
AATCGACGCCGTACTCTTTGTCAACGACTACTATTTTGGCCAACGGGAAGGCAATGCAAG
GAGTTTTTGAATATTACAAATCAGTAACGTTTGTGCTAGTAATTGCGGTTCTCACCCCTCAA
CAACTAGCAAAGGCAGCCCCATAAACACACAGTATGTTTTTTGA

YGL032C, 87 aa (SEQ ID NO 94)

MQLLRCSIFSIVASVLAQELTTICEQIPSPLESTPYSLSSTTTILANGKAMQGVFEYYK
SVTFVSNCGSHPTTSKGSPI NTQYVF

YGL043W, 1430 bp, CDS: 501-1430 (SEQ ID NO 95)

TCGGGATGGTGGGTGTTCTGTACCCCGCATTCACACCGCTCTGCCTATTCATTTTATC
GTTTTCTGCTTTTCTTCAATGTATTGATAAATAACGTGCTATGTGATGCTATTGGTAT
ATAGCCTTTCTGTATATCCCTCTAACAATTATTACAAGTGTTTCTGTTTAAAGCAAGTG

FIG. 1 - 33

CTAGAAGTGACTCGGTTCTCTTAGGAAATTCTAAACGCAAGATTTCTCTTATGGTGATTG
TAACAATTATGAGATACTTCACTAGCCACCTTAACCTTACGGACCTTCTTTTGAAACGA
TGCTTCGAATGACAACGCCTTTTTGATATATAATATCCAATTTTATTATAGGGAAATTTT
CAACTCTTACCCGCCCACTGTGCTGATATGACCAAGTGATCACTCGATGATGGGACTAC
GTATTGAAAAATATTGAATGAAAAATTACTCAAGCAGCAGAACATTACAGTGTAGTCAG
TCCGCATAAGAGCATTTCATCATGGATAGTAAGGAAGTACTGGTACATGTTAAGAATCTAG
AAAAGAACAAAAGTAATGATGCTGCAGTTCTAGAAATCTTACATGTCTTGGATAAAGAAT
TCGTCCCCACTGAAAAGTTACTGAGAGAAACAAAAGTTGGTGTGGAAGTCAACAAGTTTA
AAAAATCCACTAATGTAGAGATCAGCAAACCTCGTGAAGAAAATGATTAGCTCTTGGAAAG
ACGCAATTAATAAAAAATAAGCGTTCCAGGCAAGCACAGCAGCATCATCAAGATCATGCGC
CAGGCAATGCAGAGGACAAGACAACCTGTAGGTGAGTCCGTGAATGGTGTTCACAGCCGG
CCTCCTCCCAGTCAGATGCCATGAAACAAGACAAGTACGTCAGCACTAAACCAAGAAATA
GTAAGAACGATGGTGTGGATACAGCTATATACCACCACAAATTACGTGATCAGGTACTAA
AAGCACTCTACGACGTTTTGGCCAAGGAAAGTGAGCATCCACCTCAATCTATTTTGCATA
CTGCAAAGGCCATAGAAAGTGAAATGAATAAAGTTAAACAACCTGTGACACCAACGAAGCCG
CTTACAAAGCCAGGTATCGTATAATTTATTCAAACGTCATATCAAAGAATAACCCAGATC
TCAAACATAAAATTGCCAACGGTGATATAACACCTGAATTCCTAGCTACATGCGATGCCA
AGGATCTGGCACCAGCGCCCTTAAAGCAAAGATAGAAGAAATTGCCAAGCAAAACTTAT
ACAACGCACAGGGTGCCACCATAGAAAGGTCAGTCACCGATAGATTTACATGTGGTAAAT
GTAAAGAGAAGAAGGTATCTTACTATCAATTGCAAACAAGATCTGCGGATGAACCATTGA
CCACTTTCTGTACATGTGAAGCATGTGGTAACAGATGGAAATTCTCTTAG

YGL043W, 309 aa (SEQ ID NO 96)

MDSKEVLVHVKNLEKNKSNDAAVLEILHVLDFKEFVPTEKLLRETKVGVENVNFKKSTNVE
ISKLVKKMISSWKDAINKNKRSRQAQQHHQDHAPGNAEDKTTVGESVNGVQQPASSQSDA
MKQDKYVSTKPRNSKNDGVDTAIYHHLRDQVLKALYDVLAKESHPQSILHTAKAIES
EMNKVNNCDTNEAAYKARYRIIYSNVISKNNPDLKHKIANGDITPEFLATCDAKDLAPAP
LKQKIEEIAKQNLNAQGATIERSVTDRTFCGKCKEKKVSYYQLQTRSADPLTTFCTCE
ACGNRWKFS

YGL102C, 929 bp, CDS: 501-929 (SEQ ID NO 97)

TGTTACGATCAACATTCCTTGTCGTAATCAGCATGGTAGTTAAACCCATTCTGTACATAT
GGTCAGATATACTTTCGCATGGGTCAATACCATGGTCAACCCAACAGTTCTTCTTTGCG
TTTTCAAAAGTTGTATAATATTCAAAAACGCTAAGTATAATTTGGGTGAGGTTTCGAAA
GAATTGCCAAAATCTCCCTAGGTATATTATCTTCTGGCTTCCAGATGTTAACTGCAGTCA
TTTTGTTTTTCTGCTTTTACCTCGAATAGGTTTTCTTGTTTTGTTATTTGTTTTCTTT
TTGGACCCTATGTTTATATATGGATTTTGAATCTTTTAAAAAAGCGATAAAAGCGTTG
GGATCTGCCACTGGTAACCTTCAAAATAGACAAGACGAAAAAACGGTGAAAATGGGTGATA
GAAATAATACAGAAGTAGATGTTGAATTAGATTAACTGAAGATATATAATTTATTGGAA
AATACATAGAGTTTTGTTGATGCGCTTAAGCGATCAATTCAACAACACCACCAGCAGCT
CTGATTTTTTCTTCAGCCAACCTGGAGACGAATCTAGCTTTGACGATAACTGGAACATTT
GGAATCTACCCCTTACCCAAGATCTTACCGTAACCGGCTGCCAAAGTGTAATAACTGGA
GCAGTTTCCTTAGAAGCAGATTTCAAGTATTGGTCTCTCTTGTCTTCTGGGATCAATGTC
CACAATTTGTCCAAGTTCAAGACTGGCTTCCAGAAATGAGCTTGTGCTTGTGGAAGTAT
CTCATACCAACCTTACCGAAATAACCTGGATGGTATTTATCCATGTTAATCTGTGGTGA
TGTTGACCACCGGCCATACCTCTACCACCGGGGTGCTTTCTGTGCTTACCGATACGACCT
TTACCGGCTGTACAAAAAAATATTGTAA

YGL102C, 142 aa (SEQ ID NO 98)

MRLSDQFNNTTSSSDFFFSQLGDESSFDNWNINWNLTLQDLTVTGCSVNNWSSFLRSR
FQVLVSLVFWDQCPQFVQVDWLPMSLLLVEVSHTNLTEITWMVFIHNSVVMLTTGHT
STTGVLVSLTDTTFTGCTKKIL

YGL103W, 1461 bp, exon1: 501-549, intron1: 550-1060, exon2:
1061-1461 (SEQ ID NO 99)

AACAAGCTATAATATTGTTAAATATAGTTGATCAACAGCATTGTAATGATTACAAGAGAC
GAGGTGGAATGAACCTTATGAAATGCGTATTATATATAAACTGTAATAAGAGCTAAGTTG
AATTGAAATCTACGATACTTGATGTTGACATTATAGCACTAGTCCCAGGAAACCCCTTC

FIG. 1 - 34

GAAAAACACAGCAAAAAACAAGAGTACTGTAACCAATGTAACATCTGTACACCAGGGACCC
ACACATTACCAAAATCAAAATTATTTTCTAATGCCGTGTTATTTTCTTATTTTCCCTCT
GGCGCGTGAATAGCCCGCAGAGACGCAAAACAATTTTCTCGCAGTTTTTTCGCTTGTAA
TGCGTATTTTCCCAGATAGGTTCAAACCTTTCATCTGTATCCCGTATATTTAAGATGGCG
TTTGCTTTCTCCGTGATTTTTTTCTTCTTAGTGATTTTTTTGCATTAAATCCCAGAAC
AATCATCCAATAATCAAGAATGCCTTCCAGATTCCTAAGACTAGAAAGCACAGAGGTC
ACGTCTCAGGTATGTAGTTCCATTTGGAAGAGGGAATGAAAGAACCAAGACGGTGACTTT
TTTTTTAGTGTTGTGCAACCAATATGTCGTGTATATCATGGTACAGGAGAATGTCAAT
CAGCTAAGTGACTCAACATATTTCTTTGTGTTTTGATTGCGAATTTGTATTACCATCT
CACTGTTGAGACGGCTTATTTGAGGTAATAGCTCGAGTAAATGTACTCTTCCATCGCAA
CTGAGCAAAAAGAAAGTGTGCATAGCCTTTGTCATACTTCTCCTTTATTATACCATGATA
TTCAGAACAGTCATACTGTCTACTCATTTTACGGCTATAAAAGGTAACCTTTCATTTAGAT
TATGGAAGCACTAATTATCGCTGTATCAAATGGTTGTAGAGAGCGCAATTATGAAAAAG
AGTTACCACGTTTCTTTTGTTCGATAAAATGTCCAGTTGAAAACCTGTTTTACTAACGA
TTTAAAAATTGTATTTCAATACAATATTTTTTTGTACAGCCGGTAAAGGTCGTATCCGT
AAGCACAGAAAGCACCCCGGTGGTAGAGGTATGGCCGGTGGTCAACATCACCACAGAATT
AACATGGATAAAATACCATCCAGGTTATTTCCGTAAGGTTGGTATGAGATACTTCCACAAG
CAACAAGCTCATTTCTGGAAGCCAGTCTTGAACCTGGACAAATGTGGACATTGATCCCA
GAAGACAAGAGAGACCAATACTTGAATCTGCTTCTAAGGAACTGCTCCAGTTATTGAC
ACTTTGGCAGCCGTTACGGTAAGATCTTGGGTAAGGGTAGAATTCCAAATGTTCAGTT
ATCGTCAAAGCTAGATTCGTCTCCAAGTTGGCTGAAGAAAAATCAGAGCTGCTGGTGGT
GTTGTTGAATTGATCGCTTAA

YGL103W, 149 aa (SEQ ID NO 100)

MPSRFTKTRKRGHVSAGKGRIGKHKHPGGRGMMAGGQHHHRINMDKYHPGYFGKVGMR
YFHKQOAHFWKPVNLNLDKLWTLIPEDKRDQYLKSASKETAPVIDTLAAGYGKILGKGRIP
VPVIVKARFVSKLAEKIRAAGGVVELIA

YGL130W, 1880 bp, CDS: 501-1880 (SEQ ID NO 101)

TTTTGGTACTTGAATTTCTCGTTTTCTACTAGCTGGATTGCTTGTCTTTTACAATTCCTG
GGAGTTTGGCTATTGCTACCCTTGGTCTTAGCACCACCTTTTTTCCGCTATTTGTATTTGT
TGAATAATTTAGTATCTATTTCCATTTCAATTATAATTCACGTTTTTAGCAGCCTCTCTT
CTTCTAGGTAATTGGAAATCTTCTTCTTTAGGCATAGCGTGACCAGCTGAAAGGCAGATG
ATCTCAATATGTCCCGATAGGCCAATTTTGCCACCAGATAGTTGATGGCATTTTATTTT
TAGTCTTTTGAAGCAATATCATAAAATATATAGTTCTCCATGATGTTCCGGTTCAGT
CGTCCGAAGCGTAACCTAGTATAATAAATAGTTTCATTGCAGAAAATAACGAAAGAAATG
GTGGAATACGATCTGTTATATCTAACTAAAGCTAACTAACGGAATAAGCAAATACGAAT
CGACCGCTAATTTAACAAATATGGTTTTAGCAATGGAAAGTAGAGTGGCACCAGGAAATTC
CTGGGCTCATTCAACCTGGGAATGTCACGCAAGACTTGAAGATGATGGTCTGTAAATTAT
TGAATTTCCCAAAACCTACGAAAACATTCCTTGGTTCCCAGCCTGTGTCTTTTACGATT
CTGATGTGGAAGAGAAGCTGCTTGGCGATGATTACTACGTTTGTGAGAAAACAGATGGTC
TGCGGGTGTGATGTTTATAGTGATAAATCCTGTGACGGGTGAGCAAGGATGCTTTATGA
TTGATAGGGAAAATAACTATTATCTGGTTAATGGATTTAGGTTTCCCAGATTACCCCAA
AGAAGAAAGAAGAGCTGCTAGAGACTCTTCAAGATGGCACCTTATTAGATGGTGAACCTG
TCATACAAACTAACCCAATGACAAAATTACAAGAGTTGCGTTATTTAATGTTCGATTGTC
TTGCTATCAATGGTAGATGTCTCACACAATCACCAACAAGTTCTAGACTAGCCACCTTG
GAAAGAATTTTTTAAACCATACTTCGATTTAAGAGCAGCGTACCCTAATCGTTGTACTA
CTTTTCCGTTCAAAATTTCCATGAAACATATGGATTTTCAAGTTACCAATTAGTAAAAGTTG
CTAAAAGTTTAGATAAACTACCACATCTTTCTGATGGTCTGATATTTACTCCTGTGAAGG
CACCTTACACTGCCGGCGGAAAAGATTCAATGTTATTAAAATGGAAGCCAGAACAAGAAA
ACACCGTGGACTTCAAATTTGATTTTAGATATCCCAATGGTGGAGGATCCTTCTTTGCCTA
AAGATGATCGGAACAGGTGGTATTACAATTATGACGTTAAGCCAGTTTTCAGCTTATATG
TCTGGCAAGGCGGAGCTGATGTCAATTCACGTTTAAAACATTTTCGACCAGCCTTTTCGATA
GGAAGGAATTTGAAATATTAGAAAGAACATACAGAAAATTTGCAGAGTTGAGCGTTTCAG
ATGAGGAATGGCAAAATTTGAAGAACCCTAGAACAGCCATTAAATGGTAGAATAGTAGAGT
GCGCAAAAACCAAGAGACTGGGGCGTGGGAAATGTTAAGATTCAGGGATGATAAGTTAA
ATGGTAATCATACATCGGTGGTCCAGAAAGTTTGGAGAGTATCAACGATTCAGTTTCAT
TGGAGGACCTCGAGGAAATTGTTGGTGTATTTAAAAGGTGCTGGGACGAGAGAAGAGCAA

FIG. 1 - 35

ATATGGCTGGTGGTAGTGGGAGACCACTACCGTCTCAAAGTCAAATGCGACATTATCTA
CCTCTAAGCCAGTCCATTACAGCCCCCAAGTAATGATAAGGAGCCAAAATATGTAGACG
AGGATGATTGGTCGGATTAG

YGL130W, 459 aa (SEQ ID NO 102)

MVLAMESRVAPEIPGLIQPGNVTDLKMVMCKLLNSPKPTKTFPGSQPVVSFQHS DVEEKL
LAHDYYVCEKTDGLRVLVFMFIVINPVTGEQGC FMIDRENNYYLVNGFRFPRLPQKKKEELL
ETLQDGTLLDGELVIQTNPMTKLQELRYLMFDC LAINGRCLTQSPTSSRLAHLGKEFFKP
YFDLRAAYPNRCTTFPFKISMKHMDFSYQLVKVAKSLDKLPHLSDGLIFTVPKAPYTAGG
KDSLLLKWKPEQENTVDFKLILDIPMVEDPSLPKDDRNRYNYNDVKPVFSLYVWQGGAD
VNSRLKHFDQPFDRKEFEILERTYRKFAELSVSDEEWQNLKNLEQPLNGRIVECAKNQET
GAWEMLRFRDDKLNNGNHTSVVQKVLESINDSVSLEDLEEIVGDIKRCWDERRANMAGGSG
RPLPSQSQNATLSTSKPVHSQPPSNDKEPKYVDEDDWSD

YGL147C, 1076 bp, CDS: 501-1076 (SEQ ID NO 103)

CAATATTATAGTTACTACCTATTTGATTATTAAGATCAAAAAGTAATCCTTCATCTCATAT
CAAAAAGAAAGGTTTGTAAGAGCATTGGGCAGAGAGTATTTGTCCTGCGTATAGAGGA
GAAAAAATTGTACTGATGCTAATTTTGGTGTCGTTCTTCTTTTATTTTGTAAAGACTGT
TTTCCAGAAATGTTTGGGTTTATTTTAAATTTTGTAAACATTTTTTTCATCCTTTCTC
ATTTTGTCAATTCATTTTCTGTGGAATTTCACTGACGCGAAGAAGCGATGAAATTC
CAACATCCTCCCATCATCCCAATATTGGCATAACACACATGCAGCACAGCGGAACCTGCG
GAGGTCAGAGGCAATGTGGCAGAGACGCTGGCGCGCTGTATTGTATAATAGTATATTTT
ACACTCAATTCAATTTTGTATATTAAATAGTGTGTAAAAAGCTTCTGAAATCAAGAAG
CCCGTACCAGAAGTTCAATCATGAAATACATCCAACTGAACAACAAATCGAAGTCCAG
AAGGTGTCACTGTGACGATCAAGTCCAGAATCGTCAAGGTTGTTGGTCCAAGAGGTACTT
TGACCAAGAACTTGAAGCACATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA
AGGTTGCTGTTTCAACGGTGGCAGAAAGCACGTTGCTGCTTTGAGAACCGTCAAGTCTT
TGGTTGACAACATGATCACTGGTGTCACCAAGGGTTACAAGTACAAGATGAGATACGCT
ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCCAAATTCATTGAAG
TCAGAAACTTTTTGGGTGACAAGAAGATCAGAAACGTTCCAGTTAGAGATGGTGTTACTA
TCGAATTTTCCACCAACGTTAAGGACGAAATTGTCTTGTGAGGTAACCTCTGTGCAAGACG
TTTCCCAAACGCTGCTGACTTGCAACAAATCTGTGCTGTCAGAAACAAGGATATCCGTA
AATTTTGGACGGTATCTACGTTTCTCAACGGGTTTTATTACTGAAGATTTATAA

YGL147C, 191 aa (SEQ ID NO 104)

MKYIQTEQQIEVPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVTF TKVNNQLIKVAVHNG
GRKHVAALRTVKSLVDNMITGVTKGYKYMRYVYAHFPINVNIVEKDGAKEFIEVRNFLGD
KKIRNVPVRDGVITIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICRVRNKDIRKFLDGIY
VSHKGFITEDL

YGL213C, 1694 bp, CDS: 501-1694 (SEQ ID NO 105)

AATCAAAACGATCGTTATACAATTCATTGAGGAACCTCTCTAGTCCGATCCGTCCTTTCAT
CGATCATTTCCGGATCATCATATCTTCTTTGCCACCTCCTGTCCAATACACCGGGCTTTT
CAGGGAAGTCATATGGGATGGTGCTTCTTACATCTCTCTCCAATCGTGTCTTCAGTTTCC
AAAACCTCGGAATACCTTTTGTAAAGGCGCTTGTGTTGGTGTACTAACACCGTATAAAACAT
ACTTGGGGTTGATTTTAACATCGTCCACCTTGATTCTTAACTTTTCACTCATTTTCCCTA
CAGAATTAGCTGCCATCAATATCAATTATCAACCCTTATATGACTTTATTGTTTTTGT
TTGTTGGCTAATTAATTGATACAAATCTTTAGGCGAAAAATAAAAAAATATAAGTAAA
GAAGGAAAAATTAGGCGATATTAAACAAATCTTAAATAAAGACAAGAAACGAAAAAGAG
GTTAATCAAGTATTGGAAAAATGTCCAAAGTGTTTATTGCCACAGCAAATGCAGGTAAAG
CTCATGACGCTGATATTTTCTCGGTTTCTGCTTGCAATTCATTTACGGTAAGTTGTTTCAG
GTGACGGTTACTTAAAGGTGTGGGATAATAAGCTGTTAGATAATGAAAATCCAAAAGATA
AGTCATATTTCTCACTTTGTCCATAAGTCCGGATTGCACCATGTCGATGTCTTGCAAGCTA
TTGAGAGAGATGCATTTGAATTATGCCTTGTTGCTACCACTTCATTTTCTGGCGATTTAC
TCTTCTATCGTATCACTAGAGAAGATGAGACTAAAAAGTTATATTTCGAGAAATTGGATC
TTCTAGACTCAGACATGAAAAAGCATTCCTTTTGGGCATTAAAAATGGGGTGCCCTCAAATG
ACAGACTACTTTCCCATAGGCTGGTTGCTACAGACGTCAAAGGGACCACTTACATTTGGA
AGTTTCACCCGTTTGCAGATGAGTCAAATCTTTAACTAAATTTGGAGCCCCACGTTAG

FIG. 1 - 36

AATTACAAGGCACTGTGCAATCGCCTATGACTCCAAGTCAATTTGCCACTTCTGTGGATA
TCTCTGAACGAGGACTAATTGCCACAGGTTTAAATAATGGAACAGTACAAATTTTCAGAAC
TATCTACATTACGCCCGTTGTACAATTTTGAATCTCAGCATTCTATGATTAATAATTCGA
ATTCCATCAGATCGGTGAAATTTTCTCTCAAGGATCCTTATTAGCCATTGCTCACGATT
CAAATTCATTTGGTTGCATCACTCTATATGAAACTGAATTTGGTGAAAGAATAGGCTCCT
TATCCGTACCAACCCATAGCTCGCAGGCAAGTCTGGGTGAATTTGCACATTCTAGCTGGG
TCATGAGTCTATCGTTTAATGATTCTGGTGAAACATTATGCAGTGCCGGATGGGATGGTA
AATTGAGATTTTGGGATGTAAAAACAAAGGAAAGAATCACTACATTGAATATGCATTGTG
ATGATATTGAAATTGAAGAGGATATCTTAGCTGTTGATGAACATGGAGATTCTTTAGCTG
AACCTGGTGTCTTTGACGTGAAGTTTTTGAAAAAAGGTTGGAGATCTGGTATGGGAGCTG
ATTTAAATGAAAGTTTATGCTGTGTTTGTTTAGATAGAAGCATCAGGTGGTTTAGAGAAG
CTGGCGGTAAATAA

YGL213C, 397 aa (SEQ ID NO 106)

MSKVFIATANAGKAHDADIFSVSACNSFTVSCSGDGYLKVWDNKLDDNENPKDKSYSHFV
HKSGLHHVDVLQAIERDAFELCLVATTSFSGDLLFYRITREDETKKVIFEKLDLLDSDMK
KHSFWALKWGAASNDRLLSHRLVATDVKGTTYIWKFPFADESNSLTLNWSPTLELQGTVE
SPMTPSQFATSVDISERGLIATGFNNGTVQISELSTLRPLYNFESQHSMINNSNSIRS
VSPQGSLLAIAHDSNSFGCITLYETEFGERIGSLVPTHSSQASLGEFAHSSWVMSLSFN
DSGETLCSAGWDGKLRFDVKTKERITTLNMHCDDIEIEEDILAVDEHGDSLAEPPGVFDV
KFLKKGWRSRGMGADLNESLCCVCLDRSIRWFRAGGK

YGL235W, 1037 bp, CDS: 501-1037 (SEQ ID NO 107)

CTGGTTCCAACCATATCTTATGGGAAGATCTATCAGGAAACCTTAGAATCTTAGCTTCGA
TGGAGGGACAAATAGCGGGGGCCTTTGATGGTTCGTGTCCTGAATATGAATGGATTGATGCA
AGTTATTGCGCAAAAAGTCGTGCATTTGAGGTGTGGTATGTGTGCCAAAGCAATCCAGTT
GCTTCGTGGGTTCGACTGACACGGTTTCATTAGAAAACCTCATAGGGACAGGCAACGCAT
CTCCCTTCTGGACCTCCAGAGCGCTGAAATCAATGGATTCCCTTGGCCAGCCTAGCCGGAG
TGCCTGTTTTCAAACGCCCTAACTGAAAGCCCACCTCATTTTGTAGAGTATTGCTGATCC
CATATGTTGGCTGCTCGCCAATTCTTCTGCTGCAATACGCTTGTGCGCGATGTGAATTT
CTGCACTGAGAAACGTACCTGTAGTGATTATGACCTGATCTGCCCAACCTGGGTACCGT
CATCCAGAACCACACCTTTGATGACCTTGTGGCCACATCCGGGGTCATACAAGATCAAGT
CAGCAACTTTGTTCTGCAGCAGAGACAAGTTGGGGTGTGCTTTCTTGTGCGAAAGTTCCC
TTTGCATGTATTTCTTATATAACTCTCTGTCTATCTGGGCTCTGGGCCCCCACACAGCAG
GACCTTGTCTTCTGTTTCAGCATTTTGAATTGCACTCCAGCGAGATCAGTTACTTTGCCCA
TCAGCCCATCGAGAGCGTCGATTTCTTTTACAAGGATGCCCTTACCCACTCCACCAATAG
AGGGGTTGCACGAACACTTACCAATATCTGTTAACGATGGTGTAAATGAGAGTAGTATGCG
CACCAGTCTTAGATGACGCAGCTGCAGCTTCGCAGCCTGCATGTCCAGCACCGATGACCA
CGACCTGTGTCTTGGTTGTGGGTGGAAGCTTGTCAAAGAAGATATGGTCAACCGCCTCC
TGAGGACCTGTAAGGGAAATGAAGTACACGAAGACGCCAAGGTTGTTACACGCAGCATCG
TTCTTTGGGGCGTTTAG

YGL235W, 178 aa (SEQ ID NO 108)

MTLWPHPGSYKIKSATLFCSRDKLGCAFLSESSLCMYFLYNLSIHALGPHTAGPLLLFS
ILNCTPARSVTLPIPSRASISFTRMPLTPPIEGLHEHLPISVNDGVMRVVCAVLDDA
AAASQPACPAPMTTTCVLVVGWKLVKEDMVNRLRLRTCKGNEVHEDAKVVTRISIVLWGV

YGL260W, 731 bp, CDS: 501-731 (SEQ ID NO 109)

TACCATGGAACACCGTGATCATTCTGGTCACTTGGTCTGGGGCAATACCAGTCAACATG
GTGGTGAAGTCACCGTAGTTGAAAACGGCTTCAGCAACTTCAACTGGGTAGGTTCCGTT
GGGTGGGCGGCTTGAACATGTAGTATTGAGCCAAGTGAGCTCTGATATCAGAGACGTAG
ACACCTAATTCAACAAATTGACTCTTTTCGTGAGCTGAGCTAGAGTGGTGGTTGCGGAA
GCAGTAGCAGCGATGGCAGCGACACCAGCGCGATTGAAGTTAATTTGACCATTGTATTT
GTTTTGTTTTTTAGTGCTGGTATAAGCTTAACAGGAAAGAAAGAAATAAAGATATATCT
CAAAAGCATACAGTTGAAGCAGCTCTATTATACCCGTTCTCTATCAGTCATCACTACT
TAAACGATTCGTTAACAGATGCTCATTAGCACCTCACATATCCTCCATATCTCATCTTT
CACACAATCTCATTATCACTATGGAGATGCTCTTGTCTTGAACGAATCATACTCTTTC
ATAGACTTCGTATGTGGAGTATTGTATTATGGCACTCATGTGTATTCTGATGCGCAGAAAT

FIG. 1 - 37

GTGGGAATGCCAATTATAGGGTGCCGAGGTGCCTTATAAAACCCCTTTTCTGTGCCTGTGA
CATTTCTCTTTTCGGTCAAAAAGAATATCCGAATTTTAGATTTGGACCCTCGTACAGAAG
CTTATTGTTAA

YGL260W, 76 aa (SEQ ID NO 110)

MEMLLFLNESYIFHRLRMWSIVLWHSCVFVCAECGNANYRVPRCLIKPFSVPVTFPFSVK
KNIRILDLDPRTEAYC

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 111)

TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCCTAAATATGTACTCTTTTATTT
TTTTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTCTCT
GTGTAGCCTAATGTTTAAATGCCTAATTTTCTTAAATGCAGCAACATACATATGTTGA
GTCGTATAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTCAGGACA
TTTTAAACATCCGTACAACGAGAACCATACTACTTTTTTTAATATTCTTTTGTGTTT
CACCGCTTCTTTTTATTTTTATCCGAAGATCTTTTGGAACCCGCTCTGCGAATAGCGAA
GCTAGGATACCAAATTGAAACTTGGACATAACTCATCATTAAAGAAGTATACTGTTAAGA
GAGGCATTCAATTCGTGTATTATAACGTTTAGCATCAGTTACCCCTTGAAAGCCCAACATA
TACAAAATAACGCGTCCAAGATGTCTACTAAAGCCCAAAACCCATATGCGTGATTTGAAGA
TCGAGAAATTGGTCTTGAACATCTCCGTTGGTGAATCTGGTGACAGATTAAACAGAGCCT
CCAAGGTTTTAGAACAAATTATCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTG
TCAGAACTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTTACGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAACTTCTCTGCTACCGGTAACCTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTCTATGTCGTCATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACTGTTGGTAACTCCCACAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGACGCTGATGTGCTCGATA
AATAA

YGR085C, 174 aa (SEQ ID NO 112)

MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR
RNEKIAVHVTVRGPKEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKRCGTGTVGNSHKTTKEDTVSWFKQKYDADVLDK

YGR118W, 1258 bp, exon1: 501-565, intron1: 566-885, exon2:
886-1258 (SEQ ID NO 113)

AGCCATGTCGGTCGCACTAGACTTTTCTTCTCACTGTCACTTACCTGTTTTGAAATCATGT
CCTTTTTTTTTTTTGGCATTCTTATACATTTTCTTTCTTCTGAAATTAACGTACACCCA
TACCCTATATACACCCATACCCTATTTTTAAATATAAAAAGTAACTTCATTTTGAAAGA
CCACTCTGCATCAGCACGCGGGCTCTGGAAGGAAGAAATGACGTTTCGGCGGAATACCCT
TTCAGAAGGTCTGCTCTTGTGGCTGGTTCATGGGAGACACCCAGCGGAGCTCCTCCCGAG
AAAGGCCCTTCATCTCTGCCGATTGCTGACGGAAGCAGTAGCGGAGGTTTGAGTTCTC
TACGCCGAGAGTACACTGCCGTAATATCACAATGTTTCGACTAACGGTTACAGTACGTTA
AATTAGATACTGCCTATGAATTGACATATTAGATAATGTCAAATTTTACAAAAACCTAAG
ACAACAGGAATAAACAAGATGGGTAAAGGTAAGCCAAGAGGTTTGAACCTCTGCTAGAA
AGCTACGTGTCCACAGAAGAAACAAGTATGTTGACTATTTCAAAATTAACAAAACTATC
AACCCCTATTGTGATATCGTTTTAGGTGAAGGAAATGTTGTGAGCTCTGGAGTGATAAA
TTTATCAAGTAACATATCCTGGCGCAAATCAGTTTGGAGAGGCTTAAATGACACGTCAC
AGTGATAAAAAGTAATGAATAGTGAACGGTCAGCTTCGGCCATTCTTCCCAATCTATAGT
GTGGAAAATAAACCTTTTCTTCCCAAAATAACTCAGAAAGTCACAGGAGGCCGTTTTTTA
CAACGGAATCATTTTTTTTACTAACAGTTTTTTTTTATTATTATAGCCGTTGGGCCGAAAA
CAACTACAAGAAGAGATTGTTGGGTACTGCCTTCAAGTCTTCTCCATTCCGGTGGTTCTTC
TCATGCCAAGGGTATCGTCTTGAAAAATTGGGTATCGAATCCAAGCAACCTAACTCTGC
TATCAGAAAGTGTGTTAGAGTTCAATTAATCAAGAACGGTAAGAAGGTCACTGCTTTCGT
TCCAAACGATGGTTGTTTGAACTTTGTGACGAAAAATGATGAAGTCTTGCTAGCAGGTTT
CGGTAGAAAGGGTAAAGCTAAGGGTGATATCCAGGTGTTAGATTCAAGGTGCTTAAGGT
CTCTGGTGTCTCCTTGTGGCTTTGTGGAAGAAAGAAGGAAAGCCAAGATCATAA

FIG. 1 - 38

YGR118W, 145 aa (SEQ ID NO 114)
MGKGKPRGLNSARKLRVHRRNNRWAENNYKKRLLGTAFKSSPFGGSSSHAKGIVLEKLGIE
SKQPNsAIRKCVRVQLIKNGKKVTAfVPNDGCLNFVDENDEVLLAGFGRKGKAKGDIPGV
RFKVVVKVSGVSLALWKEKKEKPRS

YGR142W, 1733 bp, CDS: 501-1733 (SEQ ID NO 115)
GGACTACTTTACAGGGTAATGAATATTTGGGCGTTTTTCGCTATTTTAGCATGCTGTAGT
GTATGTACTGTGCATCGTCATGTAGCACTATTTTCAGCCGTATTTTTCTTTTTTTCTTTTCG
CACCGTCTGTGGTTGTAAAGTTACTGACACTTTTTTTTTCTAGAAAGTTCGGAAAAATTGC
GACACTCGGTGGAGCTCGAGAGTTGTATCCAGTTTTCTTGTTCGGCGATATTCGGAACCA
GGTCGGGTTGGGCTAACAGCCGCCAGGATGGAAGAATTAAGAATTTCATAGAAGCCTTC
AGTTCTTGGCGAAGTAAAGTGGCAAAACAAATGGAAGATCTATTGCATTACATATATAAA
AGCATTAGAACAATCTTTTCTCATTGACAGGTATTCCTCATTGCTCTATATATATTTTTCTT
CTTCTTGAAAGAAATATCAGTATTACAATCATAACAACAACCAAAAGAAAATAACTAATA
GACCCCATTAATATAGAAATGTTTTCCATATTCAATTCACCATGTGTTTTTGAACAGC
TGCCATCTTTTAGTCAGCCCTACATTTCGCGTTATTTTGATTGCAGTCTCCAGTGAGCT
ATTATCCGAATGTAAAAGGAGGAAAAGCAATAAAAAGCTAACCTAAGAGCTCCAAAAA
GCGATGCAAAATTGTTTCAAGACCTTTGAGGTATGCACCTTGCTGAAACACCAAAATGGTTATA
CATTAAAGCTTGTCTAAGCGGATTCCATATGAACTTTTTTCAAAGTACGTTAATGAGAAAT
TAGGTGAGCTAAAGGAGAACCATTACAGACCAACTTACCATGTTGTCCAAGATTTTTTTTG
GAAACCAGTATTATGTTGAAGATGAAGCGGATGAAGATGCTCTATTGAGATCTGCATTGA
AAGATCTGGATTTTAGAGCCATAGGAAAGAAAATTGCTAAGGATCTTTTCCAAGACTACG
AAATAGAAATTGAATCATAGAGGTGATGAATTTGAGCATATTGAGTAAGAAGGATAAAATCT
TTAAGGAATTCTCTCTAGACCAAGTGTTTGAAGATGTTTTGTTATTGGCTGTGGAGTTG
AAAACATAGATGATGGCTCGAGAGAAAAATATGCACTTTTTAAAGATTGGTTTAGTTAAGC
ATGAGGAAGAAATTTCCGAAGGTGGCATCAACGAACCAAGATGCCAATAATTGAATCCA
AAATAGACGAGTCTCACGATGATGTTAACAATGCTCTGAATCTTTGAAGGAGGAAGAAGCGG
AGAAAGCGAAAGAACCCTAACCAAGAAGACCAATAAAAAAATGGATAGAGGAAGAAA
GATTGATGCAGGAGGAAAGCAGAAAATCAGAACAGGAAAAGCTGCCAAGATGAGTGAAG
AAAGGCAAAAGAGAGAGGAAGCCAGATTGAAGGCAAGGAAAGAATCTTTGATAAAATA
AGCAAAAAACCAAGAGGTCCAGCAAAAAAATTGCAAAATTCAAATCATTGCCTATCT
CTGAGATTGAGGCCAGCAATAAAAAATAATAATAGCAATTCCTGGTTCAGCAGAAAGTGATA
ATGAAAGTATAAACAGTGATTCTGATACGACTTTGGATTTCTCTGTGTCTGGTAATACAC
TAAAAAACACGCTTCACCCCTATTAGAAGACGTTGAGGATGAGGAAGTTGACAGATACA
ACGAGTCCCTAAGCAGATCTCCAAGGGAACTCTATTATTGAGGAGATATAA

YGR142W, 410 aa (SEQ ID NO 116)
MFSIFNSPCVFELPSFSQPLHSRYFDCSSPVSYYPECKRRKAIKANLRAPKSDANCSE
PLRYALAETPNGYTLSLSKRIPYELFSKYVNEKLGLKENHYRPTYHVVDFFGNQYYVE
DEADEDALLRSALKDLDFRAIGKKIAKDLFQDYEIELNHRGDELSILSKDKIFKEFSLD
QVFEDVFVIGCGVENIDGDSREKYALLKIGLVKHEEEISEGGINEPKMPIIESKIDESH
DVMNSESLEKEEAKEKEPLTKEDQIKKWIIEERLMQEESEKSEQEKAKEDEERQKKEK
EARLKARKESLINKQKTKRSQKKLQNSKSLPISEIEASNKNNSNSGSAESDNESINSD
SDTTLDFSVSGNTLKKHASPLLEDVEDEEVDRYNESLSRSPKGNIIIEI

YGR236C, 890 bp, CDS: 501-890 (SEQ ID NO 117)
CAAAAAGTTTTTCGGATGAACCGGATTAATACAAGTAAAATCAGCAAAGATATAGAAGAC
AAAATAAGCGTGAAAACAATCATAAACCCTCACAAACGGGGTTTTTCAGCTGTTACTCCT
CCATACATACATTTTGATAAAGATATAATGTTATATTTCTTTTCGTAATTTTGTTTTACT
TCGGTTTGCTCTATAGATTTTCATCAGCCGCACCGAAAAGGGAGATCAATAAGGTACCCTT
TAAAAGGGATAAGAAGCCTACATCACCCCAATAAATGGAGTAATGGCCAGCATTGGATGA
AGAGAAGAATTACGGGATACTGGGATAACACTGTTAAAAAATGCTTCGCGACGTGAGGGT
CTTCTTCATATAAATTGAACTGCCAAATCTCTTTACATTATCCAGGATAGTTTGGAATG
TGTGTTTACTGAAGGATCAGAATCAATAAATACAATCAATACAAATATTTAGCGCATAAAA
TTCAAACAAGTTTACTGAAATGAAGTTAGATTTCAGGAATATACTCAGAGGCACAAAGAG
TTGTGAGAACTCCAAAGTTTAGATATATTATGTTAGGGCTGGTGGGCGCTGCTGTGGTAC
CGACCGCATACATGAGGAGAGGCTATACGGTTCCTGCACATAGCTTAGACAACATCAACG
CGGTAGACACAACCTAAGGCGTCTGTTATGGGTACAGAACAGAGAGCAGCTATGACGAAGG

FIG. 1 - 39

GTAAGAGTTTACAAGAGATGATGGATGATGATGAAGTAACGTATTTGATGTTCTCTTCA
ATCATGTAAGGGAATTTGTAAGTTGCTTCCCTGCATTTATGTTCTTTGCATTTTGTTCG
CATTTAATCATAGTACGACAAACGGGGAAGGGGATTGTGATTTTACATAA

YGR236C, 129 aa (SEQ ID NO 118)
MKLDSGIYSEAQRVVRTPKFRYIMLGLVGAADVPTAYMRRGYTVPASLDNINGVDTTKA
SVMGTEQRAAMTKGKSLQEMDDDEVTYLMFLFNHVREFVLGSLHLCSLHFVFAFNHSTT
NGEGDCDFT

YGR277C, 1418 bp, CDS: 501-1418 (SEQ ID NO 119)
AATCTTTGCGATTGAATTGCTGCACGAACATTAACATTAGTTCTTTTGCTAAAGTTTCTC
CAATATCTGGAATATCAGAATTTAGCAAGGCAATCAAAGCGGATAAAGCAGGGATTAGCC
TGCCATTCTGTTTGTTCAGAGTAAAATCCACAACATTTTACAAATTATGTTGCGGCCAA
TAAGTATATTGACTTGAAATAAGTCTCTGTGCGATTCTCTGTAAGTTGTCCATTGTTAAAT
TGGATATTATGGGTGAAACGTGTGACCTTATCATTTCCCAGTTTTCTCTCTGAAATTTAA
TGTCTTCATCTGTATGGTAGCGGTAGACATGCTGGTTTGTAGCCTTTTTATTCCTTTTT
AGGTTTCTTACTCACAATGCCAAAATAAATATCAGTGTAAATATAATTTTCAAGAGTACG
TAATGGAAAAAGATAAAAATAAGGACCGTCATAAAAAGAGACGTGATTA AACCTAAAAAT
CTAAAGTAAAGAAGTGTAAAGATGGTTGAGGAAAATTCAGAGTTTTGATTGTTCTTCTT
ATACACCGCCTAGTGCTACTTTGCAGAGGATTATAGGGCAAACATTCCGTTCTTAAGAG
AATGTCAAAGTCAACTAGACATCGTGATTGTACCTGAATTCAAAACCTCATCCAGTTGG
ATTCTGCGCTAGGGAAGATGTACAGTATTACCAGGGATGTCCTTTTGGGCTATGGAATGA
TCAACAGCGGAATCAACATCATATTCAACAATATTCATTTTCGTCGAGAGTAATTTGCAAT
GGAAAGTGGTTTATTGCCACAGGAATCCACTTTTGAACTTGGAAGCTAGAGTTGGGAC
AAGGACAATACCATAGTATAGAACATTATGCATTACACGATAATATAATGGAAGAGATAG
AAGGTCCCAAAGATGCTAACAAATTTTCATGTACCGCATTTGGGCGGAACGTTCCGACCACA
TTCACGATGGACATAAAATATTGTTGAGCGTCTCTACATTCATCACGTCACAAAGGTTAA
TTTGTGGAATTACGTGCGATGAGCTCTTGCAAAAACAAGAAATACAAAGAGTTGATTGAAC
CTTATGATACACGATGCAGGCACGTACATCAATTCAAGTTGTTAAACC GGATCTCT
CCGTAGAACTAGTTCCCTTAAGGGACGTGTGCGGCCCCACAGGGAAAGTACCCGAGATAG
AATGTTTAGTTGTGAGTAGAGAAACCGTCAGTGGGGCAGAGACTGTGAATAAGACTAGGA
TTGAAAAGGCATGAGCCCATTTGGCAGTACATGTGGTTAATGTACTTGGAGGAAGGGAGG
AAGACGGCTGGAGCGAGAAGTTAAGCAGCACGGAAATCAGACGCCTACTTAAGTCCTCTG
CTTCGCCAACGTGCACTCCACAAAACCTTGCGGTATAA

YGR277C, 305 aa (SEQ ID NO 120)
MVEENSRVLIVLPYTPPSATLQRIIGQTIPFLRECQSQLDIVIVPEFKTSFQ LDSALGKM
YSITRDVLLGYGMINSGINIIIFNNIHFVESNLQWKVLLPQESTFETWKLELGQGYHSI
EHYALHDNIMEEIEGPKDANKFHV TALGGTFDHIHDGHKILLSVSTFIT SQRLICGITCD
ELLQNKKYKELIEPYDTRCRHVHQFIKLLKPDLSVELVPLRDVCGPTGKVPEIECLVVSR
ETVSGAETVNKTRIEKGMSPLAVHVNVNLGGREEDGWSEKLSSTEIRRLKSSASPTCTP
QNPCV

YGR284C, 1433 bp, CDS: 501-1433 (SEQ ID NO 121)
AGAGAGCCATCCGTAACCTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGGCCA
CCACGATTGACGAACAAGTTGGTTTGATCGTTGACAGTTTGAATGACGAAGAGTTAGTGT
CCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTGAAGGAATCTG
CAAAGACTATTGTCGATTCTGGCAAACCTACCATCCAGCTTGTGTCCTACTTCGTGTGAA
TACCGTAAGAAATGGAATAGAATATATACGAATGTATACGAATATTATAGAGAACGTTCT
CTTTTATTTCTATAATGAATAGGTTCCGGTAACGGTTCCTTTTTTAGGTATTTCTAGAAG
ATGAGAGAAGAGGGAATAATGAGAAAGGCCAAAAATAAAGGACACCTTTAACGAAAGATC
AAAGGTGTCCTTATTTACTTACAATAGCTGCAATTAGTACGACTCAAAAAAGTGAAAAC
AAAACCTGAAAGGATAGATCAATGCTTTACAGAGGACCTATTGGAAATTTTGGCGGTATGC
CAATGTCAATCATCGCAAGGACCACTCTGGCGGTGCACAATTCAGATCAAACCGAACC
AATCCACTTCTGGCATCTTAAAGCAATGGAAGCATTCTTTTGAAGTTTGCCTCCAGAA
TTGAGGGGCTCACTGACAATGCAGTTGTTTATAAATTGAAGCCTTACATTCCAAGTTTGT
CAAGATTTTTTCAATTGTGGCCACCTTTTATGAAGATTCGTTTAGGATCTTATCACAATGGT
CAGATCAAATTTTTTATCTGAATAAGTGGAAGCATTACCCATACTTCTTTGTCGTTGTGT

FIG. 1 - 40

TTCTAGTGGTTGTTACCGTTTCCATGTTGATTGGCGCCAGTTTGTAGTTTAAAGAAAGC
AAACCAATTATGCCACCGGTGTGTATGTGCTTGCCTTATTTCTCAAGCATTAGTTTATG
GGTTGTTTACGGGTTTCATCATTGTCTTAAGAACTTTAGTGTATTGGTGGGTTGTTAA
TTGCATTTCAGCGATTCAATTGTTCAAAACAAGACAACATTCGGTATGCTTCTGAATTAA
ACAGCAAAAACGACAAAGCGAAGGGTTACCTGTTGTTTGTGCTGGTAGAATTTAATTGTTT
TAATGTTTATCGCTTTCACTTTCAGTAAATCATGGTTTACTGTTGTTTGTGACCATTATCG
GCACAATATGTTTCGCCATTGGTTACAAGACAAAATTCGCATCCATTATGTTGGGTTTGA
TACTAACTTTTTACAATATCACGCTAAACAACACTACTGGTTTATAACAATACTAAGAGAG
ATTTCTTGAAGTATGAGTTTACCAGAACCTTAAGCATCATGGTGGGCTTCTATTAGTTA
CTAATACTGGCGCTGGTGAATTATCCGTTGATGAAAAGAAGAAGATTTACTAG

YGR284C, 310 aa (SEQ ID NO 122)

MSYRGPIGNFSGMPMSSSQGPYSGGAQFRSNQNSTSGILKQWKHSFEKFASRIEGLTDN
AVVYKLPYIPSLSRFFIVATFYEDSFRILSQWSDQIFYLNKWKHYPYFFVVVFLVVVTV
SMLIGASLLVLRKQTNATGVLCAVISQALVYGLFTGSSFVLRNFSVIGGLLIASFSDSI
VQNKTFGMLPELNSKNDKAGYLLFAGRILIVLMFIAFTFSKSWFTVVLTIIGTICFAI
GYKTKFASIMLGLILTFYNITLNNYWFYNNTKRDFLKYEFYQNLISIIGLLLVNTGAGE
LSVDEKKKIY

YGR285C, 1802 bp, CDS: 501-1802 (SEQ ID NO 123)

CATTTAGTTCGTGATTACAGCAGAAATCGTAGCGCGATGAGACATTTTCATCAAATGGCCTT
TTTTTTTGGGCAATTTTTTATATCTTGAAATGATAGTTGCCTTGTAATTTCAACCGTT
CATTTCAATTAAGAACTTGACTAAATATGAACATTTCTTAAAAAAAAGGTTGACATATAA
AATAATCGAATATAAACGATGGAATTTTTATAAAATTAACACATATATATATATATATT
AACTATAAATATGTCAAAGAAACCATAACAATCATAGATTTATAACTATCTTTTGGATGAC
ATTAATGAACATAACGCTCCTAATACAAATGTCCAAAAAATATTACCCGCAAATACGAAT
CTTTTTTTTTTCTCGATGAAATTTTGCAAAGAGTTGCAAATTTTTATTTCAGAGCTGGT
AGAGAAAATTTCATAAGGTTTTCTACCGATGCTTTTATAAAATCTTCGTTTTGTCTCAC
ATATACCAACAAGAGTAACGATGTTTTCTTTACCTACCTAACCTCAGACATCACTGTTG
AAGTCAACAGTTCCGCTACCAAAACCCCATTCGTCCTCGTCCGGTCCGAACCGGTTGGTA
AGTTCTTTTTGCAACATGCTCAAAGAACTTTGAGAAACCACACCTGGTCTGAATTTGAAA
GAATTGAAGCTGAAAAGAACGTCAAACCGTTGATGAATCCAATGTGACCCAGATGAGT
TGTTATTCGACACTGAATTGGCCGATGAAGATTTACTGACTCATGATGCTAGAGACTGGA
AAACTGCCGATTTGTATGCTGCTATGGGTTTGTCTAAGTTGCGTTTCAGAGCTACTGAAA
GTCAAATCATCAAGGCTCACAGAAAACAAGTTGTCAAGTACCATCCAGACAAGCAATCTG
CTGCTGGTGGTAGTTTGGACCAAGATGGCTTTTTCAAGATTATTCAAAGGCCTTTGAAA
CTTTGACTGATTCCAACAAGAGAGCTCAGTACGACTCATGTGATTTTGTGCGCATGTTT
CTCCTCCAAAGAAGGGTACCGATTATGACTTTTATGAAGCTTGGGGCCCCGTTTTCGAAG
CTGAAGCTCGTTTTTCTAAGAAGACTCCTATTCTCTCTAGGTAACAAAGATTCTTCCA
AGAAGGAAGTTGAACAATTCTATGCTTTCTGGCACAGATTTGACTCCTGGAGAACCTTTG
AGTTCTTGGACGAAGATGTCCAGATGACTCTTCTAACAGAGACCACAAGCGTTACATTG
AAAGAAAGAACAAGGCCGCAAGAGACAAGAAGACTGCTGATAACGCTAGATTGGTCA
AACTTGTTGAAAGAGCTGTCAAGTGAAGATCCCCGTATCAAAATGTTCAAAGAAGAAGAGA
AGAAGGAAAAGGAAAGAAGAAAATGGGAAAGAGAAGCCGGTGCCAGAGCTGAAGCTGAAG
CTAAGGCCAAGGCCGAAGCTGAAGCGAAGGCTAAAGCTGAATCTGAAGCCAAGGCTAACG
CCTCCGCAAAAGCTGACAAAAGAAGGCTAAGGAAGCTGCTAAGGCCGCCAAGAAAAAGA
ACAAGAGAGCCATCCGTAACCTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGG
CCACCAGATTGACGAACAAGTTGGTTTGTATCGTTGACAGTTTGAATGACGAAGAGTTAG
TGTCCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTTGAAGGAAT
CTGCAAAGACTATTGTGCTGATTCTGGCAAACCTACCATCCAGCTTGTGTCTACTTCGTGT
GA

YGR285C, 433 aa (SEQ ID NO 124)

MFSLPTLTSDITVEVNSSATKTPFVRRPVEPVGKFFLQHAQRTLNRNHTWSEFERIEAEKN
VKTVDESNDPDELDFDELADLTHDARDWKTADLYAAMGLSKLRFRAESQIIKAH
RKQVVKYHPDKQSAAGGSLDQDGFVKIIQKAFETLTDSENKRAQYDSCDFVADVPPPKGT
DYDFYEAWGPVFEAEARFSKKTPIPSLGNKDSSKKEVEQFYAFWHRFDSWRTFEFLDEDV
PDDSSNRDHKRYIERKNKAARDKKKTADNARLVKLVERAVSEDPRIKMFKEEEKKEKERR

FIG. 1 - 41

KWEREAGARAEAEAKAKAEAEAKAKAESEAKANASAKADKKKAKEAAKAAKKKNKRAIRN
SAKEADYFGDADKATTIDEQVGLIVDSLNDDELVSTADKIKANAAGAKEVLKESAKTIVD
SGKLPSSLLSYFV

YHR010W, 1472 bp, exon1: 501-531, intron1: 532-1092, exon2:
1093-1472 (SEQ ID NO 125)

GACTCGGACGGAACCGTCTCATATTATACGTTCAAGTGAATATTTTTCACGGAAGAATGGA
AAGGGCCTCGAAAGACGTTAATGCATCCGTACACCTACATCTTTACATTTTTTGTCTGTTG
CACCTACACTGTTTTTTTTTTTTTTCACCTTATGAGTCTGTATTTCTTGAAAGAGCCGAT
AACAATATTCCAGGTGGAGTCCCGAGGCAGAATCAAGGCTGCGGAGAGAAGTTCCTCTCA
AAGTAATGGGAGTGATCCGCTCAGTTCTCCCATCACGACAGAAGTGTCTGAGACAAAGTC
TTTCCAGCAGAGTCCGCTACGCTCTTGCTGCAGAGATTGCGCCGAAGGCAGGTTTCCTG
AAATTCTTTTCACTAGTAAAGTGTTGCTTCATGTAAACATACTGCCGTAGTTTTGAGCT
AAAATTAAAGATATATTAGATTTTTAGAATTTCTTAGATAGTCTCAACGTGTTAAACAA
AAGCATAACCAAGAAAAAATGGCTAAGTTCCTTGAAAGCTGGTAAAGTTGGTACGTATC
ATTTTCAGTTTTTGGACATCAACAAAAAACCGTGCAACTGTGGTATTAGAAATCCAAGTT
ATTAGCAGTTGATGTTGTATAATTTGAGTTTGAATTCGAGTATTGTATCTTCATATGGGA
GTAGGGAGGAAAAAGCGTGGAGATGTAGATCTGGGAAAAAACCTTTAAATTTGAATGAT
AGCTTATTAATAGAAATATTGGACAAAAAGATGAATGATTTAGGAGCGAAACTAACGATT
ATTTCATATTCATTGAGCTATACGAGGCAGTGGAAGGGTTATCAAAAAGTTGTAATTTAAA
AGAAAAAGCATCAATAGCCACCAATAAGATGGTGAAAGTTCCGCGATATATTTGCTAA
GACCATAGGCACATGTACGCAGGCGACAGGGCCTTTTATTTACTGTAGTTCTTTCCATG
CCCTATTAATAATTCGTGGGCCTATGATAATTTTCTCTCCCTAGTATTGAAGAACAAAA
TTGAGAATTCGCCAAACTTTAAGAAGGGTTCATTTACTAACTATTTCTTTTCTTCTCT
TTTTTTACACAGCTGTGTTGTCGTTGTCGTTACGCCGGTAAGAAGGTTGTTATCGTTA
AACCACATGATGAAGGTTCCAAGTCTCACCATTGTTGGTACGCTTTGGTTGCCGTTATTG
AAAGATACCCATTGAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTTGCTAAGAGAACCA
AGATCAAGCCTTTTCATCAAGGTCGTCAACTACAACCATTTATTGCCAACAGATACACTT
TAGATGTTGAAGCTTTCAAATCCGTTGTTTCTACTGAAACTTTTGAACAACCTTCCCAAC
GTGAAGAAGCTAAGAAAGTCGTCAAGAAGGCTTTTGAAGAAGACACCAAGCTGGTAAGA
ACCAATGGTTCTTCTCTAAGTTGAGATTTTAA

YHR010W, 136 aa (SEQ ID NO 126)

MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEGSKSHPFHALVAGIERYPLKVTKKHGAK
KVAKRRTKIKPFIKVVNHNHLLPTRYTLTDLVEAFKSVVSTETFEQPSQREEAKKVVKAFEE
RHQAGKNQWFFSKLRF

YHR021C, 1299 bp, exon1: 501-503, intron1: 504-1053, exon2:
1054-1299 (SEQ ID NO 127)

TTACTTACGTCTATTATAACCTTCCGCGTAAAAAAGAAATATTGACATCCTTTCTTGTAT
TTAGCCCATACATTTTCACCCATGCACCATTGGATTATAAAGAAAAAATTTAATAAAAA
TCTGCCGGGGAAATTTTCAAGAAAAAAGGAAGGTGTGTTTCGCATTTAACACGGGCCACC
ATAAACTTTTGTGTTGCCACCCATCTAGACGGGATCCGCCCCGCCCAAGGCTCTCTTCCTC
TAGCTAGGCAATGTGGCTCTCGGAAAGGAACTCCCACCAGGACGTGGTGGGAAATGCAG
CAATTCCCCTCTGCTTCCCGCTGACCTTTCTTGGGCCCAGTTTAGTAAGTATGCTCTCAT
CTTTTCATGTGTGCTGTAACCTTGCAAGTCATTAACACTATCTATAATTGATATTAGACGTT
AAAAGTTCTATATAGCATTTGCTTTTATTTAGAGAATACGAAAAACACCAGATAATTAG
TGCATATATATTAGATCAATATGGTATGTGAAAGAGATATTAAACATAAGATGTGAAGGA
AACAGAAGAGAACAATATTGAGGAATGAATTCGGATGAAATTTCTAGTAGAAGAAAAAAG
CCTAAAAATAAAAGAAAAGAAAGGAAAAATAAAGCAGTAATCAACCTCTGACATTTGATAGG
AGTATGCGTTTCCGCAAAATCAACAAATCATGCATTAACCTGGTAACGGAGACTTTAAAG
ACGTGCAAAGAAAGCAATTAATTTTTAGATAGGGAATTGAAAGGCTCTGTATAGCAGAAA
ATTTGAGATCTACTGTGGAGATAAGCATATGGTGTGAGTTATGGGTAATCTAACAAATAA
TAGAAACTTATAGCAGTTGAAGATGGCGGATCATGATGCCGGATACTGCTGGGTAATGAT
TTATCCTTCTTTTTTTGGAGCACAAATGCTCACTTTTTCTGTCTCCTCTAACTTTTCTG
ATGTATCCTACCCAACCTTACAGTTTTCAAATTACTAACATCAATTTTTTTGTGAAACGA
CTTTTCGTTTTCGTTTTCTATTTATTTTATTACAGGTTTTAGTTCAAGATTTGTTGCACCCA
ACTGCTGCTTCTGAAGCCAGAAAGCACAAGTTAAAGACTTTGGTTCAAGGCCCAAGATCC

FIG. 1 - 42

TACTTCTTGGATGTCAAATGCCCAGGTTGTTTGAACATCACCCTGTTTTTCTCATGCT
CAAACCTGCTGTCACTTGTGAATCATGCTCTACTGTCTTATGTACTCCAACCGGTGGTAAG
GCCAAATTATCTGAAGGTACTTCTTTCAGAAGAAAAGTAA

YHR021C, 82 aa (SEQ ID NO 128)

MVLVQDLLHPTAASEARKHKLKTLVQGPSYFLDVKCPGCLNITTVF SHAQTAVTCESCS
TVLCTPTGGKAKLSEGT SFRRK

YHR141C, 1262 bp, exon1: 501-504, intron1: 505-945, exon2:
946-1262 (SEQ ID NO 129)

TAAAACATGGCATTTTTAAATAGTACTGCCAAAATTTAATGCAATGGCAATTAGTTGGCTA
TGTTGCTACATATTATTTTCCATAGCATTCTCTGTACAAAACCTCAAATAAAAAGACAGT
GACATCCGAACATCCGATACACCCATACATCATGAAAATAAATCCTGACATTGGAAGAAG
TCTTGATACAAAAAAGATCGCTGTCAAAAATGCGGCCAGACTGCCGCTGCATCGTACCA
ACAGTGCCTATGTTTCAGACGGAGAGACGACCTCTAGAGAGACGTCCGTCGGTGCAGCAAC
GCTGACGGTTTAGTTGTTTCGACGGGATGATGGGTTCCGCCAGGGGGAGGGAAGGCTTTCC
ACCAAGAGAGGTAATAATTATTCGTGCAAAATGAACTCAGAGATACATCCATATTGTTGACA
ATGTATATCTTAATTGATGTGGTATTTTCACTGTTTTAACGTAAATTTGAAGGAGATTAAG
CAAAAAACAATCAGTAATAATGGGTATGTGGACGATTAGGAATAGACAAACCATGTTAT
TTATCTCCATTAGGGCGTGAGAGTGAATTAGTACACAGGTACTACTAGAATGCTAAAGA
ACTTTTPTAAATATCCTGAATCGTAGGGCAAATCCATGTCAAGCAAGAACTAATAGTTA
TTAAACTTCATTTACTTTTGAGCTAGTTAAATATTTTCATCATTTCCCTAAAGTACTGAAC
ACCTGAATGATACTTTTATTGGCCCTTTTAATAAGAACTCTGGTTAGAAAATATATTGAG
GATATCATTAGTAATACTCATTAGATATTTGTGAATTTAGCCGTTTCCCATTACAGAAA
AAAGATACAACATAATTACATGTGCAGTCAAATTACTTTTTTTTAAAGATCAATTAAAC
AATCAACTATCATGCTAAATTTGCTGTGATATCATTTTGAACCAGTTAACGTCCCAAAGA
CCAGAAAGACCTACTGTAAGGGTAAGACCTGTCTGTAAGCACACTCAACACAAGGTTACTC
AATACAAAGCTGGTAAGGCTTCCTTGTTCGCTCAAGGTAAGAGACGTTATGACCGTAAAC
AATCTGGTTTCGGTGGTCAAACCAAGCCTGTTTTCCACAAGAAAGCTAAGACTACCAAGA
AGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACTAGAGCCCAATTAACCTTGAAGA
GATGTAAGCACTTCGAATTGGGTGGTGAAAAGAAGCAAAAGGGTCAAGCTTTGCAATTCT
GA

YHR141C, 106 aa (SEQ ID NO 130)

MVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGFGGQTKPVFHK
KAKTTKKVVLRLCEVKCKTRAQLTLKRCKHFELGGEKKQKQALQF

YHR217C, 962 bp, CDS: 501-962 (SEQ ID NO 131)

CATCGCTTGATTTCCGGCCTGCAAAAATAAAGTAGTCGGTACGTACTTTTCGTTTTCAATT
TCCATGGTGCACAGTATCTTAACTATCTGCTTAGTCGAGGAGAACAGGATTCTGTTTCGT
TGCTCAGCCGCTTCGTGGATATTCTCTTGGATACTTTAAACATGGACCTACGTTCCGCTC
TCGAAAAGACCAATATAATAAAAAGTTATAAATTACATTTCTTATTAGGTATACGACCT
CGCGCTTCGAAGTAGAGGAGCCCTTTTGGCGTACCTACATATGGCGCGTCAGACAGACA
AACTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATTACCCACGAC
GTATCAAGTTACTTCCTTGGTGCAATGTCCCACTATAAAAAAATTCCTTGACGCTAGATC
GTTGGACTAAAATCTGCGTCACAATCGCCTAACAGGAAATATTGCCTATTTTCGTACAA
GGTTACTTCCTAGATGCTATATGTCCCTACGGCCTTGTCTAACACCATCCAGCATGCAAT
ACAGTGACATATATATACACACACCCACACCCACACCCACACCCACACACACCCCA
CACACACACCCACACACACCCACACCCACACCCACACCCACACACACCCACACCC
CACACACACCCACACCCACACCCACACCCACACCCACACACACCCACACCCATCTA
ACCTGTCTCTTAACCTACCCCTACATTACCCCTACCTCCCCACTCGTTACCCTGCCCCACT
CAACCATAACCACTCCCAACCAACCATCCATCTCTTACTTACTACTACCATCCACCGCCCA
TCATAACCGTTACCCTCCAATTACCCATATCCAACCTCCACTACCATTACCCTGCTATTAC
CTACCATCCACCATGTCTACTCACTGTACTGTTGTTCTACCCTCCATATTGAAACGTT
AA

FIG. 1 - 43

YHR217C, 153 aa (SEQ ID NO 132)
MSLRPCLTPSSMQYSDIYIHTPHPHPHPHPTHTHTPHPTPTPTPHPHPHPTPHPHPTTPTP
TPHHTHTPHHTLSNLSNLPSHYPTSPVLTLPHSTIPLPTTIHLSTYYYHPPPIITVTLQ
LPISNSTTITLLLPYHPPCPHTCTVVLPSILKR

YIL112W, 3752 bp, CDS: 501-3752 (SEQ ID NO 133)
TTCCATAGGGCTTATTTTCCAGTTGATGGAATGGGAGGTTGCTCTTAACGCGAAGACTAA
CGTGCAAGCCAACAGTTATAGAAAAGTACCGTGAGAGAGAAAAAAGATATAGCA
TTCAATGAGGCTTATTTGAGGGGCACGATGCTCTTTTTTCTTCTGTACTTTATAAATAA
TTCCGTATTTCTTCGCTTTGTTTCATGCTCTGTTCTGAGCTTTTAGTTTCTCTTATTGAG
AGCCTTTTCCAATCAAGGCTCAGGAAGTGACTCGTCTTAGAAGAACAAGTTTGGATT
TGGTAGGGTTCTTGACGAAGTTCTCAATATAATTTGCGCATTTACTGTACGGTTTCATAC
TAGTTTATTCCGGGTAACAAGTTTCTTGTGATGCTAAATCAATGTGTATATTGAGAAAA
CTATGTAGTAAGTTACACAAAGCAACAAGGATATTATTATATGTGACAGAGAAGAATTG
CTGTAGAGATTCATGACAATATGAATGAGACTACTACAAAACAGCCGCTAAAGAAAAGGT
CCCTGAGCAGCTATCTTTCAAACGTGAGCACGAGACGGGAGGAGCTGGAAAAGATTTCTA
AACAAAGAAACATCCGAAGAGGAAGATACTGCCGGCAAGCATGAACAAAGGGAAACACTGT
CGGAAGAAGTAAGTGATAAGTTTCCAGAAAATGTTGCATCGTTTCGCTCACAGACTACAA
GCGTTTCATCAAGCCACCCAAAATAACCTGAATGCAAGGAATCCGAAGACCTGGCCCAT
AGAATGATGCGAGTTCACACGAAGGAGAGGTTAATGGGGACAGCCGTCCGGACGATGTTT
CTGAAACGAATGAAAAATAAGCCAAGCAATACGAGCGAAAATTTTCGTATCATCATCAT
CACCCAATGTACGTAATGTTGATATCCAAAACCATCAACCTTTTTTCGAGAGACCAACTTC
GAGCGATGTTGAAAGAACC AAAAAGGAAAAC TGTGATGATTTTCATAGAAGAAGAGGGTT
TGGGAGCTGTTGAAGAAGAGGATTTAAGTGATGAGGTACTTGAAAAAATACACAGAAC
CAGAAAATGTGAAAAAGATATAGAGTATAGCGACTCAGATAAGGACACAGACGATGTGG
GAAGCGATGATCCACGGCACCCAACTCACCATAAAACTTGGTTCGTCGCAAACTTGGTTA
GAGGTGACCAACTTGATGCAACAACAAGTTCCATGTTTAATAACGAATCAGATTCTGAAT
TATCAGATATCGATGATAGCAAGAATATTGCTTTTATCCAGTAGCCTATTTAGAGGCGGTT
CTTCACCTGTGAAAGAGACAAACAACAACCTTTCAAATATGAATTCTTCACCAGCACAAA
ATCCAAAAGGGGTTCTGTCTCCAGGAGTAATGATAGTAACAAGAGTTCTCATATAGCTG
TTTCCAAGCGCCCCAAACAGAAGAAGGGCATATATAGGGATTCTGGTGGTAGAACAAGAC
TACAGATTGCTGTGACAAGGGCAAATATGATGTAGTCAAAAAGATGATTGAAGAAGGAG
GTTACGATATTAAATGACCAAGACAATGCTGGTAATACAGCATTCATGAAGCGGCGTTGC
AAGGTCATATTGAGATTGTGGAAC TGTGATAGAAAATGGTGCAGATGTAAATATCAAGT
CTATTGAAATGTTCCGCGATACTCCCTTGATCGATGCTTCCGCCAATGGACACTTGGATG
TTGTCAAGTATCTTCTTAAAAACGGTGCGGACCCAACTATACGTAACGCTAAAGGGTTAA
CTGCGTTTGAATCTGTCGATGATGAATCTGAATTTGATGATGAAGAAGACC AAAAGATTT
TGCGTGAAATAAAAAAAGGTTGAGTATAGCCGCTAAAAAATGGACTAACAGAGCAGGAA
TTTCATAATGACAAATCTAAAAATGGCAATAAGTCTCACACAATAGATCAGCCACCTTTTG
ATAATACCACAAAAAGCCAAAAACGAAAAGGCCGCTGACTCACCTTCAATGGCTTCCAATA
TTGATGAGAAAGCTCCGGAAGAGGAATTCATTGGACAGATGTTACTTCTAGAGCGGGAA
AAGAAAAACTGTTTAAAGCTTCGAAGGAGGGACATTTACCATACGTTGGTACGTATGTAG
AAAATGGTGGTAAGATAGACTTAAGGTCATTTTTCGAAAAGCGTTAAGTGTGGCCATGAAG
ATATTACAAGTATCTTTTGGCATTCCGATTTCCCGTAAATCAAAC TCAAGGGATAATA
AAACATCCGCTTTAATGGTAGCTGTAGGTCGTGGCCATCTTGGAACTGTTAAACTGCTAT
TAGAGGCAGGTGCAGATCCAACCAAAAGAGATAAAAAGGGTCGTACCGCTTTGTACTATG
CCAAAAACAGCATAATGGGAATAACAAACAGTGAAGAAATTC AATTGATTGAAAATGCTA
TAAATAACTATTTGAAGAAGCACTCTGAAGATAATAATGATGATGATGATGATGATA
ATAATAATGAAACATATAAACATGAAAAAAGAGAGAGAAAACGCAATCACCCATATTAG
CAAGCCGAAGAAGTGCCACTCCTAGAAATTGAAGACGAAGAGGACGATACGAGGATGCTCA
ATCTGGCAGACGATGACTTTAATAACGATCGTGATGTCAAGGAATCTACAAC TTCGGATT
CGCGCAAGAGATTGGATGACAATGAAAATGTTGGTACTCAATACTCATTGGACTGGAAAA
AACGTAAAACAAATGCCTTGCAAGATGAAGAAAAAATTA AAAAGTATCTCACCACCTCTCTA
TGGAACCTCATTCTCCAAGAAGGCAAAATCTGTAGAGATAAGTAAAATACATGAAGAAA
CGGCTGCTGAAAGAGAAGCAAGACTCAAGGAAGAGGAAGAATACAGAAAAGAAAAGATTAG
AAAAGAAAAGAAAAAAGAACAGGAAC TACTACAAAAGCTGGCCGAAGATGAGAAAAAA
GGATCGAAGAACAGGAGAAGCAGAAAGTCTTAGAAATGGAAAGATTGGAAAAAGCTACTT
TAGAGAAAGCAAGAAAAATGGAAAGGGAAAAAGAAATGGAAGAAATCTCTTATAGAAGGG

FIG. 1 - 44

CAGTAAGGGACTTATATCCGTTAGGACTGAAGATTATTAACCTTCAACGATAAACTTGATT
ACAAAAGATTTTGGCCGCTATATTATTTGTAGACGAAAAAACGATAAAATTTGTGCTCG
ACTTGCAAGTAATGATATTGTTGAAGGATATCGACTTGCTCTCAAAGGACAACCAACCAA
CTTCTGAGAAGATTCCCGTCGATCCCTCGCACCTGACTCCATTGTGGAATATGTTGAAAT
TCATTTTCTGTATGGAGGTAGTTATGATGATAAAAAGAACAACATGGAAAATAAAAGAT
ATGTTGTAAACTTTGATGGGGTTGATTTGGACACAAAGATTGGGTATGAGCTTTTGGAGT
ACAAAAAATTTGTTAGTTTGGCCATGGCGTGGATTAAATGGGATAACGTTGTTATTGAAA
ACCACGCAAAAAGAAAAGAAATTGAAGGAAATATGATTCAAATATCAATAAACGAATTTG
CACGATGGAGAAACGATAAGCTGAACAAAGCGCAGCAGCCGACGCGCAAACAGCGTTCTC
TAAAAATACCTCGAGAGTTACCGTTAAATTTCAACACCGTATGAGCATATCCTCCGTCC
TCCAGCAGACATCCAAAGAACCATTTTGGTAA

YIL112W, 1083 aa (SEQ ID NO 134)

MNETTTKQPLKRSLSYLSNVSTRREELEKISKQETSEEEDTAGKHEQRETLSEEVSDK
FPENVASFRSQTTSVHQATQNNLNAKESEDLAHKNDASSHEGEVNGDSRPDDVPETNEKI
SQAIRAKISSSSSSPNVRNVDIQNHQPF SRDQLRAMLKEPKRKTVDDFIEEGLGAVEEE
DLSDEVLEKNTTEPENVEKDIEYSDSDKDTDDVGSDDPTAPNSPIKLGRRKLVRGDQLDA
TTSSMFNNESDSELSIDDSKNIALSSSLFRGGSSPVKETNNNLSNMNSSPAQNPKRGSV
SRSDNSNKSSHIAVSKRPKQKKGIYRDSGGRTRLQIACDKGKYDVVKMIEEGGYDINDQ
DNAGNTALHEAALQGHIEIVELLIENGADVNIKSIEMFGDTPLIDASANGHLDVVKYLLK
NGADPTIRNAKGLTAFESVDDSEFDDEEDQKILREIKKRLSIAAKKWTNRAGIHNDKSK
NGNNAHTIDQPPFDNTTKAKNEKAADSPMASNIDEKAPEEEFYWTDVTSRAGKEKLFKA
SKEGHLPIYVGTYVENGGKIDLRSFESVKCGHEDITSIFLAFGFPVNQTSRDNKT SALMV
AVGRGHLGPTVKLLLEAGADPTKRDKKGRNALYAKNSIMGITNSEIOLINAINNYLKK
HSEDNNDDDDDDDNNNETYKHEKKREKTQSPILASRRSATPRIEDEEDDTRMLNLADDDF
NNDRDVKESTTSDSRKRLDDNENVGTQYSLDWKKRKTNALQDEEKLKSI SPSLMEPHSPK
KAKSVEISKIHEETAAREEARLKEEEYRKKRLEKKRKEQELLQKLADEKKRIEEQEK
QKVLIMERLEKATLEKARKMEREKEMEEISYRRAVRDLYPLGLKIINFNDKLDYKRFPL
YYFVDEKNDKFVLDLQVMILLKDIDLLSKDNQPTSEKIPVDPSHLTPLWNMLKFIFLYGG
SYDDKKNMENKRYVNFDFGVDLDTKIGYELLEYKFFVSLPMAWIKWDNVVIENHAKRKE
IEGNMIQISINEFARWRNDKLNKAQQPTRKQRSCLKIPREL PVKFQHRMSISSVLQOTSKE
PFW

YIL115C, 4883 bp, CDS: 501-4883 (SEQ ID NO 135)

TTTCAATGCGCTACAACCTGACTGAACCACTCCACAAATTTGGCTGCTCTATCGTTCTC
GCCCTGAGAGATTTTATTTTCTTATAAAATTTTACTAAATAAGGATTTGTACTTTTGATAG
AGTTTTTTTTTTTTCTGACGTTTGTGTTAGTTAATATTATATAATAGTATTTAGGAACTA
GGTGGGAGGGGACATCGCAACTTTTATCGTGACCTACGACCACTGTTTTCATTGTTT
GATCAAAAGAGAAAAAAGACAAAGGACCGAAGGATAGTTGCACGCATAAACTGGAGAAA
AAATGTGTTTGACATCGGCGTTTAGGCTTGTTTGTCTGTGTCACACATACGCTGCTTCAC
ACCAATTCATATTTCTCAGGTTAATTTGTCTCCTCTCCAACCTTCAATAACGATTTTGGCT
GAAGGTTTAATTTTCATTATTGCAATTTTAGCAGAGAAACGCACATAAATATATATATATT
GATTACAGAACCATTATAACATGTCTTCTTTGAAGGATGAAGTACCCACTGAGACTTCCG
AAGACTTCGGTTTTAAGTTTTTAGGTCAAAAACAAATCTACCTTCTTCAATGAAAAAC
TGCCATTTGCATCTCTACAAAATCTCGATATTTCAAACAGTAAGTCTTTATTCGTTGCTG
CCTCTGGTAGTAAGGCGGTGGTCGGCGAATTACAATTACTGAGAGATCATATCACCTCCG
ACTCTACTCCGTTAACGTTCAAGTGGGAGAAAGAAATCCCAGATGTAATATTTGTGTGCT
TTCATGGTGATCAGGTTTGGTTTCAACCAGAAATGCATTATATTCGTAGACTGGAGG
AATTGAGTGAATTTTGAACGGTCACTTCTTTTGAAGGAGCCAGTTTTCATTGAAGAACG
TTAATAACACTTTAGTAATTTTAAATTCAGTCAATGATTTATCAGCACTGGATTTAAGAA
CAAAATCGACTAAGCAACTGGCACAAAACGTTACCTCTTTTGATGTCACAAATTCGCAGT
TAGCAGTTCTACTAAAAGATAGAAGTTTTCAAAGTTTTCATGGCGAAATGGCGAAATGG
AAAAACAATTTGAGTTCTCTCTACCGTCAGAATTAGAAGAGCTTCCAGTAGAAGAATATT
CCCCTTTGAGTGTTACCATCTCTCTCCACAGGATTTTTTGGCGGTTTTCGGTAATGTTA
TATCAGAGACCGATGACGAAGTTTCATACGATCAAAAATGTACATTATAAAGCATAG
ACGGCAGCGCCTCATTTCAAGAACTTTTGTATATTACACCTCCATTTCGGGCAATAGTAA
GGTTCATATATGTACAAAGTTACCTTGTCTGGTTTAAATTGAACCTGATGCAACGTAA
ATGTGCTAGCATCATCATGTTCAAGTGAAGTAAGTATATGGGACTCGAAACAAGTTATTG

FIG. 1 - 45

AACCTTCCCAGGATTCTGAACGAGCAGTATTGCCCATCAGTGAGGAAACAGATAAGGACA
CAAAATCCAATAGGTGTGGCAGTTGACGTCGTTACTTCAGGCACATTATTCTAGAACCTTGTT
CCGGTGTTGATACGATAGAGCGATTGCCGCTCGTTTACATATTGAATAACGAAGGTAGCT
TACAGATAGTCGGGTGTTTCATGTGGCAGCAATCAAAAGCGGCCATTATAGCATAAATC
TGGAACTCTTTAGAACATGAGAAATCTCTCTCTACATCAGAAAAAATTCCTATTGCTG
GACAGGAGCAGGAAGAAAAAAGAAAAAATGAATCAAGTAAGGCTTTATCAGAGAATC
CTTTCACATCAGCAAATACATCAGGCTTCACTTTTCTTAAAACACAACCAGCCGCTGCCA
ATAGCCTGCAGTCTCAAAGTTCTTCAACCTTTGGTGCTCCCTCATTTGGATCATCCGCAT
TTAAATTTGACTTGCCATCAGTCTCATCTACCAGTACTGGTGTAGCGTCCAGTGAACAAG
ACGCAACAGATCCTGCTTCTGCTAAGCCAGTATTCCGGCAAACCCGCGTTCCGAGCTATTG
CCAAAGAACCGTCAACATCAGAATATGCCCTTTGGCAAGCCATCTTTTGGTGCTCCCTCCT
TTGGCTCTGGAAGTCATCTGTTGAATCGCCTGCCTCCGGATCTGCCTTTGGTAAAGCCCT
CTTTTGGTACTCCTTCCCTTTGGCTCTGGAAATTCATCTGTTGAGCCGCTGCCTCCGGAT
CTGCATTTGGTAAGCCCTCTTTTGGTACTCCTTCTCTTTGGCTCTGGAAATTCATCTGCTG
AGCCGCTGCTTCCGGATCTGCCTTTGGTAAGCCCTCTTTTGGTACATCTGCATTCGGAA
CTGCATCAAGTAACGAAACTAACTCTGGATCCATATTTGGAAGGCTGCATTTGGTTTAT
CATCTTTTGCACCCGCCAACAATGAACCTTTTCGGATCAAACCTTTACTATTTCAAAACCTA
CAGTTGACAGCCCAAAGGAGGTAGATTCAACGTCACCTTTCCCATCTTCTGCGCATCAAA
GTGAAGATGAGTCTAAGAGTGATGTAGACTCTTCTTCGACACCTTTTGGTACGAAACCTA
ACACCTCTACGAAACCAAGACCAATGCCTTTGATTTTGGGAGTTCTTCTTTGGATCTG
GATTTTCAAAGGCTCTGGAATCTGTTGGTTCCGATACAACCTTTTAAATTCGTTACTCAGG
CTTCACCTTTCTCTTACAGTTAGGAAACAAATCACCATTCAAGTTCTTTCACAAAAGATG
ATACTGAAAATGGATCTTTAAGTAAGGGCTCTACCAGTGAAATCAATGACGATAATGAAG
AACACGAAAGCAATGGTCCCAACGTAAGCGGTAATGATTGACAGATTCTACGGTTGAGC
AAACATCTTCTACTAGATTACCGGAACTCCCTCGGATGAAGATGGTGAAGTTGTGCGAGG
AGGAAGCGCAAAAATCCCCATAGGCAAGCTAACTGAAACTATAAAAAAAGTGCCAATA
TTGACATGGCTGGTTTAAAAAATCCTGTATTGGAATCATGTCAAAGCAAAATCCGAAT
CGCCGTTTTCAGCATTTGCAACAAATATTACCAACCAAGCTCTACAACACCTGCTTTT
CGTTTGGTAACCTCCACAATGAATAAAAGTAATACATCTACGGTTTCAACCAATGGAAGAAG
CTGATACTAAAGAACTAGTGAAAAGGGCCCCATAACCTTGAAGAGTGTGGAGAATCCGT
TTCTACCAGCGAAAGAAGAAAGAACTGGAGAAAGTTCTAAAAAGGATCATAACGATGACC
CAAAAGATGGTTATGTATCAGGAAGTGAAATATCTGTAAGGACTTCTGAAAGTGCTTTTG
ATACCACAGCAAAACGAAGAAATTCAAAGTCACAGGACGTGAACAATCATGAAAAAGCG
AAACAGACCCCAAAATATAGTCAACATGCTGTGGTTGATCAGGATAACAAGTCTAAAGAAA
TGAATGAAACTTCGAAGAATAATGAAAAGGAGCGGTCAACCAATCATGGTGTCCAAGGAG
ATGGAATAGCATTGAAAAAGACAATGAAAAAGAGAATTTTGATTCAAATATGGCAATAA
AGCAATTCGAAGACCACCAATCTTCAGAAGAGGACGCGAGCGAAAAAGACAGTAGACAAA
GCAGTGAAGTTAAAGAATCAGATGATAACATGTCACTCAACAGTGACCGGGATGAAAGTA
TATCTGAGTCCCTACGATAAACTGGAAGATATTAATACTGATGAGCTACCTCATGGTGGAG
AAGCTTTTAAAGCACGTGAAGTGAGCGCTTCCGCTGATTTTGATGTACAACTTCATTAG
AAGACAATTATGCTGAATCTGGCATACAGACAGACCTTTTCAGAAAGTTCCAAGGAAAATG
AAGTTCAAACGGATGCCATACCCGTGAAACACAACAGTACACAACTGTTAAGAAGGAAG
CAGTCGACAATGGTCTGCAAACTGAGCCTGTTGAAACATGTAATTTTTCTGTTCAAACAT
TTGAAGGTGACGAAAATTATTTAGCAGAGCAATGCAAACCAAGCAATTGAAAGAATATT
ACACAAGTGCAAAAGTATCAAATATTCCTTTTCGTTTCAAAAATTTCTACGTTAAGGTTGA
TTGAGAGTACATTTTCAGACGGTCAAGCTGAGTTTACTGTTCTGATGGAAAACATCCGGA
ATATGGATACTTTTTTTACTGATCAATCGAGCATCCCTTTGGTGAAGCGTACAGTCCGGT
CTATCAATAATCTGTATACTTGGAGAATACCAGAGGCTGAAATTTCTATTAAATATTTCAGA
ATAATATCAAGTGTGAACAAATGCAAAATAACAAATGCTAACATTCAAGACCTGAAGGAAA
AAGTTACAGATTATGTCAGGAAAGATATTGCACAAATAACTGAAGATGTAGCCAATGCAA
AAGAGGAGTATCTGTTTAAATGCATTTTGATGATGCTTCGAGTGGATACGTTAAAGATC
TCAGCACGCATCAATTTAGAATGCAAAAGACATTACGTCAAAAGCTATTTCGATGTGTCCG
CCAAAATTAATCATACTGAAGAGTTGCTGAACATTTTAAATTTGTTCACTGTAAAGAATA
AGAGATTGGACGATAATCCATTAGTGGCAAACTAGCTAAAGAATCTCTTGACGAGTACG
GTTTACTAAAAGAAATCAAATTTATGCGTGAGCAAGTGAGTAGGTTACAATTTGGAGGAGA
AAGGTAAAAAGGCTTCGTGCTTCGATGCATCCTCTTCAATAACAAAGGACATGAAAGGAT
TTAAAGTAGTAGAAGTTGGGTTGGCCATGAATACGAAAAAGCAAATTGGTGATTTCTTCA
AAAATTTGAACATGGCAAAATAG

FIG. 1 - 46

YIL115C, 1460 aa (SEQ ID NO 136)
MSSLKDEVPTETSEDGFKFLGQKQILPSFNEKLPPFASLQNLDISNSKSLFVAASGSKAV
VGELQLLRDHITS DSTPLTFKWEKEIPDIVFVCFHGDQVLVSTRNALYSLDLEELSEFRT
VTSFEKPVFQLKNVNNTLVILNSVNDLSALDLRTKSTKQLAQNVTSFDVNTNSQLAVLLKD
RSFQSFPAWRNGEMEKQFEFSLPSELEELPVEEYSPLSVTILSPQDFLAVFGNVISETDDE
VSYDQKMYIIKHIDGSASFQETFDITPPFGQIVRFPYMYKVTLSGLIEPDANVNVLASSC
SSEVSIWDSKQVIEPSQDSERAVLPISEETDKDNTNPIGVAVDVVTSGTILEPCSGVDTIE
RLPLVYILNNEGSLQIVGLFHVAAIKSGHYSINLESLEHEKSLSPTEKIP IAGQEQUEEK
KKNNESSKALSENPF TSANTS GFTFLKTQPA AANSLOSQSSSTFGAPSFGSSAFKIDLPS
VSSTSTGVASSEQDATDPASAKPVFGKPAFGAIAKEPSTSEYAFGKPSFGAPSFGSGKSS
VESPASGSAFGKPSFGTPSFGSGNSSVEPPASGSAFGKPSFGTPSFGSGNSSAEPPASGS
AFGKPSFGTSAFGTASSNETNSGSIFGKAAGSSSFAPANNELFGSNFTISKPTVDSPE
VDSTSPFPSSGDQSEDESKSDVDSSSTPPFGTKPNTSTKPKTNAFDGSSSFSGSGFSKALE
SVGSDTTFKFGTQASPFSSQLGNKSPFSSFTKDDTENGSLSKGSTSEINDNEEHESNGP
NVSGNDLTDSTVEQTSSTRLPETPSDEDEGEVVEEEAQKSPIGKLTETIKKSANIDMAGLK
NPVFGNHVKAKSESPFSAFATNITKPSSTPAFSGNSTMNKSNTSTVSPMEEDTKETS
EKGPITLKSVENPFLPAKEERTGESSKKDHNDPDKGYVSGSEISVRTSESAFDTTANEE
IPKSQDVNMHEKSETDPKYSQHAVVDHDKSKEMNETSKNNERSGQPNHGVOGDGIALKK
DNEKENFDSNMAIKQFEDHQSSSEEDASEKDSRQSSEVKESDDNMSLNSDRDESI SESYDK
LEDINTDELPHGGEAFKAREVSASADFDVQTSLEDNYAESGIQTDLSESSKENEVQTDAL
PVKHNSTQTVKKEAVDNGLQTEPVETCNFSVQTFEGDENYLAEQCKPKQLKEYYTSKVS
NIPFVSQNSTLRLEISTFQTVAEFTVLMENIRNMDTFFTDQSSIPLVKRTVRSINNLYT
WRIPEABILLNIQNNIKCEQMQITNANIQDLKEKVTDYVRKDIAQITEDVANAKEEYFL
MHFDDASSGYVKDLSTHQFRMQKTLRQKLFVSAKINHTEELLNLIKLFVKNKRLDDNP
LVAKLAKESLARDGLLKEIKLLREQVSRQLQLEEKGKKASSFDASSSITKDMKGFKVVEVG
LAMNTKKQIGDFFKNLNMAL

YIL148W, 1321 bp, exon1: 501-508, intron1: 509-942, exon2:
943-1321 (SEQ ID NO 137)

TCGATCAACTCTATCCAACAATTCTATAATATCCACTGTTCATTAACGAATATTGGTCTT
TTTCCCTTATGGTGAAGTAAATTTTCCATGCAATATCCGGGTAAAGCTATCGACAAGTTTA
TTGACTGCAATTTGAGTTTATTACATCCGTACATTACTAAGATGTATGGTTTTTCTATTT
TTGTGCTCCGTGTCGATATTTCTGTGGAGCAAACCAGAAAAGATGCGGAACCTCTTAGCAC
TCCGCTGACATAGGCGGAGCATATTCCTCCTATGGGATGGGTTTTGTGTACTCTTTT
CTCTCTAGACAGGACCTCCGATTGCCTCCCTGAGGGTGAGATGGTTTCCGCGCTCAGGAC
GGCCTTCTCCAGTTTCTAGCGAGGCATACATTCCAACCAAAGGTGTATCAAGAATATCTG
AAATTAAGGTAGTTGAATCTCTATTTGTGTGTGTATTACCGCTTATTATCCCATAGTT
GAGACGACCAAGATTCAAACATGCAAAATGTATGCACCATATCCATTCTAAACATAGTTTT
TCGAACGTTTCAAGCTTAAAGGGACAATTATTTTAGAACTGAATTTTTTACCCAGTGGA
TAACATCGTATCTGTAAAGTCTACAAAATTTTTATCCATCAAAAATTAAACAAAGAAA
ACTGCCAAACTGAATATGAGGAACCTTCTCTCTAGGAATGACTTAGTGAATGTACAGTG
ACTTGTGGAAAATATGATTAGATTTTGTAGCGGGTGATGCGACTTAACAGTCTCATTGCCT
AAGAAATATCCAAATTTGTGGTTTCATGCTCTCCCCAAGATATGACGATGAGAGCTCGTT
TAAAATTTTGTCTTCTTCCGAACAGTTATGAAAAAACTATTACGTGTTTTTATGATATCC
TTACTAACTTGTCATTTTTTTTATAAAATATTTTTTTTAAACAGTTTTGTCAAGACTTTGAC
TGGTAAGACCATCACTTTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCAAA
GATTCAAGACAAGGAAGGTATCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCA
ATTGGAAGACGGTAGAACCTTGTCTGACTACAACATTCAAAAAGAATCCACTTTGCACTT
AGTCTTGAGATTGAGAGGTGGTATCATTGAACCATCTTTGAAAGCTTTGGCTTCCAAGTA
CAACTGTGACAAATCTGTTTGCCGTAAGTGTTATGCTAGATTGCCACCAAGAGCTACCAA
CTGTAGAAAGAGAAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTAAAATG
A

YIL148W, 128 aa (SEQ ID NO 138)
MQIFVKLTGKTTITLEVESDITDNVSKSIQDKEGIPPDQQRLLIFAGKQLEDGRTLSDYN
IQKESTLHLVRLRGGIIEPSLKALASKYNCDKSVCRKCYARLP PRATNCRKRKCGHTNQ
LRPKKLK

FIG. 1 - 47

YIL150C, 2216 bp, CDS: 501-2216 (SEQ ID NO 139)
AATATTCAACCTGAAGTTGCAGTCAAAGCGGCGATTAACTTTTCCAACGTAACCGATCTA
ACTAACAATAGCACCGATGGAGCAAAAATAACAGAAATTGGAAGTACATCTAAACGGCCA
ATTGAGAGCGGTACATCTTCTGATCCAGACACCAAAAAGGTTAAAGAGAGTCCAGCAAAT
GATCAAGCTTCCAACGAGTGATGTAATATTAAACAATGTAATTATATAAATATGAAACAT
CTACATATTTTAAATGTCATAATGTCATTACAGAGGACATAAAGTGATTTATGACACAT
CCGTACTAGTAGTTAAGTATGAACAAATTTTGGGTTTATTTGCCATTTTTCACGCGG
GTTTCTTGGATGCGCAAACCCACCTTTTCTAACACCACTAAGAAATATCAACTTTATAGG
CCATCGAAGATAAAGGAACGTAAGTTTGTCAATTCAACCTCACATTTTCAACGCACATTA
AGCACTTGGTTCGTGGAGAAATGAATGATCCTCGTGAAATTTTAGCGGTTGATCCGTACA
ATAATATTACTTCTGATGAAGAGGATGAGCAAGCCATCGCGAGAGAACTTGAATTTATGG
AACGAAAGAGGCAGGCCTTAGTGGAACGATTAAAAAGAAAGCAAGAATTTAAGAAACCCC
AGGATCCTAATTTTGAAGCCATCGAGGTACCTCAATCTCCTACCAAAAACCGTGTGAAAG
TGGGGTCTCATAATGCTACACAACAAGGCACAAAATTCGAAGGTTTGAATATTAATGAAG
TAAGGTTATCTCAATTACAGCAGCAACCAAAACCAGCTAGTACAACCACATACTTTA
TGGAGAAATTTCAAAACGCAAGAAAGCAAGATAAACAAATTGCCAAGTTTGAAAGCA
TGATGAATGCAAGAGTACATACGTTTCAAGTACCGATGAGAAGAAATATGTGCCGATAATCA
CAAACGAATTAGAAAGCTTTTCAAATCTTTGGGTTAAAAAGAGGTACATACCTGAAGATG
ACTTAAACCGGGCTTTGCATGAGATCAAAATCCTTCGGTTGGGCAAACTTTTGTCTAAAA
TTCGCCCCACCTAAATTTCAAGAGCCTGAATACGCCAACTGGGCCACCGTAGGCCTCATTA
GCCACAAATCGGACATCAAATTTACATCATCTGAAAAGCCAGTCAAATTTCTCATGTTCA
CCATAACGGACTTTCAGCATACACTAGATGTTTATATCTTCGGGAAAAAGGGTGTAGAAA
GATATTATAATCTTCGCCTGGGTGATGTGATAGCAATATTAACCCAGAAGTACTACCAT
GGAGACCCTCAGGGCGAGGAAATTTTATCAAATCCTTCAACCTTCGAATTAGTCATGACT
TCAAATGTCTGGAGATAGGTTCAAGTAGAGATTTAGGTTGGTGTCCCATAGTGAATA
AAAAGACTCACAAAAAATGTGGCTCTCCCATTAACATATCTTTCATAAGTGTTCGCGATT
ACCATAGAGAAGTGCAATTTCTGTGGAACAAGTGCTAAAAAGAAATTGAATTTAAATGGTGGGT
ACGCCTTGGGCGCGCTTACGAAAGTGGACTCTCAACCAAGCCTATATAAGGCCAAAGGGG
AAAACGGGTTTAAATATAATCAAAGGTACTCGTAAGCGCCTGTCAGAAGAGGAGGAAAGAC
TTAAAAAGAGCTCTCACAATTTTACGAATAGTAATTCTGCCAAAGCATTTTTCGACGAGA
AATTTCAGAATCCAGATATGCTGGCAAACCTTAGACAATAAAAGAAGGAAAAATAAGAAA
CTAAGAAATCGACAGCACTGAGCCGCGAATAGGCAAAATTATGAGAAGGAGGGAATCCA
GCGGATTAGAAGATAAGAGCGTCGGAGAGCGACAGAAAAATGAAACGAACCAAGAAAGTG
CCCTCCAGACAGGGCTTATCCAACGCCTAGGATTGATCCCACTCATGGAAAAATTTCCC
AAGTACTCAAGTCTTCTGTATCAGGGAGCGAACCTAAGAACAACCTTACTCGGTAAAAAAA
AAACTGTTATAACGATCTCTTGCATTACAAGAAGGAAAAAGTCATTCTCGCACCTTCAA
AGAACGAATGGTTCAAGAAAAGAAGCCATCGCGAAGAAGTTTGGCAAAAACATTTTCGGAT
CCAAGGAACTAAAGAACTTCTGACGGTAGTGCCAGCGATCTTGAGATAATATAA

YIL150C, 571 aa (SEQ ID NO 140)
MNDPREILAVDPYNNITSDEEDEQAIARELEFMERKRQALVERLKRKQEFKKPQDPNFEA
IEVPQSPTKNRVKVGSHNATQQGTFEGSNINEVRLSQLQQPKPPASTTTYFMEKFQNA
KKNEDKQIAKFESMMNARVHTFSTDEKKYVPIITNELESFNLWVKRYIPEDDLKRALH
EIKILRLGKLFAKIRPPKFQEPYANWATVGLISHKSDIKFTSSEKPVKFFMFTITDFQH
TLDVYIFGKKGVERYYNLRLGDVIAILNPEVLPWRPSGRGNFIKSFNLRI SHDFKILEI
GSSRD LGWCP IVNKKTHKKCGSPINISLHKCCDYHREVQFRGTS AKRIELNGGYALGAPT
KVDSQPSLYKAKGENGFNI IKGTRKRLSEEEERLKKSSHNF TNSNSAKAFFDEKFQNPDM
LANLDNKRRI IETKKSTALSRELKIMRRRESSGLEDKSVGERQKMKRTTESALQTGLI
QRLGFDPTHGKISQVLKSSVSGSEPKNNLLGKKKT VINDLLHYKKEKVILAPSKNEWFKK
RSHREEVWQKHFGSKETKETS DGSASDLEII

YIL167W, 1133 bp, CDS: 501-1133 (SEQ ID NO 141)
GACATTTTGAAAAAATTACATTTATAGAAGTTTATTATAACGTAACAGTTAACAACAAAG
GCTCATAGTCCGAGATCAATATAATAAATTATTCAAGGTTTAAAGGAAGAAGTTACCATGG
AAATGACTTACTATGAAAAGACACCTTTGATTCGTCAATTTTGAACAATGGTAAGACAA
ATTTCGTGGTTTACGTTAAGCATGAGATGTTACAACCAGGTGGAAGTTTCAAATCGAGAG
GAATCGGGCATTTGATAAGGAAGAGTAATGAAGAAGCGCTAAGCGAGGGTTCTGGGAAGC
TTGCTGTATTTCTAGCTCTGGGGGAAATGCTGGTTTAGCAGCAGCAACTGCCTGCAGAT

FIG. 1 - 48

CGATGGCACTTAATTGCAGTGTAGTGGTTCCCTAAAACTACAAAACCTAGAATGGTAAAGA
AAATTCAAAGTGCAGGAGCCAAAGTCATTATCCATGGTGATCATTGGGGGGAAGCAGATG
AATACTTGAGGCACGAATGAATGGCGCAAGAAAGCCAACATGGTTGGAAGACACTATATG
TGCACCCGTTTGATAACGAGACAATTTGGGAAGGTCATTCTACGATTGTGGATGAAATCA
TAGAACAAATTGAAGGAAAATGATATATCCTTACCTAGGGTGAAAGCTTTGGTTTGTAGTG
TTGGTGGTGGTGGGCTATTTAGTGGCATAATTAAAGGCCCTAGATAGGAATCAGCTTGGCTG
AAAAAATTCCGGTCGTTGCTGTAGAAACTGCCGGTTGTGACGTATTGAATAAGTCTCTCA
AAAAAGGTAGTCCAGTTACTCTTGAAAAATTGACAAGTGTTGCAACTTCTTTGGCCTCCC
CATACATAGCATCATTTCGCGTTTGAGAGTTTTAACAAGTATGGATGTAAGTCTGTAGTTT
TATCAGATCAAGACGTTCTGGCAACATGCTTGAGATATGCCGATGACTACAATTTTATAG
TGAACACAGCCTGTGGAGCATCCTTACATTTATGTTATCATCCAGAGATTCCTGAAGACA
TTCTGGAACAAAAAATATATGAGGATGATATCGTTATTATAATCGCATGCCGTGGATCAT
GTATGACGTATGAAGACTTGGTGAAAGCGTCGAGCACATTAAACGTATCATAA

YIL167W, 210 aa (SEQ ID NO 142)

MAQESQHGSKTLYVHPFDNETIWEHGSHSTIVDEIIEQLKENDISLPRVKALVCSVGGGGFLF
SGIIKGLDRNQLAEKIPVVAVETAGCDVLNKSLLKKGSPVTLEKLTSVATSLASPYIASFA
FESFNKYGCKSVVLSQDVLATCLRYADDYNFIVEPACGASLHLCYHPEILEDILEQKIY
EDDIVIIIACGGSCMTYEDLVKASSTLNVS

YJL034W, 2549 bp, CDS: 501-2549 (SEQ ID NO 143)

CCATGAACTCAGCATGTGCTACTCCAGTTAATGACTTGTTCTGATCGTTCATGCCATAAG
CCATCACCTGGCCAGTTGGCGTATGTACAAAGATGCAAGCTACCGGTGTCATCGTGGT
CAAGAGCGTATCTAGCCAAACGGACAGCTGTCTCATATGTTTAATATGCTGCATAGTGT
GAGTCTCTAGTTTTTACCGCAGCCACCAGCCGCTTCTCGAGCAAAGTGATAGTCCATT
AGGATCATCATTCATCTAATTTTGTCTATGTTAGCTGCAACTTCTATTTTAATAGAAC
TTCTGGAAAATTTACCCGGCGCGGCACCCGAGGAACTGGACAGCGTGTGCAAAAAGTTGC
TTTTTTATATAAAGGACACGAAAAGGGTCTCTGGAAGATATAAATATGGCTATGTAATT
CTAAAGATTAACTGTGTTACTGTTTTACTTTTTTAAAGTCCCAAGAGTAGTCTCAAGGGA
AAAAGCGTATCAAACATACCATGTTTTTCAACAGACTAAGCGCTGGCAAGCTGCTGGTAC
CACTCTCCGTGGTCCGTGTACGCCCTTTTCGTGGTAATATTACCTTTACAGAATCTTTTCC
ACTCCTCCAATGTTTTAGTTAGAGGTGCCGATGATGTAGAAAACACGGAACGTGTTATCG
GTATTGACTTAGGTACTACTTATTCTGTGTTGCTGTGATGAAAAATGGTAAGACTGAAA
TTCTTGCTAATGAGCAAGGTAACAGAATCACCCCATCTTACGTGGCATTACCCGATGATG
AAAGATTGATTGGTGATGCTGCAAGAACCAAGTTGCTGCCAATCCTCAAAACACCATCT
TCGACATTAAAGAGATTGATCGGTTTGAAATATAACGACAGATCTGTTTCAAGAGGATATCA
AGCACTTGCCATTTAATGTGGTTAATAAAGATGGGAAGCCCGCTGTAGAAGTAAGTGTCA
AAGGAGAAAAGAAGGTTTTTACTCCAGAAGAAATTTCTGGTATGATCTTGGGTAAGATGA
AACAAATTGCCGAAGATTATTTAGGCACATAAGGTTACCCATGCTGTCTGTTACTGTTCTG
CTTATTTCAATGACGCGCAAAGACAAGCCACCAAGGATGCTGGTACCATCGCTGGTTTGA
ACGTTTTGAGAATTGTTAATGAACCAACCGCAGCCGCCATTGCCTACGTTTGGATAAAT
CTGATAAGGAACATCAAATTATTGTTTATGATTGGGTTGGTGGTACTTTTCGATGTCTCTC
TATTGTCTATTGAAAACGGTGTTTTCGAAGTCCAAGCCACTTCTGGTGATACTCATTTAG
GTGGTGAAGATTTTGACTATAAGATCGTTTCGTCAATTGATAAAAGCTTTCAAGAAGAAGC
ATGGTATTGATGTGTCTGACAACAACAAGGCCCTAGCTAAATTGAAGAGAGAAGCTGAAA
AGGCTAAACGTGCCTTGTCCAGCCAAATGTCCACCCGATTGAAATTGACTCCTTCGTTG
ATGGTATCGACTTAAGTGAAACCTTGACCAGAGCTAAGTTTGAGGAATTAAACCTAGATC
TATTCAAGAAGACCTTGAAGCCTGTGAGAAAGGTTTTGCAAGATTCTGGTTTGGAAAAGA
AGGATGTTGATGATATCGTTTTGGTTGGTGGTCTACTAGAATTCCAAAGGTCCAACAAT
TGTTAGAATCATACTTTGATGGTAAGAAGGCCTCCAAGGTTATTAACCCAGATGAAGCTG
TTGCATACGGTGCAGCCGTTCAAGCTGGTGTCTTATCCGGTGAAGAAGGTGTCGAAGATA
TTGTTTTATTGGATGTCAACGCTTTGACTCTTGGTATTGAAACCACTGGTGGTGTCTATGA
CTCCATTAATTAAGAGAAATACTGCTATTCTACAAAGAAATCCCAAATTTTCTCTACTG
CCGTTGACAACCAACCAACCGTTATGATCAAGGTATACGAGGGTGAAAGAGCCATGTCTA
AGGACAACAATCTATTAGGTAAGTTGAATTAACCGGCATTCCACCAGCACCAAGAGGTG
TACCTCAAATTGAAGTCACATTTGCACTTGACGCTAATGGTATTCTGAAGGTGTCTGCCA
CAGATAAGGGAACCTGGTAAATCCGAATCTATCACCATCACTAACGATAAAGGTAGATTAA
CCCAAGAAGAGATTGATAGAATGGTTGAAGAGGCTGAAAAATTCGCTTCTGAAGACGCTT

FIG. 1 - 49

CTATCAAGGCCAAGGTTGAATCTAGAAACAAATTAGAAAACACTACGCTCACTCTTTGAAAA
ACCAAGTTAATGGTGACCTAGGTGAAAAATTGGAAGAAGAAGACAAGGAAACCTTATTAG
ATGCTGCTAACGATGTTTTAGAATGGTTAGATGATAACTTTGAAACCGCCATTGCTGAAG
ACTTTGATGAAAAGTTTGAATCTTTGTCCAAGGTCGCTTATCCAATTACTTCTAAGTTGT
ACGGAGGTGCTGATGGTTCTGGTGCCGCTGATTATGACGACGAAGATGAAGATGACGATG
GTGATTATTTTGAACACGACGAATTGTAG

YJL034W, 682 aa (SEQ ID NO 144)

MFFNRLSAGKLLVPLSVVLYALFVVILPLQNSFHSNVLVRGADDVENYGTVIGIDLGTT
YSCVAVMKNGKTEILANEQGNRITPSYVAFDDEDERLIGDAAKNQVAANPONTIFDIKRLI
GLKYNDRSVQKDIKHLFPNVVNKDGKPAVEVSVKGEKKVFTPEEISGMILGKMKQIAEDY
LGTKVTHAVVTVPAYFNDAQRQATKDAGTIAGLNLVLRVNEPTAAAIAYGLDKSDKEHQI
IVYDLGGGTFDVSLLSIENGVFVQATSGDTHLGGEDFDYKIVRQLIKAFKKKHGIDVSD
NNKALAKLKREAEKAKRALSSQMSTRIEIDSFVDGIDLSETLTRAKEELNLDLFKKTLK
PVEKVLQDSGLEKKDVDDIVLVGGSTRIPKVQQLLESYFDGKKASKGINPDEAVAYGA
QAGVLSGEEGVEDIVLLDVNALTGDIETGGVMTPLIKRNTAIPTKKSQIFSTAVDNQPT
VMIKVYEGERAMSKDNLLGKFELTGIPAPRGVPQIEVTFALDANGILKVSATDKGTGK
SESITITNDKGRILTQEEIDRMVEEAKEFASEDASIKAKVESRNKLENYAHSKLNQVNGDL
GEKLEEDKETLLDAANDVLEWLDNDFETAIAEDFDEKPFESLSKVAYPITSKLYGGADGS
GAADYDDEDEDDEDDGDYFEHDEL

YJL035C, 1253 bp, CDS: 501-1253 (SEQ ID NO 145)

TACCTAAGTCAATACCGATAACAGTTCCTAGTCTTCTACATCATCGGCACCTCTAACTA
AAACATTGGAGGAGTGGAAAGAATTCTGTAAAGGTAATATTACCACGAAAAGGGCGTACA
GGACCACGGAGAGTGGTACCAGCAGCTTGCCAGCGCTTAGTCTGTTGAAAAACATGGTAT
GTTTGATACGCTTTTTCCCTTGAGACTACTCTTGGGGACTTTAAAAAAGTAAACAGTAA
CACGTTAATCTTTAGAATTACATAGCCATATTATATCTTCCAGAGAACCTTTTCGTGT
CCTTTATATAAAAAAGCAACTTTTTCGACACGCTGTCCAGTTCCTCGGGTCCGCGCCGG
GTGAAATTTCCAGAAGGTTCTATTAAATAGAAAGTTGCAGCTAACATAGCAAAATTAGA
TGAATGATGAGTCTAATGGGATCTACACTTTGCTCGAGAAGCGGCTGGTGGCTGCGGTA
AAAAC TAGAGGACTCAGACTATGCAGCATATTAAACATATGAGGACAGCTGTCCGTTTGG
CTAGATACGCTCTTGACCACGATGAGACACCGGTAGCTTGCATCTTTGTACATACGCCAA
CTGGCCAGGTGATGGCTTATGGCATGAACGATACGAACAAGTCATTAACTGGAGTAGCAC
ATGCTGAGTTTCATGGGGATCGATCAGATCAAGGCGATGTTGGGCTCCCGAGGAGTTGTTG
ACGTGTTCAAAGACATTACTCTATATGTTACTGTAGAACCCTGTATAATGTGTGCATCTG
CTCTCAAGCAATTAGACATTGGAAAGGTGGTGTTCGGTTGTGGCAACGAGAGATTTGGAG
GCAACGGTACTGTCTTGTGCTAATCATGATACGTGTACATTAGTGCCCAAGAACAATA
GTGCGGCAGGGTACGAGAGTATACCGGGGATCTTGAGGAAAGAAGCAATAATGCTGCTGA
GATACTTTTATGTAAGACAAAATGAAAGGGCGCCAAAGCCACGGTCCAAGAGTGACAGAG
TGTTGGATAAAAAACACGTTTCCGCCATGGGAATGGTCAAAGTATCTTAATGAAGAAGCAT
TCATTGAGACTTTTGGTGATGATTACAGGACTTGTTTTGCGAATAAAGTTGACTTGTCCA
GTAATAGCGTCGATTGGGATTTGATTGACTCCCAACGAATAATATAATCCAAGAAGTGG
AAGAACAATGCAAAATGTTTAAGTTTAATGTACATAAGAAATCTAAGGTTTGA

YJL035C, 250 aa (SEQ ID NO 146)

MQHIKHMRTAVRLARYALDHDTPVACIFVHTPTGQVMAYGMNDTNKSLTGVAHAEFMGI
DQIKAMLGSRGVVDVFKDITLYVTVEPCIMCASALKQLDIGKVVFGCGNERFGGNGTVLS
VNHDCTCLVPKNNSAAGYESIPGILRKEAIMLLRYFYVRQNERAPKPRSKSDRVLDKNTF
PPMEWSKYLNEEAFIETFGDDYRTCFANKVDLSSNSVDWDLIDSHQDNIIQELEEQCKMF
KFNVHKHKKSV

YJL070C, 3167 bp, CDS: 501-3167 (SEQ ID NO 147)

TCCCCTGATGGTCAAATACTGTGCATGGCATCCCGTGCAGTCAAGGATGCTTTGAGACTA
GTTTCATCTGCCCTTCTTGTAGCGTGTTAGCAACTGGCCTACCAGCGGGACGCCTTTGGGT
AAAGTTACCAGTGTGCGATTTTCGCCATCTGGTGGGCTACTGGCCGTGGGTAACGAACAA
GGTAAAGTGAGGCTCTGGAAATTAAACCACTACTAAATTTCCATTTATAGACAAACTTAG
ATATTTAAAGCAATGTACAAATACATACACAAATATCACTGTAAAAAAATTGCGAAGAA
ACTTGAAATTGAATATGATTCTGCCCACTTTTTTCTTGCTGTCATTTATAGTCAGAAATG

FIG. 1 - 50

AAAAATTGTCCGAGAAATTAAATATAATATATGGAAAAAAGGGGACATTGAGTTTAAAG
AATTTGATTAAAAATGTCCTCTCAATATCCTCTGTAAAGAGTTATCTAAATCTCACTTTACT
TATTCATCTCGCTGGGAATTATGCAGGCGGTAGAGAGAAGGCCCTCGTTACTCTTTGACG
AATATCAAAATTCTGTTACTAAGCCTAATGAGACGAAGAATAAAGAAGCCAGGGTCTTGT
CAGAGAATGACGGTGATGTCTCCCCATCTGTTTTGAAACAGAAGGAAATATCAGTCGATG
ATATGGATATGATTTCTTTGCCCACGGAATTTGACAGGCAAATGGTTTTAGGTTTACCTA
TGTTTTTCGATCTTGAAGACGAAGAAAACAAAATTGATCCACTTCCTTCAGTTTCCCATC
ATTATGGAAATGGAGAAAGTGACAGCTTTGTCTCATCGTACACGCCCTCAAATCTGAAAA
CGGGTGAAGAACTAAAGATCTTTTCATTAATCCGTTTGAATTGGTTTTCTCAAATGAGAA
AAAGATACATTGCTGCTTCCAAACAAGATGGCATTTCAAACATAAAAAATGACACTGAAA
AGTGGTTTTTATACCCAAAACCACTGCCAAAGTTTTGGAGATTTGAAGACGATAAACGAT
TCCAAGATCCCTCTGACTCTGACTTAAATGACGATGGAGACAGTACTGGGACCGGAGCCG
CTACACCGCACCGCCATGGCTACTATTACCCAAGTTACTTTACCGATCACTACTACTACT
ACACAAAATCTGGTTTGAAAGGAAAAGGAAATATAAAAGTACCATACACCGGTGAATATT
TCGATTTAGAGGATTACAAAAACAATACATTTACCATTTAAGTAATCAGGAAAATACGC
AAAACCCACTTTCACCTTATCTAGTAAGGAGGAGTCACTAGAGGAAGAATTTTAAACAG
ATGTGCCTACGTTTCAAGAATTTAGGGATGATTTTGCATACATAATAGAGTTAATCCAA
CTCATAAATTCAACGAGGTTTCACGAAAGCGATTATCTTATTTATTAGATAAATTTGAAT
TGTTTCAGTACCTAAACTCTAAGAAAGAAATTTTAGCTAATAAAAAATGTTCCCTACAGAG
ATTTTTATAATTCTCGTAAGGTAGATCGAGACTTGTCTTTAAGTGGTTGTATTTCTCAAC
GTCAATTGAGTGAATATATATGGGAGAAAATAAATTTAGAACCCTGAAAGGATAGTTTATC
AAGACCCGGAACGTCAGGAACTCAGTTTGAGAGACATTTTTCAGTTTGGTTGTTCTT
CTAATGACCAACCCATTGCGATTGGGTTGAAATTGATTGATGATGAATTTCTGGATTGGT
ATAGAAATATTTACCTAATAGATTACCATCTTAACCTAACAAGTAGCAAAGTTGGTCG
GCAAAGAAATGAGGTTTTACCTATTAGCCAAAGTGTCTGGAGTTTGATAATTTCAATG
AAGGTGAGTACCTAGCAGAAATTTTCATAAAATACGTTATTATCATATCCTCGAAAAATCAA
AGTACCAATTGGCCCAAGTATCAGTTAATTTTCAATTCTATTCCAGTGGTGAAGACTGGT
ACAAGAAATTTTCTCAATGGTTGCTACGATGGAAGCTAGTATCGTATAATATCCGCTGGA
ATATACAAATTGCCAGGATTTTCCCAAATATTCAAGGAAAATGTCGTGTCAAATTTCC
AGGAGTTTTTGGATCTTATCTTCAATCCTTTATTCACTCTGGAAAAGGAGCAGTTACCAA
TAGATTATCTGTAAATACTGATATCATTGGTCTGCAGTTTTTTTTATCAAATGTGTGTT
CTATGGATCTGGTCATTAAAGAGTCGGATGAATATTACTGGAAAGAATTTACTGATATGA
ATTGTAAGCCAAAATTTTGGACAGCACAGGGTGACAATCCAACCTGTTGCGCATTACATGT
ATTATATTTATAAAAGTTTTCGCGAAAGTTAATTTTCTGCGGTCACAAAATCTTCAAATA
CAATCACCCCTAAGAAATTATGTTCTCCACTATCCAGCAGAACTTCCCAATTTGGAGTGG
ATTTATATTTTACAGATCAAGTTGAATCGTTAGTGTGCAACTTACTGCTTTGTAATGGTG
GTCTGCTACAGGTAGAACCCTTTGGGATACTGCAACAATGATTCAATATTTATTTTATC
TCTTTCAAATACCCATTTTAGCTGCGCCATTATCATCTGTTTCATTACTGAATTCGCAAA
AATCGACCTTTTTGAAGAATAAAAACGTGCTTCTAGAACATGATTATTTGAAAGACCAGG
AAACAGCCAAAATCAATCCTTCTAGAGATATCACTGTGGGCGAACAAAGATCATATGAGA
CAAATCCTTTCATGAAAATGTTTAAAGATGGGACTAAAAATTTCTTTATCATCAAAATCGA
TTCTTTTACAATAGTTTCATACACGCTAGAACCTCTCATTGAAGAATACAGTGTAGCAGCAA
GTATTTACTTGCTGAACCCAACAGATTTGTGCGAGTTGTGCGAGAACAAGTGTGCTATCTA
GTGGCTATGAAGGTTGGTACAAGGCTCATTGGATTGGCGTTGGAGTTAAAAAGGCGCCTT
ACTTTGAGGAGAACGTGGGTGGGATAGATAATTGGTACGATACAGCGAAAGATACCTCGA
TAAAGCACAACGTTCCGATGATTAGAAGAAGATATAGAAAGGAGACATTGGATCAAGAGT
GGAACCTCGTTCCGGATCACTTTGGAGTAATTAACCTCCATTGAGTAG

YJL070C, 888 aa (SEQ ID NO 148)

MQAVERRPSLLFDEYQNSVTKPNETKNKEARVLSNDGDVSPSVLKQKEISVDDMDMISL
PTEFDRQMVLGSPMFFDLEDEENKIDPLPSVSHHYNGESDSFVSSYTPSNLKTGEETKD
LFINPFELVSQMRKRYIAASKQDGISNIKNDEKWFLYPKPLPKFWRFEEDDKRFQDPDS
DLNDDGDSTGTGAATPHRHGYYPYFTDHYYYTSGSLKGKGNIKVPYTG EYFDLEDYK
KQYIYHLSNQENTQNPLSPYSSKEESLEEFLTDVPTFQEFRRDFAYIIELIQSHKFNEV
SRKRLSYLLDKFELFQYLSKKEILANKNPYRDFYNSRKVDRDLSLSGCISQRQLSEYI
WEKINLEPERIVYQDPETSRKLSLRDIFQFGCSSNDQPIAIGLKLIDDEFDLDWYRNIYLI
DYHLTPNKVAKLVGKEMRFYLLAKVFLEFDNFIEGEYLAEIFIKYVIHILEKSKYQLAQV
SVNPFQFYSSGEDWYKKFSQWLLRWKLVSYNIRWNIQIARIFPKLFKENVVSNFQEFLLDI

FIG. 1 - 51

FNPLFTLEKEQLPIDSSVNTDIIGLQFFLSNVCSMDLVIKESDEYYWKEFTDMNCKPKFW
TAQGDNPTVAHYMYIYKSLAKVNFLRSQNLQNTITLRNYCSPLSSRTSQFGVDLYFTDQ
VESLVCNLLLCNGGLLQVEPLWDTATMIQYLFYLFQIPILAAPLSSVSLLSQKSTFLKN
KNVLEHLDYLKDQETAKINPSRDITVGEQRSYETNPFMKMFKMGLKISLSSKSILYNSSY
TLEPLIEEYSVAASIYLLNPTDLCELSRTSVLSSGYEGWYKAHWIGVGVKKAPYFEENVG
GIDNWDYDTAKDTSIKHNVP MIRRRYRKETLDQEWNFVRDHFVINSIW

YJL078C, 3146 bp, CDS: 501-3146 (SEQ ID NO 149)

TTTTTCTTCGCACATGGCTGGTTCTGCTGGAGCGGCTGGGTGTTTATAGTTACCGCAAT
GCAGGTCGCTTCGTTTACTTTTCTCTGCGTGCCTCGAGAACTGATAAATACTGGTTTAGGA
AAACCGTCCACTTATGGATTTAACAAGGAGGTGAAAGGTAGGTACCATGGCAATATAGCT
AGCAACGCTACGCACTAGCTGTGTGTGCTTGCTCTCTTGTGTTCGTCTTTCGTATATTGC
GGGTTCCCGCGGTTAATTCAACAACAAATATGGTATCTAGGCAGGGACCCAGCAACGGAA
GGATGTAATTGCTATATAGGGCCGATGAAACAGTTCTCATGTTTCAACTCGGTGCAAGAA
TTCTCTAAACATATTCTATACTTCAAAGTTTCTAGCTTCTTGCTTTTCGGTAGTTGCCA
AACCAATATCGGCATAAAATTATAATTGCTGCACCCCTGCAACTCCAAACAACCTAAAAC
AATCTAAAACGAAAACGCTTATGCTGGAGTTTCCAATATCAGTTCTGCTAGGATGCCTAG
TAGCCGTCAAGGCACAAACCACGTTTCCAAACTTCGAGAGCGATGTGCTGAACGAGCATA
ACAAGTTCAGAGCGCTACATGTTGACACAGCGCCGCTCACCTGGTCCGACACTCTGGCCA
CCTATGCGCAGAACTACGCCGACCAATATGATTGTTTCGGGTGTCTTAACGCATTCGGATG
GCCCATATGGTGAGAACCTTGCCCTTGGTTACACAGACACGGGAGCGGTGGACGCCTGGT
ACGGGGAGATAAGCAAGTATAATTATTCAAATCCCGGATTTTCTGAATCCACGGGTCACT
TCACACAGGTGGTTTGGAGTCAACCGCCGAGATTGGATGTGGTTATAAATATTGTGGTA
CGAGTAGGAACAATTATATTGTGTGCTCCTACAACCCCTCTGGAAACTACCTGGGTGAGT
TTGCAGAGGAAGTGGAAACCCTTATAAGCACTGTTTCTCTCGTCTCATCTCTGCTCTCT
CTACCTCAACTACATCAGACACAGTCTCCACCATCTCATCCAGTATTATGCCCGCTGTAG
CGCAAGGGTATACAACAACGGTATCGTCTGCGGCTAGCAGCAGTCTTTAAAATCGACGA
CCATAAACCCCTGCCAAGACCGCTACCCTCACTGCGTCTCTTCTACCGTAATTACTAGTA
GCACAGAATCAGTTGGATCCTCCACTGTCTCATCAGCCTCAAGCTCTTCTGTCACTACTT
CCTATGTCTACCTCCTCGAGTACCGTCTGCTCTTAGTGATGCTACTTCATCCACTACCACCA
CCTCATCGGTTGCTACATCGTCCAGTACCCTTCTCCGACCCCTACCTCGAGCACTGCTG
CTGCTTCTTCTTCTGATCCTGCCTCAAGTTCGGCTGCCGCTTCTCCAGCGCGAGTACCG
AGAACGCCGCTTCTTCTAGCAGCGCCATCTCGAGCTCTTCATCAATGGTTTCTGCTCCTT
TGAGTAGTACTCTTACTACTTCCACCGCAAGCTCCAGAAGTGTAACCTCCAATTCAAGTTA
ATTCTGTAAAGTTTGCAAACACAACCTGTGTTTCTGCTCAAACAACCTCTTCTGTAAGCG
CCTCATTATCATCATCTGTAGCTGCTGACGATATTCAAGGTAGCACTTCCAAGGAGGCCA
CAAGCTCAGTTTCCGAACATACTAGTATAGTAACCTAGTGAACCTAATGCTGCCAATATG
CAACGAGACTTGGGTCTCTTCCAGAAAGTCTTCCGGGGCCGTCTCTTCTCAGCTGTGT
CGCAATCTGTTCTGAATTCCGTTATAGCCGTCAACACCGACGTATCTGTAACCTCAGTTA
GTAGCACAGCCCATACCACAAAGGACACCGCCACCACTTCAGTAACCGCCTCAGAAAGTA
TCACTTCGGAAACTGCTCAGGCTTCAAGTTCACAGAGAAGAATATTAGTAACAGTGCCG
CCACATCGAGTAGCATTTACTCCAACAGTGCTTCTGTGTGTCAGGACACGGGTGTAACATACG
CTGCCGAATACGCCATTACATCCGAGCAATCCTCTGCGCTTGCCACATCTGTGCCTGCTA
CAAATTGCTCTAGTATCGTGAAGACCACAACCTTTAGAAAATTCGAGTACCACAACCATCA
CAGCCATTACTAAGAGTACTACAACCTTGCCCACTACTGCTAACAACCTCCACAAGGGCAG
CTACCGCAGTAACCATAGATCCACATTTGGACCCTACCGACAACCTCAGCTAGTCCAACCG
ACAATGCTAAACACACCTCTACATATGGATCTTCTTCCACAGGCGCATCTTTAGATAGCT
TACGCACAACCACAGTATTAGTGTCTCAAGCAACACCACACAGTTAGTCTCTACCTGCA
CTTCCGAGAGCGATTATTCGGATAGTCTTAGCTTCCGCATCTCCACTGCCACCACCACTG
AAAGCAATCTGATCACAACACCATCACAGCTTCTTGTAGTACGGATAGTAATTTCCCTA
CCTCCGCTGCTTCTTCTACAGATGAGACGGCCTTCACTAGAACAATCTCGACATCTTGTA
GCACTTTGAACGGCGCTCAACCCAAACAGTGAGCTAACCACATCGCCTATGAAAACCA
ACACGGTGGTTCCAGCTTCTTCTTCCCTTCAACTACAACCACTTGTCTAGAAAATGATG
ACACTGCCTTTTCTAGTATCTACACTGAAGTCAACGCCGCAACTATCATTAACCCCGGAG
AAACATCTTCTCTCGCTAGCGATTTGCCACATCTGAAAAGCCAAACGAGCCCACTTCTG
TCAAATCCACCTCAAACGAAGGCACCTCTTCCACAACAACAACCTACCAACAGACTGTTG
CTACACTGTATGCCAAGCCCTCCAGCACAGCCCTAGGTGCAAGAACAACCTACTGGTAGCA
ACGGTCTGTTCAACTACCAGCCAACAAGACGGGTCTGCCATGCATCAGCCAACCTTCCCTCGA

FIG. 1 - 52

TCTACACTCAACTAAAAGAAGGCACATCAACCACCGCAAACTTTCTGCATACGAAGGTG
CTGCAACACCTCTTTCCATTTTCCAGTGCAATAGTCTAGCTGGAACGATTGCCGCTTTTG
TCGTAGCTGTTCTGTTTCGCCTTCTAG

YJL078C, 881 aa (SEQ ID NO 150)

MLEFPISVLLGCLVAVKAQTTFPNFESDVLNEHNKFRALHVDTPALTWSDTLATYAQNYA
DQYDCSGVLTHSDGPYGENLALGYTDGAVDAWYGEISKYNSNPGFSESTGHFTQVVVK
STAEIGCGYKYCGTTWNNYIVCSYNPPGNYLGEFAEEVEPLISTVSSSSSSSSSTSTSD
TVSTISSSIMPAVAQGYTTTVSSAASSSSSLKSTTINPAKTATLTASSSTVITSSSTESVGS
STVSSASSSSSVTTSYATSSSTTVSSDATSTTTTSSVATSSSTTSSDPTSSSTAAASSSDP
ASSSAAASSSASTENAASSSSAISSSSSMVSAPLSSTLTSTASSRSVTSNSVNSVKFAN
TTVFSAQTTSSVSASLSSSVAADDIQGSTSKEATSSVSEHTSIVTSATNAAQYATRLGSS
SRSSSGAVSSSAVSQSVLNSVIAVNTDVSVTSSSTAHTTKDTATTSVTASESITSETAQ
ASSSTEKNISNSAATSSSIYSNSASVSGHGVYAAEYAITSEQSSALATSVPATNCSSIV
KTTTLENSSTTTITAITKSTTTLATANNSTRAATAVTIDPTLDPTDNSASPTDNAKHTS
TYGSSSTGASLDSLRTTTSISVSSNTQLVSTCTSESDYSDSPSFAISTATTTESNLITN
TITASCSSTDSNFPSTSAASSTDETAFTRTISTSCSTLNGASTQTSELTSSPMKNTNVVPAS
SFPSTTTTTCLENDTAFSSIIYEVNAATIINPGETSSSLASDFATSEKPNEPTSVKSTSNE
GTSSTTTTYYQQTVAATLYAKPSSTSLGARTTGTSGNGRSTTSQQDGSAMHQPTSSIIYTQLKE
GTSTTAKLSAYEGAATPLSIFQCNSLAGTIAAFVVAVLFAF

YJL179W, 830 bp, CDS: 501-830 (SEQ ID NO 151)

TTGCATTATCAACTATAATTCCATTTCTAGAGGAGTTTTATAGTCCTGCCATCTAATT
GTAGAGCAATCTTTCCCTTTCTCAACATCCCTATTTAGTGACACCTTTTCCCAAACTTCT
GTGAAGTTTTGCTCAATCTATTTGTTTCCGTAGGAGTGTTATTCTCAATCGTGTGTCTG
TCCCCAGTGGCTGGGCATTTAATGAGTAGAATCGGGCAGTTTCAATCTTATGGAATTCA
CAATGAAGCATCCCTTCCCTTAATGATGGCAGCATTCCTGATTCTCTTTTGTAGGGTTTCG
TTTGCCTTCAAGTGTTTGTCTTATTTAGCCTTTTCCCTTACCTTAATTTTTTCTTTT
CTCTGAAGAAATGAATGAGTTTAAAGATATAGCAATTAAAAAGTAACAGTGAAGAAATT
TCTCAGATGAGCAGATGGGAATTAAGAATCTATCTACAGAGCTCTTTACTAAATTGAATC
AATAATACATACTTACAAACATGTACAGATAGCACAAAGAAATGACAGTGAGCTTAAGAA
ACGCCAGGACACAATTGGATATGGTCAATCAGCAGCTAGCATATTTGGACAGACAAGAAA
AGCTTGCTGAATTGACAAAGAAAGAACTAGAGTCTTATCCAACGGACAAAGTATGGAGAT
CTTGCGGTAAATCGTTTATCTTACAGGATAAATCCAAATACGTTAATGATTTATCACATG
CCGAAACTGTTCTTCTGGATCAAAGAAAAACATTAAAGATAAAGAAGAACTATTAGAAA
CTACTGTTGAAAAACAATAGACAATCTAAAGGCATTGATGAAGAATTAA

YJL179W, 109 aa (SEQ ID NO 152)

MSQIAQEMTVSLRNARTQLDMVNQQLAYLDRQEKLAELTKKELESYPTDKVWRSCGKSF
LQDKSKYVNDLSHAETVLLDQRKTLKIKKNYLETTVEKTIIDNLKALMKN

YJL180C, 1478 bp, CDS: 501-1478 (SEQ ID NO 153)

AATAGTTCCTTCTTTATCTTTAATGTTTTCTTTGATCCAGAAGAACAGTTTCGGCATGTG
ATAAATCATTAAACGTATTTGGATTTATCCTGTAAGATAAACGATTTACCGCAAGATCTCC
ATACTTTGTCCGTTGGATAAGACTCTAGTTCCTTTCTTTGTCAATTCAGCAAGCTTTTCTT
GTCTGTCCAAATATGCTAGCTGCTGATTGACCATATCCAATTGTGTCTTGGCGTTTCTTA
AGCTCACTGTCAATTTCTTGTGCTATCTGTGACATGTTTGTAAAGTATGTATTATTGATTCA
ATTTAGTAAAGAGCTCTGTAGATAGTTCTTTAATTCCCATCTGCTCATCTGAGAAATTTT
TTCAGTGTACTTTTTAATTGCTATATCTTTAAACTCATTCATTTTCTTCAGAGAAAAGA
AAAAAATTAAGGTAAAGGAAAAGGCTAAATAAGAACAAACACTTGAAGGCAAACGAAAC
CCTACAAAAGAGAATACGGAATGCTGCCATCATTAAGGAAGGGATGCTTCATTGTGAATT
CCATAAGATTGAACTGCCCGATTCTACTCATTAATGCCCAGCCACTGGGGACAGACA
ACACGATTGAGAATAAACAATCTTACGGAACAAATAGATTGAGCAAACTTCACAGAAGT
TTTGGGAAAAGGTGTCACTAAATAGGGATGTTGAGAAAGGAAAGATTGCTCTACAATTAG
ATGGCAGGACTATAAAAACTCCTCTAGGAAATGGAATTATAGTTGATAATGCAAGTCTC
TCTTAGCATACCTATTAAAACTGGAGTGGTCCCTATCCAGTCTTTCCATCAAACTC
ACTCTTTGCCACTAACTTCATTAGTGGCAAGATGCATAGATTTACAAATGACAAATGAGC
CTGGCTGTGACCCTCAATTAGTTGCAAGATTGGAGGCAACAGTGATGTTATAAAAAATC

FIG. 1 - 53

AGTTGTTAAGATATTTAGATACCGATACTTTATTGGTCTTTTCCCCTATGAATGAGTTTG
AAGGAAGATTACGCAATGCGCAAAATGAGTTATATATACCCATCATCAAAGGAATGGAAG
AGTTTTTACGCAACTTTTCATCCGAGTCTAATATTCGACTACAAATTTTAGATGCCGACA
TCCATGGGTACGAGGCAATCAGCAGTCGGATATCGTTAAGAATGCAGCAAAAAATATA
TGAGCAGCTTATCACCATGGGATCTTGCAATTCTTGAAAAACTGTATTAACCACAAAGT
CCTTCATTTGCGGCGTGCTATTATTAGAAAATAAAAAAGATACTGCGAACTTAATTCCCG
CCTTGAAAACTGATATGGATAATATTGTACGTGCCGCCACCTTAGAAACAATCTTCCAAG
TTGAAAAGTGGGGAGAGGTTGAAGATACTCATGACGTTGACAAAAGAGACATCAGAAGAA
AAATTCACTGCTGCGATTGCTGCTTTTAAGCAATAA

YJL180C, 325 aa (SEQ ID NO 154)

MLPSLRKGCFFIVNSIRLKLPRFYSLNQPLGTDNTIENNTPTETNRLSKTSQKFWKVS
NRDVEKGKIALQLDGRITIKTPLNGIIVDNAKSLAYLLKLEWSSLSLSIKTHSLPLTS
LVARCIDLQMTNEPGCDPQLVAKIGGNSDVIKNQLLRYLDTLLVFSMPNEFEGRLRNA
QNELYIPIIKGMEEFLRNFSSSNIRLQILDADIHGLRGNQQSDIVKNAKKYMSSSPW
DLAILEKTVLTTKSFICGVLLLENKKDTANLIPALKTDMDNIVRAATLETIFQVEKWGEV
EDTHDVKRDIRRKIHTAAIAAFKQ

YJL181W, 2336 bp, CDS: 501-2336 (SEQ ID NO 155)

GCAAGTCAGTACGATGCATCCTTGGATCAAGAAGGTGAGTCTGGAAACGGTGCTTCTAAT
GGCGATGTTTACCATTATAATGAAGGGGACTTGGCTGCCTCCTTCAAGGGATGTAGATCA
AGAGGTACGTGTGCTAGTGAAATAGGTACATGTACCAGAAAATCAAGAAATCTTAGATG
TGTGTAATCTTGCAATTTAGTTTCAAACAAGATCCTTGTATTTATATAAAACAAAGATATA
ATTTTAAAAAAAATTAGAAAAAGCAAATATAATTCAGGTCCCACTTGGAAATAATGGCA
CTGTATTGATGCATTTTCCCTTATGCTTAGTACGCGTTTTTCGCGCGTCAGTTTCAAGTTT
TTCTTGGCTTTTTTTTTTTTCATTTTCGTAAAGGGTCTTAAAAGGATTAAAAATGCAGTA
TTGAAATAAAGAACAATTACGAACGGTGAAGCTGCTATTTTGGTTATTATACCTTCCAG
GACAGTACGCGCAAACCTATTATGGAGATATTCAAGGAAGAAGAAGAAGACTTTTTTCGG
CGATAGAAGGTATAATATATGCCTGTGAGGTGTATGACCCTGTACCCCGTCATTTACATA
AAAGCAAAACAAAGATCATCAATGCTGCTAAATTAATTATAGAAACGCATCTTTCATATT
ATACAATACTCAATAACATTTTCAGATATACAAGCCTATCTTCTACTTGGCTTAGGGATC
TTGGAACGACAGGTCCATACCAACAATTTCTTTAGAAAGTATTTCTCTCATGTTTGACC
GCACTGTATCTATCTTCAGGAAATGTACGATAGAGGGAGGTTTTCCACATTTGATCGCAC
GTCTTTATCTCAGATTGAAAAGCTACCAGAAGCTCTTAAACGATGCAGGATTAAAGAATT
TTTTTTCAAGCTACGATTATGCTTTTCGGGTTGCATACAACCTTGTAATTTGCTCTGAAT
ACAGGTATGACGAAGTTCATTACATATCGAACCGCACTTACTCATTAGTTGCATCGATGA
AGATAGATCCTGCTGAAGTCATTAAAAGGGAACATTTTAGGCTTACAATTCGAAATTTA
ACATATCTAATATATTAATTGAAATTTTTCATTTGCTCGATGGATTAGCATTTTTTAAGG
TGAACCCTGATAGTTTATCTATATCTACAGCTTCAGCAGAAACAATCTTTCGCAGTATCT
CCGAAGGTAATCATCAGGTCCTAGAATTGGGGAGAAGTTAATGTTTCCATTGTTGAGGA
CTGGAGATTTTGAATCTGTCGTATTGACGACGCGGGAGCTGTCATAACATTTACAGAAG
CGAAGGATGTAAACTAGAAATAATCAGTCTGGATGAAGTTTCTTGGGTAATGCAGTGGA
AATCTTGTCTTCAAAATTATGAGAGAAGGGCAGCAAATGACAGTTCATTTATCAAAACAC
ACCTACAATTTAAGAAGGCCAACAAATTTCAATGAAGATAATAATGGGCTAGGACTAATTG
TAGACAGAAATATTCCAACAGATGATTTTACGCTAGCTTCTACAAACCGTCAAAGTCCCC
CGCCTTCAAAATACTGGTTGTTTCATTACACAGGTCTAAACCTTGTCATATCCCTTTATCAT
CTGTTATTTCGTGAAGACTTTTTATGATAGCTCTCTAAATGAGCGTATATCTAAAGACGGAG
ATAGCAGTTGTGAATCCTTCAGTGGCGCCGAAAGTATCTTATCAGACTACGATTTTCATG
ATAATGAATTTTTTAACAACCAGTCACCTCATTATTTTTCAGAACACATAGACAATAACT
CGAGAGAGGTGGTAATAACAGATGAAAATACGATAATATCTTTGGAAAAATACCAAGTAA
GTCGGTGGTCAAATTAATCATGGCAAAAAATTTACCCGCATCAATTACAGGTCTCTATTA
TCCAACCTGCGCATGGGAAACTTCATTGTGGCTTATGATTCTGATTATAACCTTCATCAGT
TCAAAATTCGTTTGTGTGACGATATAAAATGTATACAATCCACAGAGCAAGACATACAAA
TACGTGTCCCGCTCGGCGCAATAATGTGCAGCGTCACTGGTATCTTGAATATTAGGACGA
AGGACGCTGACAAGTTGCTTCGGGTATTAAGCTTTTATACCACTGACCACACGGAAGCTG
TATCGCACTCAAACAATCAAGATGCTACTGCAAGTCCACTTTCGTGAGTTTCATCAGCAA
TGGATCTCAAGCATTCATTACAGAAATGTTCTCTACAATAATGCCCCAAGAGTTGACGC
AGGACGTCATCGGTTCAAATCAGACCTAATCAGTAATATTTCGTCAAAAAATATAA

FIG. 1 - 54

YJL181W, 611 aa (SEQ ID NO 156)
MEIFKEEEEEFAIEGIIYACEVYDPVPRHLHKSCTKIINAAKLIIETHLSYYTILNNI
SDIQAYLSTGLRDLGTTGPYQTLSEISLMFDRTVSIFRKCTIEGGFPHLIARLYLRLLK
SYQKLLNDAGLKNFFSSYDYAFGVAYNLVNCSEYRYDEVHYISNGTYSLVASMKIDPAEV
IKREHFRLLTIPKFNISNILIEIFHLLDGLAFFKVNPDLSISTASAETIFRSISEGNHQV
LELGRSLMFLRLRTGDFEICRIDDAGAVITFTEAKDVKLEIISLDEVSWVMQWKSCLQNY
ERRAANDSSFIKTHLQFKKANFNEDNNGLLGLIVDRNIPDDFTLASTNRQSPPPSNTGC
SLHRSKPLHIPLSSVIREDFYDSSLNERISKDGDSSCESFSGAESILSDYDFHDNEFFNN
QSPHYFSEHIDNNSREVITDENTIIISLENTQVSRWSNYSWQKISPHQLQVSIQLRMGN
FIVAYDSYDLHQFKIRLCDDIKCIQSTEQDIQIRVPLGAIMCSVTGILNIRTKDADKLL
RVLSFYTTDTEAVSHSNQDATASPLSSVSSAMDLKHSLOKCSSTIMPQELTQDVIGSK
SDLISNIRQKI

YJL187C, 2960 bp, CDS: 501-2960 (SEQ ID NO 157)
TCTTGCAACCATCGTCTCTAAGGAAAGAAATGTGGCACCTTTAAATAGGTTCCACCTCA
CAGATGCCAACATGTGGGAGATAGGGGGCTATTTCGCAATTTATTAACGTCTCTAGTACTG
GTAAGCCTTTCTAACATTCTTGTGGTCACGTGATGTGTATGTTTCTTTTATTCTCTC
CGGGTGATAACGACGCGAAAAATATTTTTTTCATTTTTCTTTTAACCATCACAATTTGCGA
CGCGACGCGAAAAAATGCAGAGAAGTAAAAGAATGCTGGATAAGAAATCAACAACACAG
TTGAACATTGGCGTGCCCTGTGTATTAAGTAAAGGTTGTCCAAGAGGCTCTTTTTTGTA
TGTATGCGTGTGTTAACTATCCTGCACATCATCTTGCAGCTAGTCCAAATAAAAAAGGA
TTACTACTGAACAGGTCTTACTATTTTTGATTGCGTAGTGCTGGGGAAAAGTAAACACAC
ACAGGCGCACACGAGAACAGATGAGTTCTTTGGACGAGGATGAAGAGGACTTCGAAATGC
TGGACACGGGAGAACCTCCAGTTTATGGGGGAAGAAGATGTTTGGCAAAACAGGCCGCGAAG
ACGAGAGTGATGATTTTTGCTATAGGGGGTAGCACCCCGACCAATAAACTGAAATTTTATC
CATATTCGAACAACAAATTGACAAGAAGTACGGGGACCTTGAACCTGTCATTAAGTAATA
CAGCTTTGTGAGAGGCTAACTCCAAATTTCTTGGGAAAATTGAAGAAGAGGAAGAAGAGG
AGGAAGAAGGCAAGGATGAGGAAAAGCGTGGATTCTCGTATTAAAAGGTGGTCTCCGTTCC
ATGAAAATGAAAGTGTTACTACTCTATTACAAAAAGATCTGCGGAAAAAACGAACAGTC
CTATTTCTCTCAACAATGGAACACAGCGATGGTTTCCGAAAAATGATGCTCGCACTGAAA
ATACATCCTCATCCTCTTCATATAGCGTCGCTAAACCTAACCAATCAGCCTTTACGTCTT
CGGGCCTCGTATCTAAAATGTCTATGGACACTTCGTTATACCTGCGAAATTGAGGATAC
CAGAAACACCAGTGAAAAAATCACCTTAGTGGAGGGAAGAGACCATAAGCATGTCCACC
TTTCGAGTTCGAAAAATGCATCGTCTCTCTAAGTGTTCCTCTTAAATTTTGTGTAAG
ACAATAATTTACAAGAAGACCTTTTATTTTCAGATTCTCCGTCTTCGAAAGCTTTACCTT
CCATCCATGTACCAACCATAGACTCATCCCCACTGAGCGAGGCAAAATATCATCGCATG
ATCGTCACAATAACCAGACAAACATCCTGTCTCCCACTAATAGCTTGGTTACCAACAGCT
CTCCACAAACATTGCATTCTAACAAGTTCAAAAAAATCAAAAGAGCAAGGAATTCCGTTA
TTTTGAAAAATAGAGAGCTAACAAACAGTTTACAACAATTCAAAGATGATTTATACGGCA
CGGACGAGAATTTCCACCTCCAATCATAATATCAAGTCATCATTTCACTAGAAAGAACC
CTCAACCTTATCAATTTTCGTGGACGCTATGACAATGACACTGACGAAGAGATCTCCACTC
CAACAAGACGAAAATCTATTATTGGGGCAACATCTCAAACACATAGAGAAAGCAGACCAT
TGTCACCTCTCTGCCATCGTGACAAACACAACAAGTGCAGAGACGCATTCATATCTT
CCACCGATTCTTCGCCGTTAAATTCCAAAAGGCGTCTAATCTCTTCAAATAAGTTATCAG
CAAATCCAGATTCCCATCTTTTCGAAAAATTTACGAATGTGCATTCCATTGGTAAAGGCC
AGTTTTCACGGTCTACCAGGTTACGTTTGCCCAACAAACAAAAAGTATGCAATCAAAG
CCATTAAACCAACAAATATAATTCTTTGAAACGCATATTACTGGAAATTAAAATACTAA
ACGAGGTAACAAACCAATTAACAATGGATCAAGAAGGGAAGGAATACATCATCGATTACA
TCAGTTCTTGGAAAGTTTCAAAATTCATACTATATTATGACAGAATTGTGCGAAAATGGTA
ATTTGGATGGATTTTTACAAGAGCAAGTTATCGCAAAGAAAAAAGGTTGGAAGATTGGA
GAATTTGGAAATCATCGTGAATTAAGCCTGGCTTTACGATTATCCATGATTCTTGTC
ACATTGTGCATCTGGACTTGAAACCCGCAACGTCATGATCACATTTGAAGGTAACCTAA
AACTAGGTGACTTTGGAATGGCTACTCATTTACCGTTGGAGGATAAAAGTTTGAAGATG
AAGGTGACAGAGAATATATTGCACCAGAAATCATTTCTGATTGTACGTACGATTACAAGG
CAGATATTTTTCCCTGGGTCTGATGATTGTTGAAATTGCAGCGAACGTTGTGTTACCTG
ACAATGGCAACGCATGGCATAAGTTGAGATCGGGTGATTTATCGGATGCAGGAAGATTAA
GTTCCACAGATATTCTGAATCATTTATTTTCAGACATTACGAAAGTAGATACAAATG
ATTTATTTGATTTTGAAGAGACAATATCAGTGGTAATAGTAACAACGCTGGCACCTCCA

FIG. 1 - 55

CTGTTTCATAACAATAGTAATATCAACAACCCTAATATGAATAATGGCAACGATAATAATA
ATGTCAATACTGCCGCTACCAAGAATCGTCTTATTTTGCATAAAAGTTCTAAAATTTCCCG
CATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACGATGGATGA
TAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGAGGAATGCC
TGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTTTGGACCTA
AGCCAAAATTTTTTATATGA

YJL187C, 819 aa (SEQ ID NO 158)

MSSLDEDEEDFEMLDTENLQFMGKKMFQKQAGEDESDDFAIGGSTPTNKLKFYPYSNNKL
TRSTGTNLNLSLNTALSEANSKFLGKIEEEEEEEGKDEESVDSRIKRWSPFHENESVT
TPITKRSAEKTNSPISLKQWNQRFKNDARTENTSSSSSYSAKPNQSAFTSSGLVSKM
SMDTSLYPAKLRIPETPVKKSPLVEGRDHKHVHLSSSKNASSSLSVSPLNFVEDNNLQED
LLFSDSPSSKALPSIHVPTIDSSPLSEAKYHAHDRHNNQTNILSPTNSLVTNSSPQTLHS
NKFKKIKRARNSVILKNRELTNLQOFKDDLYGTDENFPPIIISHHSTRKNPQPYQFR
GRYDNDTDEEISTPTRRKSIIIGATSQTHRESRPLSLSSAIVTNTTSAETHSISTDSSPL
NSKRRLISSNKL SANPDSHLFEKFTNVHSIGKGQFSTVYQVTFQTNKKYAIKAIKPNKY
NSLKRILLEIKILNEVTNQITMDQEGKEYIIDYISSWKFNQSYIMTELCENGNDLGFLO
EQVIKKRLEDWRIWKIIIVELSLALRFIHDSCHIVHLDLKPANVMITFEGNLKLGDFGM
ATHLPLEDKSFENEGDREYIAPEIISDCTYDYKADIFSLGLMIVEIAANVVLDPNGNAWH
KLRSGLSDAGRLSSTDHSESLFSDITKVDITNDLDFDFERNISGNSNNAGTSTVHNNSN
INNPNMNGNDNNNVNTAATKNRLILHKSSKIPAWVPKFLIDGESLERIVRWMIEPNYER
RPTANQILQTEECYVEMTRNAGAI IQEDDFGPKPKFFI

YJL188C, 809 bp, CDS: 501-809 (SEQ ID NO 159)

AATTCGCCGATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACG
ATGGATGATAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGA
GGAATGCCTGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTT
TGGACCTAAGCCAAAATTTTTTATATGATAAATGGAACAAAAAACCTTGTTTTATTTACA
TACTTTTTTCCACACGTGCTTATGGGCCGCAATGTATAAATAATCCAATAACGAAAAAG
AGTGTAATTGCAGTCCGGTAGTAATACCATGTAAAACCTTAGATGAGTTTATTTTAAGTA
CAGCCGCTTCAAGCATTTTTATTTTTATTTTACAGATGTAGCAGATAACAACCGTTAAAT
TATATTATATATATATATATATATATCAAAATACGACGTATTACATATATATTGAGAAAT
AAGGGAAGGATGGAAGACAAATGACAAAAAGTTTGAAGCATAAATATGTTCTTCGCTTAG
ATGTTTCATCTTGGTTCTTCTCCAGTTTCTTCTCTTAGCGTTGTAACGGATAGTGTTGTTG
GTTCTCAATCTGATCCATTGTGGCAATGGTCTGTTTTGCTTCTTAGCCTTAGCCATTTTT
TGCTTGATTCTGAAAGACTTTTGGACCTAATTAAGGGAAACATATCGTGCACATACGA
AGTGTAACAATTGTAAAAAATGTTAGTAACAATGTTCAAACCTCATCAATATGATGCATTCA
CGGATCCAAGGCAATACCACCTGACATAA

YJL188C, 102 aa (SEQ ID NO 160)

MTKSLKHKYVLRDLVHLGSSPVSSLSVVTDSVVGSDPLWQWSVLLLLSLSHFLLDSERL
LSLIKRETYRAHTKCTIVKNVSNNVQTHQYDAFTDPRQYHLT

YJL189W, 1042 bp, exon1: 501-506, intron1: 507-892, exon2:
893-1042 (SEQ ID NO 161)

TATTCAAGAATTATTTACATCTTCCAGCGAGTAAACATGCCGCTGGTAATCGCGCGTCC
TCAATATTTGAGTTTTTCAAATAGTGAGGTGTGGATGTATAGAGGAATTACACACTTTTA
AGTATGTGATGTATGGGCGCACAGTACCAATTTAACTTTTTTTTTTTTTCATTTTTTAGC
TTGATTTTCAAAAACTTATGGGCGTTTATAGGCTCCGGCTCAAACCTACCACCACCACGCG
GCAGGCCGAGGCAACAGTACGCCTTGGCGGGGACGCCGAAGCGACTCCTTCTGTTCCAA
GCTCAATGGTCTTTCGCTTTACGCTCGCGCTGGGCTAACTAACGCAATTCGGCTTTTGG
GCTGTGAGAACCGAGAATTATTTCTTCGCCTTGATAGATACTTTAAACTTCTACTTAAT
ATACTTCTACAATTTTGGTACATTCATATTATACTGAAAATTCGAAAAAGACAAGCAA
ATAAACACAGATAGATCAACATGGCTGTATGTTAGAAAGATATTATAAATCCCAGTTAGA
TGCTGAACTGATCAATAGCAAATTATAAACACATCCATCTAAATGACCTTACCACCTAC
AATTTGGATTTGAAATAGAAGCAATGTGTAAATATAGGGAAAGGATTAGGAGTGTTAAC
CATACTAAAATTTTCTTATCCGAAACAGAAATCTAAAGTCGCCACTACGCAGATTAAAA
TATGGTCATAAACTGCTTATTCTGAGAACTTTTGGTGGTCCAGCGTGGTTTATGTCAGGT

FIG. 1 - 56

GGTATTGCCTTGGATCCGTGAATGCATCATATTGATGAGTTTGAACATTGTTACTAACAT
TTTTTACAATTGTACACTTCGTATGTGCACGATATGTTTCCCTTTTAATTAGGCTCAAAA
GTCTTTTCAAGATCAAGCAAAAAATGGCTAAGGCTAAGAAGCAAAACAGACCATTGCCACA
ATGGATCAGATTGAGAACCAACAACACTATCCGTTACAACGCTAAGAGAAGAACTGGAG
AAGAACCAAGATGAACATCTAA

YJL189W, 51 aa (SEQ ID NO 162)
MAAQKSFRIKQKMAKAKQNRLPQWIRLRTNNTIRYNKRNRNRRTKMNI

YJL190C, 893 bp, CDS: 501-893 (SEQ ID NO 163)
TCTCGACAGCCCAAAAGCCGAATTGCGTTAGTTAGCCCACGCGGAGCGTAAACGCAAGG
ACCATTTAGCTTTGGAACAGAAGGAGTCGCTTCGGCGTCCCGCCAAGGCGTACTGTTTGC
CTCGGCCTGCCGCTGGTGGTGGTAGTTTGGAGCCGAGCCTAAACGCCCATAGTTT
TGAAAATCAAGCTAAAAAATGAAAAAAGTTAAATTGGTACTGTGCGCCCATAC
ATCACATACTTAAAGTGTGTAATTCCTCTATACATCCACACCTCACTATTTGAAAACT
CAAATATTGAGGACGCGCGATTACCAGCGGCATGTTTACTCGCTGGAAGATGTGAAATAA
TTCTTGAATATGGGTTTGCAGTTAGTCAATTTCAATCTAAATAATCTTAATCGACTATTC
AATCTTAAATTGTAAGGTTTAAATGGCCTTTCAGTTCTAGTATTTTTATAAAACAA
GACCAACATACATATCCAAGATGACCAGATCTTCCGTTTATAGCTGATGCTTTGAATGCCA
TTAACAACGCTGAAAAGACCGGTAAAGCGTCAAGTTTAAATCAGACCATCTCCAAGGTCA
TTATCAAGTTTTTGCAGTTATGCAAAAGCACGGTTACATTGGTGAATTTGAATACATCG
ATGACCACAGATCTGGTAAGATTGTTGTTCAATTGAACGGTAGATTGAACAAGTGTGGTG
TTATTTCCCAAGATTCAACGTTAAGATTGGTGACATTGAAAAATGGACTGCCAATTTGT
TGCCAGCCAGACAATTCCGTTACGTCATCTTGACCACCTCTGCTGGTATCATGGACCATG
AAGAAGCCAGAAGAAAGCACGTTTCTGGTAAGATTTTGGGTTTTCGTTTACTAA

YJL190C, 130 aa (SEQ ID NO 164)
MTRSSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLQVMQKHGYIGEFYIDDHRSGK
IVVQLNGLRNKCGVISPRFNVKIGDIEKWTANLLPARQFGYVILTTSAGIMDHEEARRKH
VSGKILGFVY

YJL197W, 4265 bp, CDS: 501-4265 (SEQ ID NO 165)
CTTCTTCGGGGTTCCCAATGTCACTGCCATCTCTAAAGTAGATAGAAAGGGCGATCGCT
ATTTAAGTGTACGACTTCTTAACGAGAGGTGTTCCAGCTTCTATTTTGGCTTTCCCTAT
GTGTCATTACTCTAGGTTATGGTATCATGGCATCTGTTGTCAAGGGTAACGCAACCTCTG
CGTAAGAGATACGTCTACGATAGCATGTAACAGCGTATATATAATCTATATGTATTCGAT
TAATCCAACACTTCTGTTGTGTAGTCTAATGTTTCGAAAAAAGGTACGCTTCCCTGTTAT
AATCAGGTATATTTTCGTTATCTTATAAGCTAAAAGATTAAAAATTTTCCACTTTCCTT
GAAATTTGGTTCGGTTTCGTGAAAAATATTATTACGTATTGAAGAAGTGCATGAAGATAAA
AGATGGGATTACTGGAATAAAGGGAGGAAATCCTGCAGAACGTTGTTGTTTCAATC
GAAGGTTTCTTCATTTCGAAAAATGGGTTCTTCAGATGTTTCAAGTCGTGAATGTTCAATTGG
TTTATAATGAAGATCCCGATTTACCGATGGCACAACACCATGTGATCGGTTGGGAGTGG
ACTTGATGAATGTTCTAGATGACAAGGATGAAATAAAGCAAGAGTCTGTCCCAGTCTCAG
ATCGTGAAATTGAGGATACGGAATCCGATGCTTCCGCTGTTTCTTCATTTGCTAGCGCTA
ATGAGTTAATAGCTGAGCCACACGCTGCAAGTGAACTAATCTTGGAATAATGGTCAAG
ATGGAAGAAATGTCTTAGAACAACAAAGAGACGTGGTTGCTAGACTAATAGAAGAAAACA
AGGAAACGCAAAAAGAGGGTGATAAAGTCTGTATTGTCCCCAAGGTTTGGTACGATAAAT
TTTTCGACCCCGATGTTACCGATCCTGAAGATATAGGCCCTATTAATACACGCATGATTT
GCAGAGCTTTGAAAATTTTGTGCTTGAGGATTACAATAGATGTCCGTATCTGTCTATTG
CAGAGCCTGTTTTCAATTTTCTATCAGAAATTTACGGCATGACAAGTGCTCTTACCCAG
TGGTAATAATTTGGTTATCAACCAAAACCACAGGGGAGTTAGAGACAGAATACAATAAAT
GGTTTTTCAGACTACATTACCTGACCGAAAAACAAGACGGGAGGAAAAGGAGGCATGGCC
AGGACGATTCAATAATGTACCTCTCGATGCTCTGCGTTGAATTTAGTACGTGATTTGGTTG
AAAAGAGTATGAATCTGTTTTTGTAGAAAGCTGATCATCTAGACGTGAATGCGGTGGATT
TTAAATTTGGTTTGTGTGAGGGATCTGATATTGCCACAGATAGCAATGTTAGTACTT
TTTTGAATCTTTCATATGAAATAACTCCGCTTCAATTTCTCGAACTACCGATAAAGAAAC
TACTAATACCAGACATGTTTGAAAACCGTTTAGACAAGATAACTTCAAATCCGAGTGACC
TTGTCATAGAAATTAAACCTATAGAAGGAATCACCATTGGCCTTCAAACATTTTTGCTT

FIG. 1 - 57

ATAATAAACTCGAACCAGCATCAGGTACTACTGGTTTGGTCAATTTGGGAAATACATGTT
ACATGAATTCTGCGTTGCAATGCCTGGTACACATTCGCGAGTTGCGTGATTATTTCCCTTT
ATGATGGTTATGAAGACGAAATCAATGAAGAAAATCCTCTTGGGTACCACGGCTATGTGG
CTAGGGCATTTAGTGACTTGGTTCAGAAGTTGTTTCAAAACAGGATGAGCATAATGCAAA
GAAATGCTGCTTTCCCCCTTCAATGTTCAAATCCACTATCGGGCACTTTAATTCGATGT
TTTCTGGTTATATGCAACAGGATTCTCAAGAATTTTATAGCCTTCTGTAGACAGTTTAC
ATGAAGATTTGAACAGGATAATAAAGAAAGAATACACAGAAAAACCATCATTATCTCCTG
GTGATGACGTGAATGATTGGAATGTAGTCAAGAAACTGGCAGACGATACTTGGGAGATGC
ATTTAAAGAGAAATTGTTCCGTTATAACGGATTATTTGTTCGGGATGTACAAATCAACGC
TATATTGTCCCGAATGTCAAATGTTTCTATAACGTTTGACCCGTATAATGATGTTACAT
TGCCGCTTCCGGTTGATACAGTGTGGGATAAAAACATAAAAAATTTTCCCATGAACTCTC
CACCCTTCTTCTTGAAGTTGAGTTAAGCAAATCGTCCACTTATATGGACTTGAAGAATT
ATGTTGGTAAAATGTCGGGCCTAGATCCAAATACACTATTTGGCTGTGAGATTTTCAGTA
ATCAAATCTATGTTAACTATGAGTCAACAGAGTCGAATGCTCAATTTTAACTTGCAGG
AATTGATCAAACCTGCTGATGACGTTATTTTTTATGAATTACCAGTAACAAATGACAATG
AAGTAATTGTTCCCGTATTGAATACTAGAATTGAAAAAGGCTACAAAAATGCAATGTTAT
TTGGAGTCCCTTTCTTTATTACGTTAAAAGAAGATGAATTGAATAATCCAGGTGCAATAA
GAATGAAATTGCAAAACAGGTTTGTCCATTTAAGTGGTGGGTATATCCATTTCCTGAAC
CTGTAGGAAATCGAACCGATTTTGTCTGATGCTTTTCCATTATTAGTAGAAAAATATCCAG
ATGTTGAATTTGAACAATATAAAGATATACTACAGTATACGTCTATTAAGGTGACTGACA
AGGATAAATCCTTTTTTTTCCATCAAGATTCTGTCTGTAGAAAAGAGCAGCAATTTGCTA
GTAATAACCGAACAGGGCCTAATTTCTGGACCCCTATCTCCAGTTAAACCTTGACAAAG
CTACAGATATAGACGATAAACTTGAAGATGTGGTGAAGGATATCTACAATTATTCATCCT
TAGTAGATTGTGCTGAAGGGTCTTATGCAAGTGGATGATGAGGGAGATACCGAGGGTA
GTGAAGCAAAGAATTTTTTCCAAGCCCTTCCAATCGGGAGATGATGAAGAAAATAAAGAAA
CTGTAACAAATAATGAAAATGTAAATAATACTAATGATCGGGATGAAGATATGGAATAA
CAGATGATGTTGAAGAAGATGCAAGTACAGAGCCAGAATTAACAGATAAGCCAGAGGCGT
TAGATAAAATTAAGGATAGCTTGACTTCCACTCCGTTTGCATTCTTTCTATGAATGATA
TTATTGTTTGTGAGTGGAGCGAATTGGGTTCAAATGAGGCATTTTCCGATGATAAAATAT
ATACTGGGAAAATCCAGCTACTTTGCCTAACAAAGAGTTGGAGAACGCTAAGTTGGAAA
GATCTAACGCTAAGGAAAGAACCATAACCTTGGACGATTGTCTCCAATTATTTTCCAAAC
CAGAAATACTAGGATTAACCGATTCTGGTACTGCCCTACATGCAAGGAACATCGTCAGG
CTACCAAAACAAATACAACCTTTGGAATACACCAGATATTCTGCTAATTCACCTTAAAAGGT
TTGAAAGTCAAAGGTCTTTTAGCGATAAAATTGATGCCACGGTTAATTTCCCCATTACAG
ATTTGGATCTGTGAGGTACGTTGTCTATAAAGATGATCCAGAGGTTAATCTATGACC
TGTATGCAGTAGATAACCCTATGGTGGTTTGGGTGGTGGGCACTATACCGCGTACGTAA
AGAATTTTGGCGACAATAAATGGTACTATTTTGATGATTCTCGAGTAACTGAACTGCGC
CAGAAAATAGTATAGCTGGATCGGCTTATTGCTATTTTACATTGCGCGTCATAAAGATG
GCAATGGATTAGGCAGCTCTAAACTACAGGAAATAATCCAAAAGTCACGCCACGGATATG
ATGAGCGTATCAAAAAGATATACGATGAACAGATGAAGTTGTATGAATTTAATAAGACTG
ACGAGGAGGAAGATGTTTCTGATGATATGATAGAATGTAATGAAGATGTGCAGGCCCTG
AATATAGTAATCGTAGTTTGGAGGTTGGGCATATTGAAACTCAGGACTGCAACGACGAAG
ATGACAATGATGATGGTGAGAGGACAAATTCAGGTAGGAGAAAGTTAAGATTGTTGAAAA
AAGTCTACAAGAATAATTCAGGCTTGGGTTTCATCGAGTACGCTGAAATATCTGAGGGAT
GCCCAGAAAACGAAGTCGCTGATTTGAATTTAAAAAATGGTGTGACACTAGAATCGCCAG
AATAA

YJL197W, 1254 aa (SEQ ID NO 166)
MGSSDVSSRECSLVYNEDPDFTDGTTPCDRLGVLDLMNVLDKDEIKQESVPVSDREIEDT
ESDASAVSSFASANELIAEPHAASETNLGTNGQDGRNVLEQQRDVVARLIEENKETQKEG
DKVCIVPKVWYDKFFDPDVTDPEDIGPINTRMICRDFENFVLEDYNRCPYLSIAEPVFNF
LSEIYGMTSGSYPPVVTNLVINQTTGELETEYNKWWFRLHYLLEKQDGRKRRHGQDDSIMY
LSMSALNLVRDLVEKSMNLFEEKADHLDVNAVDFKIWFVSEGSDIATDSNVSTFLNSSYE
ITPLQFLELPIKKLLIPDMFENRLDKITSNPSDLVIEIKPIEGNHHWPSNYFAYNKLEPA
SGTTGLVNLGNTCYMNSALQCLVHIPQLRDYFLYDGYEDEINEENPLGYHGYVARAFSDL
VQKLFQNRMSIMQRNAAFPPSMFKSTIGHFNSMFSGYMQQDSQEFLAFLLDLSHEDLNRI
IKKEYTEKPSLSPGDDVDNWNVVKKLADDTWEMHLKRNC SVITDLFVGMKYSTLYCPECQ
NVSITFDPYNDVTLPLPVDTVWDKTIKIFPMNSPPLLELEVELSKSSSTYMDLKNYVGKMSG

FIG. 1 - 58

LDPNTLFGCEIFSNQIYVNYESTESNAQFLTLQELIKPADDVIFYELPVTNDNEVIVPVL
NTRIEKGYKNAMLFGVPPFITLKEDELNNPGAIRMKLQNRVHLSGGYIPFPEFVGNRTD
FADAFPLLVKYPDVEFEQYKDILQYTSIKVTDKDKSFFSIKILSVEKEQQFASNNRTGP
NFWTPISQLNLDKATDIDDKLEDVVKDIYNYSSLVDCAEGLVMQVDDDEGDTGSEAKNFS
KPFQSGDDEENKETVTNNENVNNTNDRDEDMELTDDVEEDASTEPELTDKPEALDKIKDS
LTSTPFAILSMNDIIVCEWSELGSNEAFSDDKIYNWENPATLPNKELENAKLERSNAKER
TITLDDCLQLFSKPEILGLTDSWYCPTCKEHRQATKQIQWLWNTPDILLIHLKRFESQSF
SDKIDATVNFPIITDLDSRYVVYKDDPRGLIYDLYAVDNHYGGLGGGHYTAIVKNFADNK
WYFDDSRVTETAPENSIAGSAYLLFYIRRHKDGNGLGSSKLQEIIQKSRHGYDERIKKI
YDEQMKLYEFNKTDDEEDVSDDMI ECNEDVQAPEYSNRSLEVGHIEIETQDCNDEDDNDGDGE
RTNSGRRLRLLLKKVYKNNSLGSSSTSEISEGCPENEVADLNLKNGVTLESPE

YJL198W, 3149 bp, CDS: 501-3149 (SEQ ID NO 167)

TGTCGTATTTCCACTGATTTGGATGTATGTTGCATGGTGTAGATTGTGAATAAATCATT
TCCACTGGTTTCTAGCAGAGGTAAGAAAATCAGTAGTAGCGGCAGCAGCCAAGAAAAATG
GCAGCCTGGCAAGCAGCGAAGGCCATCTGTGCTGCATTTCCACACTCCTTGTATGACTGC
ATACGCATAAAGAGGTGCCTTGCTGTAGGCGTATATGATCCTAAGCAACAGAGAAACCAC
GGTTCCTCTCTCTTCTTATTTCTGTTATTTGCTTCCCTTTTTTACTATGGGTAAAGTCGCC
TAAAGCGGGGCGCTCACAATATCGCCGAGCTACAGCCGTTTTTTTTTTTTTTTTTTTTT
TTTGCGCTGCTTCTCGAAGAATGAATGGCTCACTGAAAAATTTTGATTCATCGATATAAA
GAACACTGTTCACTTCGATGTCATCCGGCCAATAAAGTTGTTTTTAGGATAAACGAGTAA
GTGGTAGCTGGTACAGGATCATGAGATTTTCACACTTCTTGAAGTACAATGCTGTCCCAG
AATGGCAAACCATATATGGAAGTACAGCGAGCTGAAAAATCTTATTTACACGCTACAAA
CAGATGAAGTTTCAAGTTGGTGATAACGAAGAAGGATTTGGCGCAGGAAAGAGCTCTAACA
TTACAGATAGGTTCAAAAACAAGTTTCTTTTAAAAATGCGAAGGAAGATACGCTCTCCG
GTATGAACAAAGATGACAGGCATCGTTGAGGAAACCATCGAGTTGCGAGAGTTGCCTACTG
CTCAGACGGTGCCTGCCAAACCTTCTCCTTTTCAAGAATGAAGGAAAAGATATTTTACA
AAAGAAGGTCTGCTTCCGCATCGTCCGTCTCCTCCACGGCCAACGAAAAATCTGCAATTAG
ACACTTATGATACGTTTGTGTTGGTGATTTAACAGCTGAAAAACAGAAAGTAGATGATTTT
ATAAGAGGACAGAAGCGAAGTTCTACGACAAATTTGACGCGCTGGTGAAGGACCTGAAGA
AAATCGGAGTTATAGAATACGATATCGACGATGATACTCTGTTTAAACGAACCGATTGCCA
GCACAAATGACGAAGTTCCCCACTAGACTTGGATGATGACGAAGACGACGACGAATTTT
ACGATGATCAATCTAATATTGAAGATAATACTGCTTTGCTGCATCATTGCGAGTATAACA
TTAAGTCTCAGAAAAATCGCTGTTGAAGAAGTCGATCGTAAACCTATATATCGATCTTT
GCCAGTTGAAGTCGTTTCATCGAATTGAACCGCATTGGGTTTGCAAAAATTACAAAGAAAT
CAGACAAAGTTCTTCACTTGAATACAAGAACCGAAGTATCGAATCGGAGCAGTTTTTCA
AAGACACATATGCATTCCAGGCAGAAACGATCGAATTGCTAAATTTCAAAATTTCCAGC
TAGTCACATTTTATGCGCGCATCACTGACCGGCCTCATAATATCTCGCATAGCAAGCAAG
AGTTGAAATCCTACCTGCATGACCACATTTGTTTGGGAAAGAAGTAACACTTGGAAGACA
TGTTGGGACTGCTATCGCAAGCTGACGAGTTGACACCAAAGGAAACAGAAATATAATGCAA
ATAAGCTGGTAGGCAAGTTAGATTTGGAATACTACAGATGGCCACTACCCAGACCGATAA
ACTTAAATTTCACTAGTATAAACAACGTTGCATACCGAAATTATTTTACCAAGAAAG
CATACAAGATTTACTTTTATTATTCTAGTCACTGGACTCTTGTTAGGAATAAAGACCTTCA
ACGACGCTGCTCAGCACCGCTGCATGGCCCTTGTCGAGTGTGTGCGCTTTTTGTGGGCTA
GTGAGGCCATCCCATACACATTACAGCATTCCTTGTACCACTACTTGTAGTCTTTTCA
AAGTCTTAAACCTCCGACGGGGCTATAATGAGTGTGCAAGCGCTTCATCAGAAATTT
TGGCCGCCATGTGGTCTTCTACAATTATGATTTCTGCTGGCAGGTTTTACTTTGGGTGAAG
TACTTGCACAATATAACATCGCCAAAGTTCTTGCCCTCGTGGTTGTTGGCCTTCGCTGGTT
GTAAACCCAGAAACGTTCTTTTAAATGGCAATGTGTGTCGTGTTCTTCTATCAATGTGGA
TTTCCAATGTGCGACGACCTGTTCTAACAATATTCGTTGTTATCTCCCTATTGGATGCCA
TGGATGCAGATAGCCCATTTGCGCAAGCATTTGGTGTAGGTGTAGCGTTGGCTGCAAATA
TCGGTGGTATGTCTTACCAATCTCTTCACTTCAAAACATCATTTCCATGTGCTACTTGA
AACCCTATGGTATTGGCTGGGGCCAATTCTTTGCTGTTGCATTGCCATCTGGTATCCTGG
CCATGCTTTTGGTTTGGATTTTATTGTTCACTACTTTCAAGATGAATAAGACCAAAATGG
AAAAATTTAAGCCTATTAAGACGAAATTCACAGTTAAGCAGTATTATATCATCTACTGTCA
CTGTGGCCACTATTTTGTGTTGGTGTGTGGAAGCCAGATTGAAGGTGCTTTTGGGTGAT
CAGGTCAAATGCAATCATTTCCATCGTTTGTGTTTTTGGTACCGGATTACTATCAACAC
AAGATTTAAATGCCTTTCCGTGGTCAATCGTTATTTTGGCAATGGGAGGTATTGCTTTGG

FIG. 1 - 59

GGAAGGCCGTCTCATCCTCGGGTTTGCTATCAACCATTGCAAAAGCATTACAAAAGAAAA
TTGAGAATGATGGTGTGTTTTGCCATTCTATGATTTTCGGTATCCTGATGTTGGTTGTGG
GTACTTTTCGTCTCGCATACAGTATCCGCTATTATCATCATTCCTTGGTGCAAGAAGTTG
GTGACAAGCTTGGCAACCCCAAAGCTGCTCCTATCCTTGTGTTTCGGTTGTGCATTATTGT
CATCCTGTGGTATGGGACTAGCTTCTTCGGGGTTCCCAATGTCACTGCCATCTCTAAAG
TAGATAGAAAAGGGCGATCGCTATTTAAGTGTCTAGCTTTCTTAACGAGAGGTTGTTCCAG
CTTCTATTTTGGCTTTCCTATGTGTCTACTCTAGGTTATGGTATCATGGCATCTGTTG
TCAAGGGTAACGCAACCTCTGCGTAA

YJL198W, 881 aa (SEQ ID NO 168)

MRFSHFLKYNAPPEWQNHMYDSELKNLIYTLQTDDELQVGDNEEGFGAGKSSNITDRFKN
KFSFKNAKEDTSSGMNKDAGIVEETIELRELPTAQTVAAKPSPFRRMKEKIFYKRRSSSA
SSVSSSTANENLQLDYDTFVGDLTAEKQKVDDFYKRTEAKFYDKFDALVKDLKKIGVIEY
DIDDDTLFNEPIASTNDEVPLDLDDDEDDDEFYDDQSNIEDNTALLHHSQYNIKSQKKS
LLKKSIVNLYIDLQKLSFIELNRIGFAKITKKSQKVLHLNTRTELIESEQFFKDTYAFQ
AETIELLNSKISQLVTFYARITDRPHNISHSKQELKSYLHDHIVWERSNTWKDMLGLLSQ
ADELTPKETEYNANKLVGKLDLEYRWPLPRPINLKFTSINNVALPKLFFTKKAYKIYFI
ILVTGLLGKTFNDAAQHRCMALVECVAFWLWASEAIPHLITAFVLVPLLVVLFKVLKTS
GAIMSAASASSEILAAMWSSTIMILLAGFTLGEVLAQYNIKVLASWLLAFAGCKPRNVL
LMAMCVVFFLSMWISNVAAPVLTYSLLSPLLDAMDADSPFAQALVLGVALAANIGGMSSP
ISSPQNIISMSYLPYIGIGWQFFAVALPSGILAMLLVWILLFTTFKMNKTKLEKFKPIK
TKFTVKQYIIITVTVATILLWCVESQIEGAFGSSGQIAIPIVLFPGTGLLSTQDLNAPP
WSIVILAMGGIALGKAVSSSGLLSTIAKALQKKIENDGVFAILCIFGILMLVVGTFVSH
VSAIIIIPLVQEVGDKLGNPKAAPILVFGCALLSSCGMGLASSGFPNVTASIVDRKGR
YLSVMTFLTRGVPASILAFLCVITLGYGIMASVVKGNATSA

YJR049C, 2093 bp, CDS: 501-2093 (SEQ ID NO 169)

ACTGCCATCTCTTCCATTCTTTGAAAAGATTATTAAGTTCGTCTGTTAAGTTCGCAATCT
GCATTTTCATTTAAAGACGGATCATATATCTTGTGCTTTTTTGTGTTTATCTCTTTACTTA
CTTGTCGCTTCCATTTCGTTGGCCTCTTTTATGGATTTTACCTTAGACACGTTCTGGGCC
TCTGGTAACGTGAATAATCCTTGTATCCACCTGCCGACTCTGCTTGCTGCTCTTGAAATC
GTACCAGAACTGAGTTGGCCTTATCTACATTTCTACTCATTTTGAATGCACAGGTATCTG
ATTACTGATGTGGTGCGCCTTGCATATAACGGTGTGTCACTTTTATTTGCTCTTTTCATG
CATCCTGAAATTATTTACCGCACTACGCAAGAGAACGGAGAAAAGGTATAATAGGGC
AAATGATCATTGACATCGTGATCGTAAGCCAAAAAATAACAATAGGCTCCCTAAATAA
GTAGAGTAAAAGCTCTTGAGATGAAGGAGAATGACATGAATAATGGCGTAGATAAATGGG
TAAATGAGGAAGATGGTGCAAATGATCATATAACAACAATAATAACTTGATGAAGAAGG
CCATGATGAACAATGAGCAAATTGATAGAACTCAGGATATCGACAACGCCAAAGAAATGT
TGAGGAAATATCAAGTGAAGCAGCTCGCGCAGAAGCTCCCTGTTGAATAAAGATTTCAT
CTCTCGTGAACGGCAATGCAACAGTGGCGGTGGTACGAGCATTAACGGAACAAGAGGAA
GTTCTAAGAGTAGTAATACACACTTTCAGTATGCCTCCACGGCGTATGGTGTAAAGATGT
TGAGTAAAGATATATCTAATACCAAAGTGGAACTGGATGTGGAAAATTTGATGATTGTTA
CGAAACTCAACGATGTCTCACTGTATTTCTTAACAAGAGAGTTGGTAGAATGGGTTTTGG
TACATTTTCCACGTGTGACTGTTTATGTGGATTCCGAATTGAAAAACAGCAAAAAATTTG
CCGCTGGCGAGTTATGTGAAGATAGTAAATGTAGAGAATCAAGGATCAAGTATTGGACAA
AGGATTTTCATCAGGGAACATGATGTTTTCTTCGATTGGTAGTGACTTTGGGTGGCGACG
GTACTGTTCTTTTGTAAAGTTCATTTTTCAGAGACATGTACCACCGTTATGTCGTTTTT
CATTAGGGTCTCTAGGATTTTAAACAAATTTAAAGTTTGAACATTTTCAGGGAGGATTAC
CTCGGATTATGAATCATAAAATCAAGACAAATTTACGGTTGAGGTTGGAGTGCACAATTT
ATCGTAGACACCGCCCTGAAGTAGACCCAAACACGGGGAAGAAAATATGTGTGGTGGAAA
AACTAAGCACACACCACATTTTGAACGAAGTGACCATCGATCGTGGTCCAAGTCCTTTTC
TATCCATGTTAGAATTGTATGGTGACGGCTCATTAATGACCGTTGCGCAGGCGGACGGAC
TGATTGCTGCTACTCCGACTGGGTCCACGGCTATTCTTTGAGTGCAGGTGGGTGATTGG
TATGCCCCAACCGTCAATGCAATCGCTTTAACACCCATTTGTCCACATGCATTGAGTTTCA
GACCATCATCTTACCAGAAAGTATAAATTTAAAGTGAAAGTCTCGATGAAGTCAAGGG
CTCCAGCATGGGCGGCTTTTGTATGGGAAAGATAGAATTGAATTGAAAAAGGTGATTTTA
TAACCATATGCGCCAGCCCATATGCTTTTCCAACCGTGGAAGCCTCGCCCGATGAGTTTA
TTAACAGTATCAGTCGACAATAAAGTGAATGTGAGGGAACAACAAAAGTCCTTTACGC

FIG. 1 - 60

ATATTTTGTCCCAAAGAACCAAGAAAAATATGCACATGAGGCGAACAAAGTCAGAAATC
AAGCAGAACCTTTAGAGGTAATAAGAGATAAATACTCTCTGGAAGCAGACGCTACTAAGG
AAAACAACAACGGAAGCGATGATGAGAGCGACGATGAGAGTGTAAACTGCGAAGCTTGCA
AATTAAAGCCTTCGAGCGTCCCAAACCTTCTCAAGCAAGGTTTTTCAGTATAA

YJR049C, 530 aa (SEQ ID NO 170)

MKENDMNNGVDKWVNEEDGRNDHHNNNNNLMKKAMMNNEQIDRTQDIDNAKEMLRKISSE
SSRRSSLLNKDSSLVNGNANSGGGTSINGTRGSSSKSSNTHFQYASTAYGVRMLSKDISN
TKVELDVENLMIVTKLNDVSLYFLTRELVEWVLVHFPRVTYVVDSELKNSKKFAAGELCE
DSKRESRIKYWTKDFIREHDFVFDLVVTLGGDGTVLVFSISFQRHVPPVMSFSLGSLGF
LTNFKFEHFREDLPRIMNHKIKTNLRLLECTIYRRHRPEVDPTGKKICVVEKLSTHHI
LNEVTIDRGSPSPFLSMLELYGDGSLMTVAQADGLIAATPTGSTAYSLSAGGSLVCPTVNA
IALTPICPHALSFRPIILPESINLKVKVSMKSRAPAWAAFDCKDRIELQKGDFTITICASP
YAFPTVEASPDFINSISRLNWNVREQQSFTHILSQKNQEKYAHEANKVRNQAEPLEV
IRDKYSLEADATKENNNGSDDESDESVDNCEACKLPSSVPKPSQARFSV

YKR094C, 1255 bp, exon1: 501-508, intron1: 509-876, exon2:
877-1255 (SEQ ID NO 171)

AGGTTGTGTCTTCAATGATGGGCAATGCAATTTGGCGTTAAGCGCCTGAGCAATAAGGT
AACAGCGAAATTTATGACATATTATTTGCAACCTTTTACAACTAGTAGATTAGTGATT
TATTACCTATTGGCATTCAATTTGTGTTCTATATGTGGATGAGGATAGCCGCCTTTCTTCT
CATCGGAGGCCATATCATCTTTGACAATCCTTTTAAATACTATTTCATCCGTGCCTC
TAATAGATTTGTGTAGTTGTCTGGGTGCAATCTTTCCATTTTGTCTGAACTTTTTTTTT
TTTTTCATGTTTTTCAGATTCTGAAGTACCGCAATAGGATATGGCGGATAATCCGCCATAT
GATCCGCCTCATACTAGCCATTACCCATCTATCCCAGGCATTATGGGTATGCAACTCATA
ATCTCAAATACACAAATAAGAGCAACCTTATATATCACTTTTTCCCGTTCAGCAAGAGGT
AAAGCCACCAAAGGTTCAAATGCAAATGTATGTTACGGCGAATACAGAATACTATGTTC
GAAATAATATGAGGATTATACGATAGCAAAAAGCCATAAACGAAAGACATAAATGGAAA
ATGATTGACAAGCTCACAAATTTATTAACAAGTAGCAATTGAGAAAACTATTACTCGCG
GCAAGCTTCTGAGTTTACATTAAATCTGTAGAGCAAATTGAAAATGTCGCATATGTGCTG
AAGGTTTGTGTTCCATCTTATTTTGCATAAACATAGTTATATTACTTGGTCGCATAA
AAAATATTTTTTACTAACGTGAAGTTTCTTTCTTTATGATGTACGCACGCACGTCTGTGC
TTACTCCATAAATGAACTTATTCCAATTTTGTACAGCTTCGTTAAGACTTTGACTGGTAA
GACCATCACTTTGGAAGTTGAATCTTCTGACACCATTGACAATGTCAAGTCCAAGATCCA
AGACAAGGAAGGTATCCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGA
AGACGGTAGAACTCTATCTGACTACAACATCCAAAAGGAATCCACTTTACATTGGTCTT
GAGATTAAAGAGGTGGTATCATTGAACCATCTTTGAAAGCCTTGGCTTCCAAATACAACTG
TGACAAATCTGTTTGTCTGTAATGTTACGCCAGATTACCACCAAGAGCTACCAACTGTAG
AAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTGAAATAA

YKR094C, 128 aa (SEQ ID NO 172)

MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRGRGIIEPSLKALASKYNCDSVCRKCYARLPFRATNCRKRKCGHTNQ
LRPKKKLK

YLR040C, 1175 bp, CDS: 501-1175 (SEQ ID NO 173)

AGCTCTCAAACAACTAATACTATAAGTTCAAGTACAAGCACAGGAGGTGTAGGTTCAGTC
AAGCCATGTCTTTACTTCGTTTTAATGTTAGAAACAATCGCTTATTTGTTTTCTTAAACA
AATATATTAGGTTCAAGGCTTTCGCAGGTGTAAGAAAACCCGTGGTCTCCATATTCTTAA
GTATGATAAATAAAAAAACTTAATAAATTATTAATTGCTTCAAACCTTTTTCTTTTTT
TAGTTTTTAATATTTCAAACGTTATCTTCATTGAACGCCCAAATAGGGAAAAATCCTGGC
AAATTTTTTATTGCTGTCTATCCAAGGCTATGCTAGAAAATTCAAGAGCTTGGATGATTTA
AAAAGACACTCTCAATCGAGAAAGTTTATTCTTTGTTATTCTGCTTTACCTGATCATATT
CCGGCGTATTGTTTCTAATCAAGTGATTTGATATCCAGTTACGAACCATTTACAACATT
CCTGAAAATATTGCGTATCAATGATATTTGCTCCTTCTTCTCCCTCATTTAAAAATATT
TCCTGGTAAGCTTTCTAATCAGCCACAGTTTGTCTGCCAAAACCTTAACGTCTAGTTCCA
ATGACGATACACTTGCCAGGTCCGCAGCTGCAGATGCAGACATGGCATTTCTTCATGGAGT
TTTTAAACGATTTGACACCGCTTTTCCACAGTATACCTCATACATGATGCAAAACCAT

FIG. 1 - 61

TAACCCTACCTCAACCTGTTGCTGACTACTACTATCACATGGTTGATTTGGCCTCAACAG
CAGATTTACAATCTGATATTGCTCAGAGTTTTCCGTTCACTCAATTCCAAACATTCATTA
CGGCCTTTCCATGGTATACCTCTTTGCTAAACAAAGCCTCCGCCACCACCATATACCTTC
CCCAACACTTCATAACAGGTGAGACAGAAGCTACCATGACTAACTCATCTTATGCCAGCC
AAAAAACTCCGTTTCCAATTCTGTTCTTTCTCGACAGCGAACGCAGGCCAGTCCATGA
TTTCCATGGCTAATGAAGAAAACAGTACAACAGCACTTATATCCGCATCAAACCTCTTCTT
CAACATCCAGAACTAGTCAATCACAGAATGGTGCCCATGCCAAAAGCTTATATTTCCCA
TGGCGTTGTTCCGAATCTTTGCAGTTGCCCTTTAA

YLR040C, 224 aa (SEQ ID NO 174)

MIFAPSFSLIKNILLVSFLISHSFAAKTLTSSSNDTLARSAAADADMAFFMEFLNDFDT
AFPQYTSYMMQNHLTLQPVDYHHMVDLASTADLQSDIAQSFPTQFQTFITAFPWYT
SLLNKASATTIYLPQHFIITGETEATMTNSSYASQKNSVNSVPFSTANAGQSMISMANEE
NSTTALISASNSSSTSRTSQSQNGAHAKSLYFPMALFGIFAVAL

YLR048W, 1618 bp, exon1: 501-590, intron1: 591-949, exon2:
950-1618 (SEQ ID NO 175)

GCACCCTTTTTCTTTTTCAATAACAAAAAGAGCTTGGGCATTACGTTTTCAACACTTTT
AATATTTCCCTTTTTACATCCGTACATATAAATGTAAACCCATGCATTCATGACAATTT
TACCTATTTCTTAAAGGCCTTTGTCACTTCTTTATGGGAATGGCGCTACTTTAATTTTCC
GCCTACTTTGAAAAATTTACCAAGGCGAAATTGAGTGCGCTAGGCGGAAGTTCAGGGCA
CGGTCACCGAACCTTTGTGCTGTTTCGAACGAGGGTCCCCTGGAGGTTGACCGACGCGG
GAGGAGCTGGAAAGATGGAATGGAAGGACTGCAACACTCAGTAAGAAGGTTCTGTTAGG
GAACATCACCTTCTCTAGTTCTGTAATAATATGATCAAGTTTGAATCCTCGTATTG
AAAAATCGCGAGTTATTAAGTGTGTAATTTAGAATACCGAAATAGCACAAAGAGATAA
GATAAGATACTGATAGGATAATGTCTTTACCAGCTACTTTTGATTGACTCCAGAGGATG
CCCAACTTTTGTGGCCGCTAACACCCATTTAGGTGCTAGAAACGTTCAAGTATGTACAC
ATATCCCATACGATTATGTTCTATAGATGATAATAGGTCTCGAAAAGAATATGTCCCCGA
TTAATCATATTTGGAGGTCAGAGGACCAAAGGTAATTTAGAGGAATTTGAACACGCC
GGGTTTAGAAGAGTTAGAATTTCACTTCTTAGTGAGGGTAAGGAGAAGAACTCAATAAG
AATATACATCCTCGACTGTGTCAAAGATTATGAACTCCGATGAAACAGTAAACGTCAAA
AAATTCACGGGATATAATTCGGTACTTTATTGGATATGGAAGAAAACATTATATATGCA
CAAATGAACGCTCTTACTAACATAATTTATCTTTCTCTCTTTTTTTAGGTCCACCAAGA
ACCATACGTTTTCAATGCTAGACCAGATGGTGTTCACGTTATCAATGTTGGTAAGACCTG
GGAAAAGTTGGTTTTGGCTGCTAGAATTATGCTGCCATTCCAAACCCAGAAAGATGTTGT
TGCCATCTCTTCCAGAACCTACGGTCAAAGAGCTGTCTTGAAATTTGCTGCTCACACTGG
TGCTACTCCAATCGCCGTAGATTCACTCCAGGTTCTTTCACTAATTACATCACCCGTTT
TTTCAAGGAACCAAGATTGGTTATTGTTACCGACCCAAGATTAGACGCTCAGGCCATTAA
GGAAGCTTCTTACGTTAACATTCCAGTCATTGCTTTGACTGATTTGGACTCCCCATCTGA
ATTTGTTGATGTGCGCATCCCATGTAACAACAGAGGTAAGCACTCCATCGGTTAATCTG
GTACTTGTGGCTAGAGAAGTTTTGAGACTAAGAGGTGCTTTGGTTCGACAGAACTCAACC
ATGGTCCATCATGCCAGATTGTACTTCTACAGAAACCCAGAAAGAAGTTGAGCAAGTTGC
TGAAGAAGCTGCTGCCGCTGAAGAAGGTGAAGAAGAAGAAGTTAAGGAAGAAGTCACTGA
AGGTCAAGCTGAAGCTACTGAATGGGCTGAAGAAAATGCAGACAACGTTGAATGGTAA

YLR048W, 252 aa (SEQ ID NO 176)

MSLPATFDLTPEDAQLLLAANTHLGARNVQVHQEPYVFNARPDGVHVINVGKTWEKLVLA
ARIIAAI PN PEDVVAISSRTY GQRAVLKFAAHTGATPIAGRFTPGSFTNYITRSFKEPRL
VIVTDPRLDAQAIKEASYVNIPVIALTDLDSPSEFVDVAIPCNMRGKHSIGLIWYLLARE
VLRRLGALVDRTPWSIMPDLYFYRNPEEVEQVAEEAAAAEEGEEEEVEKEEVTEGQAEAT
EWAEEENADNVEW

YLR088W, 2345 bp, CDS: 501-2345 (SEQ ID NO 177)

CTTCCCATGTAGAATATCATTTGTCAAACATACTACTACCGTGAGAATCCAATCTACTAAA
AAGACCCAGCTAAAGTCCTTTTGGTGTGTCAATGGAACACCACGTAATTGTGAAATAGCT
TCCATGCTTGCTAACTTATTACCGTCAATAGAAGACTTGAGTCAGGTGGCTTTAATGAGT
ACTATTCTTTTTTTTTTCCAAAGAGCACTATGTTGATAATACCGCAGTAATTTTTTTTG
AGTATCCTGTAGCCTAGAAAGGTTGAAGCTTATAAAACCGTGCCAACAGCTTTATAGTGG

FIG. 1 - 62

GGAGTTTGGCTTCCCTCTATTTGTATATTGATCGCCATCCCTACGAAGTTATTGGGAACG
CATCGTGAACCTCTCACTTTAATGCCAGCGGTAGAAAAAAGTCATAAACAATACACGC
CGGCTACACCTAGAAAAGAAATGACATTTGCTGTCTTATAAAAGGACTTGACAGACCAAAG
ACGCGTATAATACACCAAGAATGGCCTTATTGGAGAAGTTGCATCGAAGGATTGTTGATA
TGGGGCTTGTCCCGGTATAATCGCCTTATTACCAGTTATTTCCATGCTATGCGCTCTAT
TTGGGTTTATTTCTATAGCTATTCTGCCTATGGATGGACAGTACAGAAGAACATACATTT
CTGAGAATGCATTTGATGCCTTCACAAGCGTATAGTTACTTTAGAGAATCTGAATGGAACA
TTTTGAGGGGCTATCGATCTCAAATTAAGAAATGGTAAACATGACTTCTATGGAAAGAA
ACAATTTGATGGGTTCTTGGTTACAAGAATTTGGTACTAAGACTGCTATTTACGAAAATG
AACAAATATGGAGAAACATTGTACGGTGAATGCACGCTCCTAGGGGTGATGGAACAGAAG
CGATGGTGCTTGCCGTTCCATGGTTTAATTCAGATGATGAATTCATATTGGCGGCGCAG
CTTTGGGTGTATCTTTAGCAAGATTTTCTCACGTTGGCCAGTATGGTCCAAGAATATAA
TTGTTGTCTTCAGCGAAAATCCTCGTGCAGCATTAAGATCATGGGTTGAGGCATACCATA
CTTCCTTAGATTTGACTGGTGGTTCATTGAAGCTGCTGTTGTGTTGGATTATTCGAGTA
CGGAAGATTTCTTCGAGTATGTAGAAATCTCATACGACGGTCTGAATGGTGAGCTGCCCCA
ATTTGGATCTTGTCAACATCGCTATATCCATTACGGAACATGAAGGTATGAAAGTTTCTT
TGCAGGTCTACCCAGTGATCAGTTAACTAATAATAATTTCTGGTCAAGATTAAAAATAT
TATGCCTGGGAATAAGGGATTGGGCGTTGTCCGGTGTAAAAAGCCCCATGGTAAACGAGG
CATTTAGCGGCTGGAGGATTCAATCTGTAACATTGAAAGCACATGGAAACAGTGGTCATG
ATATTACTACATTTGGACGTATACCCGAAGCAATGTTTCGCTCTATTAATAACCTTTTGG
AAAAATTTACCAATCGTTCTTCTTTTATTTGTTATTAGCACCACGTGAGTTTCGTATCCA
TTAGTAGTTATTTGCCAAGCGCTGTGGCTTTATCTATAGCATTCGCCATAAGTTCATTAA
ATGCATTTATAAACAATGCTTATGCAAATATATCCTTATTTTCCGAGTATAAATTTGGTAG
CGTTGTTGGTTTGGTTCGTGTCATTGGTGATATCATTTGTTGTTTCAAGCGTTTCTTTC
TAATACCTTCATCGGGATTATTGATGACAATTAGCATGGCATCTTGTTTTTTACCTTTGA
TACTTTCCAGAAAAATTCACATCTCAGAACCCTATCATACAGGTTGAAAAATGTTGCTT
TTTTATATTTTCACTTTGGTTTCAACATCTTTGCTAATGATAAACTTTGCAATGGCTTTAC
TGATCGGCACATTGGCATTTCCCTATGACATTTGTGAAGACCATTGTTGAAAGTTCTAGCG
AACATGAGGTGACAACTCAATCCTCTAACCCAATAAAAACTGAGCCGAAAGATGAGATAG
AGCTCGTCGAGAAATCACATGGATACAACGCCAGCAACCCCCCAACAACAGAAAACAAAAAC
TAAAAAATTTAGTACTATTAATTTTGACAAATCCATTTATTTCAATAACCTTATTCGGAC
TATTTTTTTGATGATGAATTTTCATGGATTGATATAATAAACAACAACTGGTTTTCAGCATGGT
TGGATTTGAAATGTTGGAGTTGGTTTGTACTTTGTATAGGTTGGCTTCCATGTTGGCTAT
TGATATTAGCGTCATCGTTTGAATCTAAATCTGTCTAGTAAGGTCGAAAGAAAAGCAA
GTTAG

YLR088W, 614 aa (SEQ ID NO 178)

MALLEKLHRRIVDMGLVPRIIALLPVISMLCALFGFISIAILPMDGQYRRTYISENALMP
SQAYSYFRESEWNILRGYRSQIKEMVNMTSMERNNLMSGWLQEFGTKTAIYENEQYGETL
YGVMHAPRGDGTAMVLAVPWFNSDDEFNIGGAALGVSLARFFSRWPVWSKNIIVVFSN
PRAALRSWVEAYHTSLDLTGGSIEAAVLDYSSTEDFFEYVEISYDGLNGELPNLDLVNI
AISITEHEGMKVS LHLPSDQLTNNNFWSRLKILCLGIRDWALSGVKKPHGNEAFSGWRI
QSVTLKAHNGNSGHDITTFGRIPAMFRSINNLEKFHQSF FFYLLAPRQFVSISSYLPS
AVALSIAFAISSLNAFINNAYANISLFSEYNLVALLVWFVSLVISFVVSQAFLLIIPSSGL
LMTISMASCFLPLILSRKIHI SEPLSYRLKNVAFLYFSLVSTSLLMINFAMALLIGTLAF
PMTFVKTI VESSSEHEVTTQSSNPIKTEPKDEIELVENHMDTTPATPQQQKQKLNVLVLL
ILTNPFI SITLFLGFFDDEFHGFDIINKLVSAWLDLKCWSWFVLCIGWLPWLLILASSF
ESKSVVVRSEKQSQS

YLR159W, 845 bp, CDS: 501-845 (SEQ ID NO 179)

TCCGTCCCAAAGATAGCTTGATCATCCTAAGCGGGTCGCATTTTACTATCCCCAGTTCCG
AAGAATAACAAGGCTCAATGCATATGCTGTTTATCGTGCTCACAAGGCGGTATGACGTTT
TTAGCAATGTAATTATATTAAGATCTTCAGTCACTATGAGTGGTTGATTGCCCCATA
GAGAGCTATAAGCCGACGTGAAAGCTGCTGGTTCCAGCTTGGCTCATGTCTGCACAGTC
ACTAGTCACTTGGTCGCATTCATTGCTACTCATCTGCGAGTGAGCATATTTGAGATCTGA
CTTGCCAAGGGATTAGAATCACGTAAGACTCTTGATCCTTAGAAGATATTTCTGACAAAG
AACCACCTAAGCCATGCAAGTTTTTTTTTTTCATTTGGTGGCGAAACAAAGGTGATGAAAG

FIG. 1 - 63

TTTCTTCTTGACAAACGCCAAGCCCGATAGGTGAGACAATTCTTGAAGTAATGGACCTC
TGAGTAAGCATATCAGTCGAATGAAGTTCCAATATGCGTTGGCCAAGGAACAGCTAGGCA
GCAACTCGCGCAGTGGCGTCAAAAACTAATAAGTAAACACCACTGGCTTCCGGAATACT
ATTTCTCTGATCTCTCATTTTCTGTTGTACAGCAGTGGGACAGTAGAGCCATTGAAAAA
CTACAATCATATCTTGTATGCGGCCCGCAAACCAAGAGATTATCCTTTGAGACATTGTG
AGACCCTCCGTTTCGCAACCGTGCTCTCTGTTTTTCATCACTATATGCACGCTCTTTCCAAA
GCTCCTGCACCTTTCACGTTGGCGGAGCCATCGCCCGGCTTCCATATGTACGGCTGCCACA
CCTAA

YLR159W, 114 aa (SEQ ID NO 180)
MKFQYALAKEQLGSNSRSGVKKLISKHHLPEYYFSDLFSVQOWDSRAIEKTTIISCM
RPNQEIYPLRHCELTLSQPCSLFSSLYARSFQSSCTLHVAEPSPGFHMYGCHT

YLR167W, 959 bp, CDS: 501-959 (SEQ ID NO 181)
ATCAAAAGAGTGTTCAGTAAGTAAAAACATTTGAGCCTCCCCATTTGTTGAAAGGAGA
GAAATTAAACTTGGTTGGGGTTAATTATTTGATGGGTATATTAATTTGCAACCGCAAGGT
ATCGATAATAAATATTTACAAAACCTTTATCAATAGTGGTGAAGTCTTTAGTGCGATCT
ACCTGGGGTTAATGAACGAGAAGTTCTTGAGATATCTTTCCCTGTTTACCTCCGTGCATCC
TGTAAGGAATTGGGTTTATCATTTATCATTTATTTTAGTACAACTTTTTTTTTTGGCCC
GGGCGCACTTTTTCAAGCGGTGGGAACCTCATCAAAATGAAAACTAGATACTTTTAGACT
TATTAAATGGTTTAAATATTTTGAGATGTTTCGTTATATCAGAACTTCCTTACTTCTATC
TTTTATTCCAATACAAAGAAGTCACAAGATTACTTGGTAAGAAAGAAGCAGTTAATTTTT
AATTTGCCGACAAGCCAAGATGCAAATTTTCGTCAAGACTTTAACCGGTAAGACTATTA
CCCTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCCAAGATCCAAGACAAGG
AAGGTATTCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTTGGAAGATGGTA
GAACTTTGTCCGACTACAACATCCAAAAGGAATCTACTCTACACTTGGTCTTGAGATTGA
GAGGTGGTGGTAAGAAGAGAAAGAAGAAGGTCTACACCACCCCAAGAAGATCAAGCACA
AGCACAAGAAGGTCAAGTTGGCTGTCTTGTCTTACTACAAGGTGATGCTGAAGGTAAGG
TTACCAAAATTGAGAAGAGAATGTAGCAACCCAACCTGTGGTGTGGTGTCTTCTTGGCTA
ACCACAAGGACAGATTGTACTGTGGTAAGTGTCAATTCGCTCTACAAGGTTAACGCTTAA

YLR167W, 152 aa (SEQ ID NO 182)
MQIFVKTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRRLRGGGKKRKKKVYTTTPKKIKHKHKVKLAVLSYYKVDAEGKVTKLRRE
CSNPCTGAGVFLANHKDRLYCGKCHSVYKVNA

YLR232W, 848 bp, CDS: 501-848 (SEQ ID NO 183)
AGCCACCAATTCCACCAGGCCCGGCATTCAAGTACTTGTAAAGAACACCAACAGGCAAAGT
CAACACCCCAATCATGAAGTTGCAATGGGACGTTCCCTACAGCGTGTGCTAAATCCCATC
CAACCAATATGTCGGGGAATTGGTGGGCAAATGAGGTGATTTCGGCCAATATCGAAATATT
GCCCCGTGTAATACTGAACACCTGACAAACAGACCAGCGCCAATTCATCTTGATTTACCT
CTATGGTATCCAGGATATCTTGAGTTCTGATATAAGTCTCTCCCTCGCGTGGCTCGATCT
GAATAAAAACATTCTCAGGTTCCGAAATTCATGAATTTTGCACCTGGTTGTAGAAAGCAT
AATAGTCTGATGGAAAGGAGCCCTTTTCAAAAAGGATCTTGAATCTTTCTCAGTAGGTT
TATAAAACGTAATTAACAATGAATTCAAATTTGCAGTGAGACTATTCACTACTGCAACTT
CATTTTCTTGAGCACCCACGATGGGGGCTAGTAGTGGAAGAATAGGTAAGTCAATGCTGA
CCCAAGGCACCTTTCTCTGGCTTCTTCAGGATGTTTGAAATGCGATTCCACAGCACAAT
CGCTCCACGCATCTAGCTCAGCATTAAATTGAATTCCTAGTTGACTTCGGCATCAAACCTA
AAGAATTCCCGCATAAGTACGTACAGGCTTATCGTCCGACGATAGTCCCATGGATTTAA
ATGTAGGGATGTTGAATTCATCCCTCAGAGATTCCGGATATTCTCCGTCTAATTCCAAAG
CTTTCTCCATAATTACCAGTTTGTCTTTTTTCCACAGAATATTTAGGCTTAATATGTA
CGTATTGA

YLR232W, 115 aa (SEQ ID NO 184)
MGASSGRIGKSMLTQGTFLASSGCLKCDSTAQSLHASSSALIEFLVDFGIKPKEFPHKY
VTGLSSDDSPMDLNVGMLNSSLRDSGYSPSNSKAFSIITSLFLFSTEYLGICTY

FIG. 1 - 64

YLR233C, 2600 bp, CDS: 501-2600 (SEQ ID NO 185)
GCGCATTTTCCCCACCCATGCGAATCATGGCTGAAATCAATGCCTGTTAGGTGCCCTGCA
ACACTAGTCATGGTAACCTTCGCAGTTAGCCCCATTTCTGGCAAACGGGAACCCACTAAAC
ATGAAATCATAGTTCTTTACATACATGTAGCCGGAATCCCTTGAAGTTGATCTGCCTCCT
CCTAGGATCTGTGAAACTGCCTTCGCTATAGAATTTTTCTCTGCGACACATAGCACTTTC
ATTATGTCTATAATACACCTTTACGTAGCTGAAGCGAGCGCACAGACGAAGGTGCTTTC
AAAAGCGATGCCCTCTTTATTGACAGTTACTAATTCGCCAAACTGCTTTTTTTTATCAAT
GTGATTTTCGCGTTCACGCCATTATCCAATGTCAAAAAGGATAATGGAAATGTTAACATG
CCTGTATGATCCGACCGTTTTTAGCAAACCTATCAGGGGAAAAAGTATATTCCATTAAAT
GACACATGCCACCATAGATAATGGATAATGAAGAAGTTAACGAAGAATGTATGAGATTAT
TTTTCAAGAACGCTCGTGCGCATCTGGATAAACATCTAACATCAAGGTTGACATGCGATG
AAAATGCATATATCACGTTTCAGATGCTTCCTGGATGGAATACATCGCAAATCTACTAGGT
TTCTCGAAGAGCTACTTTTGAACAAGAAAAATATGTACCATAATAACAATTACGAACGCA
TAAATGATTCGGTGATACCATTGGTTCTGAACTTTTATGGCTTCAAATTCACGAACCTA
CACTCCAATGGTTTGAGCACTGGTTCCATGATATCATGCGACTAAGTAACAGAAGAAAGT
TCAGAGTTTTTAGAATTTTTCAAAAAAATGATTCAATTTTTCAAAATTACACACAGGT
ATTACTATGACATCATCGAACACCTATGCGCAAAGTACGATATGAATTCGGTTATTTCAA
ATGCTCTCTTCGCGAAGTTGAATTTAATGCAATACACAGATGGACTTTCAACTCATGAGA
AAATTATCTTAAACACGAGTAATCCACTGACGTTTTCCATTGTAATCTCACTACAAAGAT
GCGTGATTAATCTAGGTTCCACACATTTTTATAAAACACTACTAAACAAGCCGTCTAACA
AACCCAAGAGTGTGGAAGGTTTTGAGAAGTCTATTAGGTACTTGAATATTCCTCACTCT
ATCTCCCAGCCGTTGGAGATACTTATTTCAACGAGCGAAAATTTACTTGATCACTGGGA
AATCTCACTGTATTTCTTTGAATTAGTAAGAGGAGCATTTGGTAAGGATTCGGTCTAAAT
GTGCGTTAAACAATTTGAAAGATTTTCATTTTGACTCCTGATTTTCCGGAAGAACGTC
TGATGAAAAAATTTGGCAATTCTTGTGTCAAAAGATCTCAAAGGTGAGAAATCATTCTTTG
AAGGTCAAATTTGTTTTGCAATTTCTATCGATAGTAGAACACACTTTGGTTCCACAGTCAT
GGAACGCATCACGTGCTTCTAATTGTTGGTTATTGAAAGAGCATTTACAAATGGCTGCAT
TAAAGTATCATTCAGGTAATATTAATGTTTACTTGAAAATTTGGCTGCCACAATGGGAA
GTTTCGATCTTATGTTTACAACCTGAAAAAGTAAGGAACAAAAGAACAACCTCAAATATG
CAGATTTGAGTGAGCGCCAGGTTTTTTTTTTTAGACTTGAGCTTTGATTTTATGCTAATA
TCATAGACGTCGTCATCAAACCCTCCTGGCAAAAAACATGGAAGACTTTCGATATCTAG
CCATTATTCGTTTGCTTATGTGCTGGATTAAGTCATATAGATCTATTTTGCAGTACACTC
ACAGACACAGGAAGTTTTGCACTTCATTCGCCCTTGTGCTGAACGACTTGATAAATAGTC
CACTGAATTTGTTTCAGGAAATATATATAGCCACAGGCCGAAAAGAAGCTATCTTTTAGAG
AAGATATTATTTTCAGGGAATTTCTTGCAATTAACCTTTGCACTAACAGATTTTAATGACG
ATTATGTGATGATTCTCCCGACATGATTAATAATATAATTTGGATGCCCTACATTGACTA
AAGTGCTTTCTCCAAAAGAAGAATGTGTTCTGCGAATTAGATCAATAATATTTTCTGGCA
TGAAATTTTATAGAGAAAAATGACACCGCGTCATATGGAATGCCAGCAAATATAAGTTTG
ATTTAATAAGCCCAAATATTAATAATAAACGCCAAATAGCATTATCGGAAATTTCTCTCA
AAATAAATGTAAAAACACAACAGGAAAGAGTAGTCTCTTCGAGAAAAGTTGAGGCCAAAA
GAGATGAACAACAGCGCAAAAGAGCCGGGAAAAATAGCTGTGACAGAACTGGAAAAACAAT
TTGCAAAATGTCCGGAGAACAAAAAATTTGCTCCGCTCCAGAAAAAGATGGCGTTTTCTT
CTGAGTTGGTAAACATGCTGCTTCACGAGGGAGAAAACTATCACTGGCCCACTATCCT
CTGATTTTCTCTCATATCCAGACGAAGCAATTGATGCTGATGAGGACATCACCGTCCAAG
TGCCAGATACTCCTACTTGA

YLR233C, 699 aa (SEQ ID NO 186)
MDNEEVNEECMRLFFKNARAHLDKHLTSRLTCDENAYITFRCLDGIHRKSTRFLEELL
KQENMYHNNYERINDSVIPLVLKLLWLQIHEPTLQWFEHWFHDIMRLSNRRKFRVFRIF
QKKMIQFFKITHRYYYDIIHLCAKYDMNSVISNALFAKLNLMOYTDGLSTHEKIILNTS
NPLTFSIVISLQRCVINLGSTHFYKTLNKPSPKPSVEGFESIRYLNIAASLYLPAVGD
TYFQRAKIYLTGKFSLYFFELVRGALVRIPSKCALNNLKDFILTPDFPERRLMKKLAI
LVSKDLKGEKSFFEGQIVLQFLSIVEHTLVPSQSWNASRASNCWLLKEHLQMAALKYHSGN
INVILENLAATMGSFDFLMTTRKSKEQKNKLKYADLSERQVFFLDLSFDFIANIIDVVIK
PSWQKNMEDFRYLAIIRLLMCWIKSYRSILQYTHRHRKFCTSFALLLNDLINSPLNCSGN
IYSHRPKRSYLFREDIIFREFSCINFALTDFNDDYVYDSPDMINNIIGCPTLTKVLSPKE

FIG. 1 - 65

ECVLRIRSIIFSGMKFLEKNDTGVIWNASKYKFDLISPNIKIKRQIALSEISSKINVKTQ
QERVVSSRKVEAKRDEQQRKRAGKIAVTELEKQFANVRRTKKLSPLPEKDGVSSELVKHA
ASRGRKTIITGPLSSDFLSYPDEAIDADEDITVQVPDTP

YLR234W, 2471 bp, CDS: 501-2471 (SEQ ID NO 187)

AATGGTATCACGGAATCATTTATGCGTTCGTAATTGTTATTATGGTACATATTTTCTTGT
TTCAAAAGTAGCTCTTCGAGAAACCTAGTAGATTGCGATGTATTCATCCAGGAAGCAT
CTGAACGTGATATATGCATTTTCATCGCATGTCAACCTTGATGTTAGATGTTTATCCAGA
TGCGCACGAGCGTTCTTGAAAAATAATCTCATACATTCTTCGTTAACTTCTTCATTATCC
ATTATCTATGGTGGCATGTGTCAATTAATGGAATATACTTTTCCCCTGATAAGTTTGTG
AAAAACGGTTCGGATCATACAGGCATGTTAACATTTCCATTATCCTTTTTGACATTGGATA
ATGGCGTGAACGCGAAAATCACATTGATAAAAAAAGCAGTTTGGCGAATTAGTAAGTGT
CAATAAAGAGGGCATCGCTTTTGAAAGCACCTTCGTCTGTGCGCTCGCTTCAGCTACGTA
AAGGTGTATTATAGACAATAATGAAAGTGCTATGTGTGCGAGAGAAAAATTCATAGCGA
AGGCAGTTTTCAGATCCTAGGAGGAGGCAGATCAACTTCAAGGGATTCCGGCTACATGT
ATGTAAAGAACTATGATTTTCATGTTTAGTGGGTTCCTGTTGCGAGAAATGGGGCTAACT
GCGAAGTTACCATGACTAGTGTGTCAGGGCACCTAACAGGCATTGATTTAGCCATGATT
CGCATGGGTGGGAAAAATGCGCCATCCAAGAGTTATTTGATGCGCCACTGAACGAGATTA
TGAATAACAACCAAAAAAAGATAGCAAGCAACATCAAGCGAGAGCGAGGAATGCAGACT
ATCTGATGATATGGACAGATTGCGACCGGGAAGGAGAGTACATCGGTTGGGAGATATGGC
AGGAGGCCAAGAGAGGCAACAGGCTCATACAAATGATCAAGTATACCGGGCAGTCTTTT
CGCATCTCGAAAGACAACACATATTAAATGCAGCACGAAACCCAAGTCGATTGGATATGA
AGAGTGTGCACGCTGTAGGCACGCGGATTGAAATCGATCTTCGAGCAGGTGTTACATTCA
CCGACTCTTAACAGAAACGCTACGAAATAAACTGAGAAACCAAGCCACCATGACCAAGG
ATGGTGCATAAACACCGCGGTGGTAACAAGAACGACTCAAAAGTCGTATCGTATGGTACAT
GCCAGTTTCCAACGCTCGGCTTTGTAGTAGACAGGTTTGAAAGAATACGAAATTTTGTTC
CCGAAGAGTTCTGGTATATCCAATTGGTAGTCGAAAACAAAGACAACGGCGGAACAACAA
CGTTCAGTGGGACAGGGGCCACTTGTTCGACCGGCTGAGCGTGTAAACGTTTACGAGA
CATGCATCGAAACCGCCGGAATGTTGCTCAAGTAGTAGACTTGAAATCAAAGCCAACAA
CGAAATACAGACCTTTACCTCTGACCACAGTGGAGCTACAAAAAACTGCGCCCGGTACC
TGCGTCTGAACGCCAAACAATCACTAGACGCGAGCAGAAAAAGCTATACCAAAGGGGTTCA
TATCGTATCCAAGAACAGAGACTGATACTTTCCACACGCAATGGACCTAAAATCCTTGG
TCGAAAAGCAAGCTCAATTGGACCAACTCGCTGCAGGCGGCAGAACCGCTGGGCATCGT
ACGCGGCATCGCTGCTCCAACCCGAAAACACAAGTAACAATAACAAGTTCAAGTTTCCAC
GAAGCGGCTCCCATGACGACAAAGCGCATCCACCAATCCACCCCATCGTAAGTCTGGGGC
CTGAAGCAAATGTTTCGCCAGTGGAAAGAAGAGTATACGAGTACGTGGCCAGGCACTTTT
TGGCATGCTGCTCAGAGGACGCCAAGGGCCAATCGATGACCTTGTGTTGGACTGGGCCG
TTGAACGCTTTCTCAGCTTCAGGTCTCGTAGTCTAGAGAGAAATTTCTCGATGTTTACC
CTTGGGCCCCGATGGGAAACCACCAAGCAGTTACCGCGGCTTGAAATGAATGCCCTCGTAG
ACATCGCGAAGGCCGAAATGAAGGCGGGCACTACGGCGCCGCCAAGCCGATGACTGAGA
GTGAACTCATTCTCCTCATGGATACAAACGGCATTGGCACAGACGCCACCATTGCGGAGC
ACATAGACAAGATCCAAGTACGTAATTACGTTAGGAGCGAGAAAGTAGGCAAGGAAACCT
ACTTACAACCCACGACCTTGGGTGTCTCACTAGTGCACGGCTTCGAGGCCATCGGCCTCG
AAGACTCCTTTGCAAAGCCCTTCCAGCGCAGAGAAATGGAGCAAGACCTCAAGAAAATCT
GCCAAGGTCATGCCTCCAAGACTGATGTTGTAAAGGACATAGTCGAGAAGTATAGGAAGT
ACTGGCACAAAGACGAATGCCTGCAAGAATACTCTCTTGCAAGTTTATGACCGTGTCAAGG
CATCCATGTAA

YLR234W, 656 aa (SEQ ID NO 188)

MKVLCAVEKNSIAKAVSQILGGGRSTSRDSGYMYVKNYDFMFSGFPFARNGANCEVTMTS
VAGHLTGDIFSHDSHWGKCAIQELFDAPLNEIMNNNQKKIASNIKREARNADYLMIWTD
CDREGEYIGWEIWQEAQRGNRLIQNDQVYRAVFSHLERQHILNAARNPSRLDMKSVHAVG
TRIEIDLRAVTFTRLLTETLRNKLNRNQATMTKDGAKHRGNGKNDSQVVSYGTCQFPTLG
FVVDREFIRNFVPEEFWYIQLVVENKDNNGTTTFQWDRGHLFDRLSVLTFYETCIETAG
NVAQVVDLKSPTTKYRPLPLTTVELQKNCARYLRNLNAKQSLDAAEKLYQKGFISYPRTE
TDTFPHAMDLSLVEKQAQLDQLAAGGRTAWASYAASLLQPENTSNNNKFKFPRSGSHDD
KAHPPIHPIVSLGPEANVSPVERRVYEVVARHFLACSEDAKGQSMTLVLDWAVERFSAS

FIG. 1 - 66

GLVVLERNFLDVPYWARWETTKQLPRLEMNALVDIAKAEMKAGTTAPPKPMTESELILLM
DTNGIGTDAITAEHIDKIQVRNYRSEKVGKETYLQPTTLGVSLVHGFEAIGLEDSFAKP
FORREMEODLKKICEGHA SKTDVVKDIVEKYRKYWHKTNACKNTLLOVYDRVKASM

YLR238W, 1937 bp, CDS: 501-1937 (SEQ ID NO 189)

TTTCGGTTACACCTTAATATTAATAAACAGCTCTTTCTTAATAATAACATATACACTAGAT
ATATAATACCAAATAAATTAAAAAAGAAAAACAAAAATAACGTAGCTTTGTTACAG
TCGTAAAAAAGAACAATAAACCAATCTTATTGCCAGCGTCTAACTAGTCCTATTATAT
TCCAATATATTAAAGGGTAAGGACTACTATTATTCGCCCTGAATTGAAATCTTTTAGAAA
GCACCTGTTCTCTCTCTGGTGTCTTTTTTCTCATCTATTATCTAATTTCTTCAACCTT
CGTTATTTGTTGTTATTCCGTAATCTGGTGTCTCAACTTTTGAAATTTCACTTGTTCAC
ATAACGGAACATAATTAATAATTGTTCTTGAAGAGCACAAGCACTACGTGAACAAAA
TTAAGGCAAGAGTGACAAAGTAAACCTCACAAGGAGCCTGTCGTTGGTTATATTGGAAGC
TATAGATATAATCGAATCCAATGACTGGTCTGGACCTGAAATAAATAAGGAGGAGCACC
CCAGTTCTCCGGGCAAGAAACAGATAACATATAATAGTATACCCAAGAATGCAATCTAA
TTGATGGATCTACGAATTCATCGAAGAGGCCAATTGAAAAGTATGACAAGAGAATAGCCG
ACCCAACAAAAAGCTATTTTCCACATAGCATATCAAGAACACCAGGAGAAAAATATACCT
ACATTCTAGTCTTCACATCAATAATTGGAACCTTTTGAGAGCAAAACATGTGGTGATACCT
TTAAACCTAGATGGTTTGAAATTGGGAAGGCCTGTTGCTTAATAGTAATGACAGCTCCAGTT
CATCGCTCAGGGGCGGTAAAAGAGTGGATTACACACACTTTTCCCAAGTAAGGTCCGATA
ATGGTAATTTTCGATTCAAGAGTACTCTCCAGGAATCATGCATTGTTAAGTTGCGACCCGC
TCACGGGTAAGGTATATATACGAGACTTAAATCCAGTAATGGTACGTTTATTAACGGTC
AAAGAATTGGCTCAAATGACGTAGAAATCAAAGTTGGCGATGTGATAGACTTGGGAACAG
ATATAGATACGAAAAATTGAGCATCGAAAAATAAGTGCCACAGTTGAAGAACAATTTGTAC
AACCTTTATTAGAATCCCGATTTTTGAAAAATGAAGATAGTGATTGCCATACAAATTA
CAGAAAAAGAGGAGGCTGCTGCCATAAAGTCAAGATATGTTGGTGATTCCAACAACCTAG
AATTGGAAGAAGTTATCCTGGGCTCTGATACAGAAATACTGAGTGGAATTTTTATTAATA
ATTGTATTGGTACGAGCCCGACTTTATCTAATATCATCAAAACCCCTGGCAATGGAAATTC
CATTTTCCAAATGCGATAAATTTTAAATTACAGTCGATGGAGAATTTCTTAATTAATTATA
CGACACATCTAGAATACACGAACAAACTTTAGTGGAAAAAAATGATCAGCAACTGGTAA
AGCTGCAAAATGGATTAGAAGGAACTGTGCGGAAATACGAAAAGATTATCGAACAAA
ACAGAAATCAAGTAAAAACAGTTGGAAGGGACCATATGTTTTTCAAAAAGTCATTTGAAG
TGAAGAAAAGAAGAAATAATGAAAAGCAAAAAAGCATGGAAAGGGAATAGAAGACTTGA
AACTAGGTTAGAAGTGAACGATATAAGAATTCACAAATGATGAAGAAGAACAAACAGA
AAGAACAAGAACTCTCAACTGCATCTAAAAAAGAGCTACCGAACATGACACTAGAGGCG
TCCCGGGCATGAATCCTAAGGGTACTGACAAATTTAGCATCAAGAACACGCTATGTAATC
ATTTACACATTAATCAATTTGGAACATTTTCCATCGGGATTATAGCTATTGTCTTCAAGA
TCCTTTTCCCCCACTAG

YLR238W, 478 aa (SEO ID NO 190)

MTGPGPEINKEEHPSSSPGKKQITYNSIPKANLIDGSTNSSKRPIEKYDKRIADPTKSYF
PHSISRTPRRKYTYILVLTSLNGTFESKHVVI PFKPDGLKLRPVANSNSSSSSSSLRGGK
RVDSHTFSQVRSDNGNFDSRVL SRNHALLSCDPLTGKVYIRD LKSSNGTFINQGRIGSND
VEIKVGDVIDLGTDIDTKIEHRKISATVEELFVQPLLESPIFENEDSDDCHTITEKEEAA
AITSHIYGDSNNLEEEVILGSDTEILSGIFINNCIGTSPTLSNIIKTLAMEIPFSKCDN
FKLQSMENFLINYTHLEYTNKLLVEKNDOQLVKLQGLRRLKSGYKEKIEQNRNQVKQ
LERDHMFFFKSKFEVKKRNRNEKQKSMEREIEDLQTRLEVERYKNSQMMKKNKQKEQLST
ASKKKKTEHDTRGVPGMNPKGTDKFSIKNTL CNHETLLTFTGISIGIIAIVEKILSPN

YLR241W, 2849 bp, CDS: 501-2849 (SEO ID NO 191)

CGAACATACCTGATATCAGAATAGATCCCAATGGTGCTATATTACGTGTAAGAGAGAGAT
TTAATTTGAATATGTCCGAAGAAGATGCCACAGTGCATTTTCAGAATCTAATCAATGATA
GTGTAAATGCTTTGCTGCCATATCGTGATTGATCATTTACATAATCTGGCACAATACTGGC
GGACCTGATTGGTTGATAATTGGTGCTTCAAAATTTAAATTTTCGTCACTCTAATTFATACT
TAACATAATAAATGGTACCTTCAATATATCTTCTTAGTAAAAAGTAGCATGATTTTGTGTT
AATTTGCACCTTTTATTATTTAAAAATAAAAAACACAGTTAATTTTTTCATGATCTTGCAA
GACACGCCTCCCCCTAATGTGGCGATATAAACAATTTGTAATCAGAAAAAATCAACATT
TAACATAATGGCGGGCAGCAAGGCTAAACAAAAAAGAATTTAGCATTGAATGCCTTTTTTGG

FIG. 1 - 67

GTACAATAGAACAGTACTGAATGACATCATATATCGAAAGGCTCAAGTCGGCAGCATCGT
ATCTTGATACAGTTCAGATGAGCATCATGATTTTCAGAAAACCCACCGCCAAGGTTGTAA
CGACGCAACTGACTATTGCTACTTCACTAGGTATTTTTGCTTTGCTTTCTCAATTC
TACTAAAAAAGTGGCCTAGATTATACGCAAGCAGACGATATAAAGATGACGGGAACCTTC
GCTTACCGTCTCTGGAATCAGTCAAGTTTATTCGGCTGGTTAACAGTGTTGTATAAGATAC
GGGACGAACAGATTCTGGAATATGCAGGTTTAGATGCGTATGTGTTTTTGTAGTTTTTCA
AAATGTGCATCAAATTACTTTCTATTTTTTGTCTTCTCTGTGTGCGTTATATCTCCAG
TAAGATATCATTTTTACTTGAAAAATTGATGACGGCAACGATGATGATGACAGTGAAAGTT
CTTTAATACATCTGGTAAAAAGAATTGTGGAGGGAAGTGGCGATGGTGACAATCATTCAG
CTCCCGAACGTACAAATGTGTACCTCTGGATGTATGTTCTCTTCACATATTTCTTCACCT
TCATAGCAATTAAAAATGGCAGTTGCGGAAACAAAGCACGTGCTAAGTACTAGGCAAGCTT
ATCTTGGGAAGCAAAATACGATTACTGATAGAACGATAAGGCTCTCAGGCATCCCGATAG
AGCTTCGTGATTTCGGAAGCCTTAAAGACCAGAATTGAACAATTAAAAATCGGCACCGTTT
CATCAATCACTATTTGTGAGAGTGGGGTCTTTGAACAAGCTATTTTCATTGTGCGGAAGA
AAATACTCAAAAACCTGGAATTAAAAATATTCAGAATGTCCAAGGGAGCTCCGTACTCGAC
AACCATATTCGGGAGAACTATCATTTATTGGGAAACGAGCAATCAGGCGCAGTTACACATG
GAGAAAATGTTCCATCAAGCAATAATAATGACGAGGATACTATACTATATTCTCAAATTT
CTCTTGGAGAGAGACCAAAAATGAAAATTGGATATCGTGGTATCTTTGGGAAGGAAGTAG
ATGCCATAGAGTACCTGGAGCAGCAATTAAAAATTTATTGATGCTGAAATTTATTGAAGCGA
GGAAACAACACTACTCCGCAACACCTACGGCATTTCGTTACGATGGATTCTGTTGCTAATG
CGCAAATGGCAGCTCAGGCGGTATTAGATCCTAGAGTACATTACTTCATAACCAGATTGG
CTCTGTCACCTCACGATATCAAGTGGGATCATGTTTGTCTTTCTAGAAAGGACCGGTTAA
CAAAAGTTTATTCTACTACCGTATTTATAGGCCTTTCAAGTTTGTTTTTAGTCATTCTCTG
TATCATACTTAGCCACATTGCTAAATTTGAAAACACTTTCGAAATTCCTGGCCAAGCGTAG
GGCAGCTACTAAAAGATCACCAGTGGGCCGCTAACATTGTAACGGGGCTATTACCAACCT
ATCTCTTACAGATTGCTTAACTTTTGAATCCCTTATTTTTTACGAGTATTTGACTTCTTATC
AAGGATTGGTATCATAACAGCGAAGAGGAAATCTCACTTGTTCAAAAAATTTCTTTTATA
TTTTTGTCAACCTTTTCTTAGTTTTTACATTGGCAGGTACAGCATCTAATTACTGGGCGT
ACCTCAGCGATACCACCAAAAATTGCTTATCAACTTGCTACATCTGTGAAGGAGTTCTCCT
TATTCTATGTCGATTTGATTATATTGCAAGGTATTGGTATGTTCCCGTTTAAAGTTGTTAT
TAGTTGGTAGTTTGATCGGCTTTCTCTAGTGAAATCAAGGCTAAGACACCTAGGCAAC
GGAATGAACCTTACAATCCACCGATATTTAATTTGGACTACAATTACCACGCAATTC
TGATTTTGATTATAACGTTGATCTACAGTGTAAATGAGCACGAAAATTTTGACTTCAGGGC
TGGCGTACTTTATTATTGGGTTTTACGTCTATAAATATCAATTGATTTTTGCCACAGATC
ATTTGCCCCATTCTACAGGAAAAGTATGGCCATTAATTTTTAGAGAATCATCGTTGGAT
TGCTATTGTTTCAATTAACAATGACAGGAACACTGGCAGGATTCGAAGGAGGATGGGTTT
TGTCATCTTGCCCTTTTCCCGCTTCCAGTAGTGACATTATGTTTCTTATATGATTTTCGAGA
AGAACTATTTGCCGTTGTCAAAATATATCGCATTGAGTTCAATTTCGCGAGTACGAAAGAG
ACAATTCTACGGTGAATTCTGCCAATGAGGAAGTCTGATGCATACCCCTACGCTGTGA
GTGAATTAGAGGTTCCGATGTTGGATTGA

YLR241W, 782 aa (SEQ ID NO 192)

MTSYIERLKSAASYLDTVPDEHHDFRKPTAKVVTTQLTIATSLGIFALLSFSILLKKWPR
LYASRRYKDDGNLRLPSWNQSSLFGLWTLVLYKIRDEQILEYAGLDAYVFLSFFKMCIKLL
SIFCFFSVCVISPVRYHFTGKIDDDNDSESLIHLVKRIVEGSGDGNHSAPERTNV
YLWYVLFYFFTFIAIKMAVAETKHVVSTROAYLGKQNTITDRTIRLSGIPIELRDSEA
LKTRIEQLKIGTVSSITICREWGPLNKLPHCRKKILKNLELKYSECPRCLRTRQPYSENY
HLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPKMKIGYRGIFGKEVDAIEYLE
QQLKFIDAEIIEARKQHYSATPTAFVTMDSVANAQMAAQAVLDPRVHYFITRLAPAPHDI
KWDHVCLSRKDRLTKVYSTTVFIGLSSFLVPIVSYLATLLNLKTLKFWPSVQGQLKDH
QWAANIVTGLPTYLFTLLNFGIPYFYEYLTSYQGLVSYSEEEISLVSKNFFYIFVNFLF
VFTLAGTASNYWAYLSDTTKIAYQLATSVKEFSLFYVDLIILQGIGMFPFKLLLVGSLIG
FPLVKIKAKTPRQRNELYNPPIFNFGQLPQPILILIIITLIYSVMSTKILTSLGLAYFIIG
FYVYKYLIFATDHLPHSTGKVWPLIFRRIIVGLLLFQLTMTGTLAGFEGGWLVSSCLFP
LPVVTLCFLYDFEKNYLPISKYIALSSIREYERDNSTVNSANEEESYAYPYAVSELEGPM
LD

FIG. 1 - 68

YLR321C, 1781 bp, CDS: 501-1781 (SEQ ID NO 193)
TTCAAGTGCACCTCTTTGTAAGGAAGATTACAAGTCTCCAGTGGTCACAACTGTGGCCAT
TATTTTTGTGGATCGTGTTTTGCCAAAGATATGAAAAAGGGCACCAAATGCTTTATATGC
CACAAGGAGACCCACGGCAGTGCAAAAGTAGCATCTGACTTACAGAAGATGCTAAATAAA
AGGAAAAGTTGATGGAGAATGCCATATCACCCCAAAATTACACGCACCCGATGCTAATG
TACAGGAATTATAGAGCACATGACCCATAGATTTATCGAGCATTGTTGCAATTTTCGAAAG
ACTCTTTTACATAATAAAGTATGTAACTATATAGATAGAAGATGTCCCGTGTCTTTTTTG
TCTACTAAATGATGATCTGCTCATTTAAAGTCGCCGCGACTACTTTGACAAAAA
ACTTAGAAAATACGACAAAATAGAGATTATTGAATGAAGTACATTGAAAAAAGAAAGA
AAGGCACATAGCAGCACACAATGTTCGACCAAAACCAGCTTATCCACAAGCTTATATTT
CTAATTTTACAGATTGACAAACGAAGTATGATGGTATCCCCATCTTTACAATGGCTC
AACAAACAAGGCAGCATAAAAGGGCTAAAGTGGTCAACTATGCGGAATATGACAACGATC
TCTTTGATGAATTCAATATGAACGGTTCTAATTTCAACAATGCTGATACACACTATAAAG
ATAATGCAGTGTCTCATGAAAATACTCCGGCACTTACAAATGGTGTACCATGGACGGTT
CCGAATACAATGTCTAGAGAACATGAATGGAGCTGATAGTATTATCTCTAACAACAAAT
ACGATGCGGGTTCAAACATGGTTGTGGAATCTTTATCCGGTTTGAATAGCAATAACAACG
CCAGCATGGTCCGAGCAACAAAGCGCAGGCACAGGATATTGGAAACGCCGTTCTACCGG
ATCTGCAAGACCAACACCACAACCCCTTCAACATATTGAGATACCCCTAAAAATAAGAGATA
CTTTCATTAACGGAAGTGGTGTCTCCATATAGACTCAACACTGATCAAGAAACGAAGG
CAAACGCCAATTCTGGAGAGGCAATCATGATACCAATTACTTTGGATATAGAACATATGG
GTCATACCATAAAAGACCAGTTTCTCTGGAACACAATGACGACTCCATATCTCCGGAGG
AATTTGCCTCTATATACTGTAAAGATCTTGATATGACTTCCGCTACCTTACAACTCAA
TTGCGAATATAATAAAGAGCAGTTGAAAGACCTCGAAAATATTGCAGCCACTGAGATAA
TGTCTGACCTCCACGTGATAATCAACCTAACCTGCAACTTACAAGACAGATTTTTTGAAG
ATAACTTCCAGTGGAACTTGAACGACAAATCACTTACTCCAGAAAGATTTGCTACATCCA
TTGTACAGGACCTTGGCTTAACAAGAGAGTTCATCCCCTTAATATCTCAATCGCTTCATG
AACTATCTTGAAGATAAAGAAGGACTGGGTAGATGGCCACTTGATTGAGGACCATGTCC
CAAACGATGCCGCTTTGGGTACTTATCTGGTATAAGGCTGGATATTGATGAACGGGCT
CCAATTGGTGCCCAAGGGTGGAAATATTAACAAAAGAAGAAATACAAAAGAGAGAAATTG
AAAAAGAAAGAACTTAAGAAGATTGAAAAGAGAACTGATAGATTATCTAGAAGGGGCA
GGAGAAGATTAGATGACTTAGAAACCACAATGAGAATGTAG

YLR321C, 426 aa (SEQ ID NO 194)
MSHQNLIPQAYISNHFHRLTNEDDGIPIFTMAQQTRQHKRAKVVNVAEYDNDLFDEFNM
NGSNFNNADTHYKDNAVSHENTPALTNVMTDGSSEYNVLENMNGADSIISNNKYDAGSNM
VVESLGLNSNNNASNGPSNKAQAQDIPDLQDQHHPFNILRYPKIRDTFINGKV
VSPYRLNTDQETKANANSGEAIMIPITLDIEHMGHTIKDQFLWNYNDDSIISPEEFASIYC
KDLDMTSATLQTOQIANIIEQLKDLENIAATEIMSDLHVIINLTCNLQDRFEDNFQWNL
NDKSLTPERFATSIVQDLGLTREFIPLISQSLHETILKIKKDWVDGHLIQDHPNDAAFG
YLSGIRLDIDELGSNWCPRVEILTKEIQKREIEKERNLRLKRETDRLSRRGRRLDDL
ETTMRM

YLR322W, 815 bp, CDS: 501-815 (SEQ ID NO 195)
GTCATATCAAGATCTTTACAGTATATAGAGGCAAATTCCTCCGGAGATATGGAGTCGTCA
TTGTAGTTCCAGAGAACTGGTCTTTTATGGTATGACCCATATGTTCTATATCCAAAGTA
ATTGGTATCATGATTGCCTCTCCAGAAATGGCGTTTGCCTTCGTTTCTTGATCAGTGTG
AGTCTATATGGAGACACCACTTTCCGTTAATGAAAGTATCTCTTATTTTAGGGTATCTC
AATATGTTGAAGGGGTTGTGGTCTTGGTCTTGCAGATCCGGTAGAACGGCGTTTCCAATA
TCCTGTGCCTGCGCTTTGTTGCTCGGACCATGCTGGCGTTGTTATTGCTATTCAAACCG
GATAAAGATTCCACAACCATGTTTGAACCCGCATCGTATTTGTTGTTAGAGATAATACTA
TCAGCTCCATTCTATGTTCTCTAGGACATTGTATTTCGGAACCGTCCATGGTAACACCATTT
GTAAGTGCCGGAGTATTTTCATGAGACACTGCATTATCTTTATAGTGTGTATCAGCATTG
TTGAAATTAGAACCGTTCATATTGAATTCATCAAAGAGATCGTTGTCATATTCCGCATAG
TTGACCACTTTAGCCCTTTTATGCTGCCTTGTGTTGTTGAGCCATTGTAAAGATGGGGATA
CCATCATCTTCGTTTGTCAATCTGTTATGAAAGTTAGAAATATAAGCTTGTGGAATAAGC
TGGTTTTGGTGCACATTGTGTGCTGCTATGTGCCTTTCTTCTTTTCTTTTCAATGTAC
TTCATTCAATAATCTCTATTGTGCTATTTTCTAA

FIG. 1 - 69

YLR322W, 104 aa (SEQ ID NO 196)
MRHCIIIFIVCISIVEIIRTVHIEFIKEIVVIFRIVDHFSPFMLPCLLSHCKDGDIIIFVCQ
SVMKVRNISLWNKLVLRHCVLLCAFLLSFFNVLHSIISICRIF

YLR325C, 737 bp, CDS: 501-737 (SEQ ID NO 197)
CCACATGTCACAACACTTTGTGAAGTTGCAATGCGTGATTAGTATTATAAACATCATA
GCCTTGCCAAATAAACTCGCTTCCCAGAAAAGACGCCAAATTAAGTCCGCTGTTATGTG
ACAAAACAGGGCATCTCACATATTCGCGTACTGGTGTCTTTTAGCTCATTCGGATATTA
TTCCAAGACGGAATTTTCATCTAGAGAAAATGCATCCGTGCATTTTCATAAACCCACACA
ATTAAAAATGCCTTGCGAAAAGGAGGACTCGTCCGTGCAACTGTTGAAAAAATAGACGGA
GCATCATACGTTTCGAGTGGAATAATTATGGAGAGTTTCCAAGCTCTATGGCATGTAGAGT
CGTGATTGCTGCTGTACGCTTTTGCACAATATTGAATCTTCAATCTAAAGAATTAAATTT
TCTAATTTCAATGTAGAAATATTTCAACTGTTAGTTTTTTATTTTCAGGTTGAATATAGTA
CGACAAAATATCAAGGAAAAATGGCTAGAGAAAATCACCGACATCAAACAATTTTGGAAAT
TGACCAGAAGAGCTGACGTTAAGACCGCCACTGTTAAGATTAACAAAAAATTGAACAAGG
CCGGTAAGCCATTTCAGACAAACCAAGTTCAAGGTTAGAGGCTCTTCTTCTTTGTACACTT
TGGTTATCAACGATGCTGGTAAGGCTAAGAAATTGATCCAATCTTTGCCACCAACTTTGA
AGGTTAACAGATTATAA

YLR325C, 78 aa (SEQ ID NO 198)
MAREITDIKQFLELTRRADVKATVVKINKKLNKAGKPFRTKFKVRGSSSLYTLVINDAG
KAKKLIQSLPPTLKVNRL

YLR344W, 1331 bp, exon1: 501-519, intron1: 520-966, exon2:
967-1331 (SEQ ID NO 199)
TAAGGGCTGTCAATTTTTCATTTCCCTCAAAGTTAATGCGCAAGAGTTAGGATGATCTTG
ATTATTAGTTATTTGTTTGTTCATCAATTATGCCGACGTCCATGAATGCTATTGAAGTA
TCGATTACTTATGCTATTCTATTGTATTTTGAGCCGGCGCTAGTAAACAAGACAGCATAC
CTTTCCAACATCCGTACATATTGATTATTGTATCTATGATTTTCATGTAATGTATGGGTT
AACTAATCCTTTCTCTTCTTTTCTTTTCTGAAAATCAGTAGCTAGAGGAACCTGTTT
GTGAAAGATATGGAATATTCCGTCTAGGGAAGAGCCGAGAGCTGAGAGCAGTATCCATCG
GATGGAATCTTGCCCTGGATGCGTAACGACGACAGCTTGTCTAGAAGGCGAAGTACAAGAT
ACTAAGAAGACTATAACAACAGAAGACAATTTTGTAGTGCGATTCTATATTATTGACGTA
ACCAACAAAAAGTATCAGAATGGCTAAACAATCATTAGGTATGTGCACAAATGCTAAAT
CACTGAAACCTGTAGAGCTGGAATTGAAAATATAGTTTGTACCTTTTGCCCTGAGGGCAG
AATGACTCAATGTTATCTTAATTCGATTAGAAAAAGAAGGTGCGTTATCCAAGGTTGAAA
CTTGTAAGTATTTAGGTGATGTCTCATAACTGCAACCACTGGAAAATGACGCAAATATC
AAAATAATAGGGAGATAAAGTCTCACGACATGAAAAAATCATAGAATTATTGTTCAATTT
ATCTAGCCGTATCTTACCTTATGGAAAAAGTGTGAATATGTTTTTCTAAATCGAGCTTCC
CGGAAATTACACTATATTATGCATCCGTGATACATCTGAAATTCAATACTTTCTCCAAGG
TCCTGCTTACTAAGAGGGTAAGATTTGTTGAAACTCGAAATACTAACATTATTTTCATTA
TTTTAGACGTTTCTCCGACAGAAGAAAGGCTAGAAAGGCTTATTTACCGCCCCATCCT
CCCAACGTCGTGTTTGTCTATCTGCTCCATTATCTAAGGAGTTGAGAGCTCAATACGGTA
TCAAGGCCTTGCCAATCAGAAGAGATGATGAAGTTTGGTTGTTCTGTTGTTCCAAGAAGG
GTCAAGAAGGTAAGATTTTCATCTGTTTACAGATTGAAATTTGCCGTTCAAGTTGACAAGG
TTACCAAGGAAAAGGTCAACGGTGCTTCCGTTCCAATTAACCTGCACCCATCCAAGCTTG
TCATTACTAAATTACATTTGGACAAGGACAGAAAAGCTTTGATCCAAGAAAGGGCGGTA
AGTTGGAATAA

YLR344W, 127 aa (SEQ ID NO 200)
MAQQLDVSSDRRKARKAYFTAPSSQRRVLLSAPLSKELRAQYGIKALPIRRDDEVLLVVR
GSKKGQEGKISSVYRLKFAVQVDKVTKEKVNASVPINLHPSKLVITKLHLDKRKALIQ
RKGGKLE

YLR367W, 1376 bp, exon1: 501-633 intron1: 634-1116, exon2:
1117-1376 (SEQ ID NO 201)
ACTTTTGTCTGCTGCTGGTCGTTTGTCTTTTCGTTTAAATTTGCGCTAGACAAGTAAAC
AGGGATTGCTTAAGAATCAAAGTAGCTTAACCTCTAAAGTATTATTTTCTCAGTTGTGGG

FIG. 1 - 70

CCCATGTGTTGGAGGGAAGGAATATATTGAAATGTAAATGTTCTTAAGTTCGGTTGAACT
TGGATATTGTTACAAGAGTTCTAGTCTTTGATACCATTTTACGCAATTACAACCGCATT
ATTTACCTTTTTCATCTTCAGTTTTACGGTTCAGTTTATTTCTGTTACGAAAGAACTATGGT
GATTCAAAGGCGAAGTGCCTAGGATTGTAACCTATATCTTTAGGATACTTACAATTTT
GTACTGTTTTCAAGACCACTGTAACCGATAATAAACCGGAGGACACATTTTAACCCACTA
TTTTTTTTCAGAAGATCAGATCCGAGAGCTCGAAGCATAAGTATAATACTAACGTTTTCAAA
ACATAGTAATTAGGTAAAAAATGACTCGCTCTTCCGTTTTAGCTGATGCTTTGAATGCCA
TTAATAACGCCGAAAAGACCGGTAAACGTCAGGTTCTATTGAGACCTTCTTCCAAGGTTA
TCATCAAGTTTTTACAAGTTATGCAAAAGCATGGTATGTTCCAACATTTTTTCAATATTT
TCACATGTGTTTTCAATTTCTGCTTATTTTTTAAATGTTACCACGAGGTTTGTCCAAGTTCA
ATGTTGCGCAACTCTAACGAAGAAATAATTATTGCCATTGTTTTTTACTCCGGGCTGATA
ACTAGATGGTGTGATCGGGCAGTATACTAATTTTACTTGACAAAGACTCGTAAAAGATG
TTCCTTTGTCTTAGTCCCATACTGTTTTTTTAAAGTGTCCGGGATATTTAATCCCATGTGGA
AATGCTTCTTACACGGTTATGGATTACACCTCATGTGTAGCTACTATATCCATTACCGTT
TACTTTTCCCTCAAATCTCACTCTTAAATTTTTCAATGGCAAATTTCTTCCGCACAACTT
AGACAACATTTTCTTGTTTTTTATGAAGTAAGCAAAAATTTTCAATCAACAACGCTCCAT
GAGATTCTTCAATACTAACATTTACTCCTTATTTAGGTTACATTGGCGAATTCGAATACA
TTGACGACCACAGATCTGGTAAGATTGTCGTCCAACCTGAACGGTAGATTGAACAAATGTG
GTGTTATTTCCCAAGATTTAACGTTAAGATTGGTGACATTGAAAAATGGACCGCCAACCT
TATTGCCAGCCAGACAATTTCGGTTACGTTATTTTGACTACTTCTGCGGGTATTATGGACC
ATGAGGAAGCTAGAAGAAAGCACGTTTCCGGTAAAATCTTGGGTTTTGTCTATTAA

YLR367W, 130 aa (SEQ ID NO 202)

MTRSSVLADALNAINNAEKTGKRQVLLRPSKVIKFLQVMQKHGYIGFEYIDDHRSKG
IVVQLNGRLNKCGLVISPRFNVKIGDIEKWTANLLPARQFGYVILTTAGIMDHEEARRKH
VSGKILGFVY

YLR393W, 1340 bp, CDS: 501-1340 (SEQ ID NO 203)

CCCTCAACCCGCATTTTGCTGAGAATTTTCACCAAGGCCCTAGGTGATATTAGATTCCAC
CTGACTAATTGCATTACAGCCGACCCAAGGCAATATCAGTTTAATAAAATATCATGTATC
TCACCTCTTCTTGGTATTAGTAAAGAGACGCCTGATCTTGTAAACAGTGGTGAAGATTGT
ACTAGAGCAGAATCAAGAATTTAAAAAGTGTAAAGGCAAGGCAGAGGCGATGTACATAAA
ACTTCGAAGTAAGAAATATTTAATAGTTCTCGCCACATCACTATGCAGCTATATAAAAAAC
TACTATAAACGTTTGTGTTTGTTCCTTACGCACAATATCCTTGCCCTAGAAATCGTTTTTGA
AATTTAAATTTTTATTACCATTATTTTGATTTCGCTTCAGAAAAATATGGAAGAGTGCAT
ATTTAAAAAGGACTATTTTACGATATAGTAAAGTCAGGTTATTTGTTTATTTGCGATAT
CAGAGTAACTTAACTAAGTATGCAGGGCACTTTTAAAGGTTTTTACCATCCCACGCTTA
CGCGGATGTCCTTCTTGGATAAATTCCTCAAGCCTATGATGGCAACGGCTTCCCCAAAGG
AATACCAGATCAAACAAGTGGTCAAGCCAATAGGCTTAACACAAGCACCAAGGAAAAGCA
CCAAATACTCCCAGGGGAAGTCTTTGAGGGATATGTTTGATTTCGGAAGACAAACCACA
GAGTTAAAGAGTTGGCCGTTGAATTCAGCAAAATCTGGACTTTATGACGTGCAAGTCTTCC
AAAAGACAAAGGGGAAATTGTTTATAGCTCCAGTTTCATATTGGAAGAAGATAAAGCTT
TGTTTTTTCCTCATTGATAGGAACGGCAATGGATGGTACGAAACAACAGAATATCGAGG
ATATGTTAAGGGGTAAAACCAGTATAGTGAGGTTATTTAGTACAGCATCTGGCGATAAGT
TGAGTAGTTTCATACTTCCAAGGAATCGTAGACGATAACAAAAAACTGACTACTTGACTG
AAGCTGATGCGGCTTTAAGTTTAAATGACAGTAACGTCCAAATCATCGAGGTCAATCTTG
TAGAAAACGCTGTGAAAAGTGCTCTAGTGAAAACGCTTGCTCGTTGGGCCAATCGCGTTC
CATCCTGGCGCCAGCCATTTTATTTTCAATGTTCTAGAGGCCAATGGCCATTTTCCGTCA
GGGAAGAGCTCTTTTGCATAATGTCTTTTCTGGATACGCTTTTCTTGTGGACCAGCAGT
TAAAAATTAGGTGGGCAGCTTGGCGGGAGGCTACTCCATCTGAAAAGGAAGCATTGTGGA
AGTTTGCCAAACGCTCTGTGA

YLR393W, 279 aa (SEQ ID NO 204)

MQGTFKRFYHPTLTRMSFLDKFLKPMMATASPKYQIKQLVKPIGLTQAPRKSTKYSQGN
SLRDMFDSEKTNHRVKELAVEFSKSGLYDVQVFQKTKGKLFAPVSYWKEDKALFFPHLI
GTAMDGTKQNIEDMLRGKTSIVRLFSTASGDKLSSSYFQGI VDDNKKTDYLT EADARLS
LNSDNVQIIEVNLVENAVKSALVKTLARWANRVPSWRQPFYFEC SRGQWPFSVREELFCN
NVFSGYVFLVDQQLKIRWAACGEATPSEKEALWKFAKRL

FIG. 1 - 71

YLR423C, 1754 bp, CDS: 501-1754 (SEQ ID NO 205)

TTCTATTGGTGTAGTTATACCAGAACCATCCTTCCCAAGGCCTTTTCCCAGCAACATATCC
CATACTCGAAAGTAACTTCGCACCAATACCATATGTCTTCGTTAATTTTGAGATCGTTGG
GGCATTGCCGCTACTAGTTTTCAAGGCATCATTAGTGTATGTCATGTCATTCATGCT
TGAATTAAATATCTTCTCATCGCTATAAATPATAGGAATCGATTCTTCTTTTGGAAAA
GAACTTTTTATCTGTGTGGAGTCCGAATCCTCCATGTTTTGGCGTACTGAAGGCTTAAG
TTCTTCGACCTCTCTCGGTTGTACTATTTTCGAAATTTTGGATTTTGTATTGTTTTGAC
ATAATGTAAATACTAGATGCGCGCTCTAAGGCCTCAGTATTAAAAATTGCAAGATATCCC
TAACTTGATAATTAATTTGAAAGTCGCATAACGTACGATAAATTCGATACTGCGAGGATAT
TATCAACGTATTTAACACCTATGAACGAAGCAGATGTTACAAAATTTGTTAATAATGCCA
GGAAACCGTGACCGATGCTCAACTTTTATGTTCAAGTGCTAATTTAAGGATTGTAGATA
TTAAGAAAAAATGTTCATCTTGGCAGTTGAGTATTTCAAACTCAATTTTCTAATAGTTG
GCTTGAGACAGCAAGGAAAGTTTCTTTACACTATTTTAAAGGAAGGCATTGGGACAAAGC
TAATCCAGAAACAATGGAATCAAGCTGTCTTAGTGGTCTTAGTTGATGAGATGAAGTACT
GGCAATATGAAATCACTTCTAAAGTACAAAGGTTGGATGGTATAGTAAATGAATTGAGCA
TATCAGAAAAAGATGATACCGATCCCTCTAAACTAGGAGATTACATCTCGAGAGACAACG
TTAACTTATTGAATGACAACTGAAAGAAGTGCCAGTAATTGAGCGTCAAAATGAAAAACA
TTAAGCTTCAATACGAAAAATATGGTCAGAAAAGTTAACAAGAAGTATGATACCAAGT
TGACGGACGTAACCTCAAAAATTCAAAAGTAAATTTGGTATAGATAAACCCTGATGGAACAA
ATGTTGCAGAGCAGTTTAGCAGGGAACCTAACGGACCTTGAAAAAGATTTAGCAGAGATAA
TGAATTCATTGACACAGCACTTTGATAAGACATTGCTGTTACAAGATAAAAAAATTGATA
ACGATGAACGTGAGGAGCTGTTTAAAGGTGGTACAAGGCGACGACAAAGAAGTATACAACA
TTTTCAAACTCTGCATGAGGTAATTGATGACGTGGACAAAACAATCTTAACTTGGGTC
AATTTTTGCAGGCAAAAATAAAGGAAAAGACAGAAGTACACAGCGAAGTTTCTGAAATAA
TAAACGATTTCATAGAAATTTGGAATATCTATTAATCTTTAAAGATATTTCCAATCTGA
TTGATAGCTTCAAAAATTCCTGTACACAAGATATTCAACAACATAAGGAACCTTGTGAAT
TTTATGATAATTTTGAAGAAAGCTACGGTAACTTAGTTCTAGAAGCAAAGAGGAGAAAGG
ATGTGGCAAACAGAATGAAAATATATTGAAAGATTGTGAAAAGCAGTTGCAGAATTTAG
ATGCTCAGGACCAGGAAGAACGTCAGAATTTTATAGCGGAAAATGGAACCTATCTTCTCTG
AGACAATCTGGCCCGGTAAAATTGACGATTTTCTTCCCTGTACACTTTAAATTACAACG
TGAAGAATCCTTAG

YLR423C, 417 aa (SEQ ID NO 206)

MNEADVTKFVNNARKTLTDAQLLCSSANLRIVDIKKKLSSWQLSISKLNFLIVGLRQOGK
FLYTILKEGIGTKLIQKQWNQAVLVVLVDEMKEYWQYEITSKVQRLDGI VNELSISEKDDT
DPSKLGDIYSRDNVNLNDKLKEVPVIERQIENIKLOYENMVRKVNKELIDTKLTDVTQK
FQSKFGIDNLMETNVAEQFSRELTDLEKDLAEIMNSLTQHFDKTL LLDQDKKIDNDEREEL
FKVYQGGDDKELYNIFKTLHEVIDDVDKTILNLGQFLQAKIKEKTELHSEVSEIINDFNRN
LEYLLIFKDISNLDISFKNSCTQDIQTTPKELCEFYDNFEESYGNLVLEAKRRKDVANRMK
TILKDCEKQLQNLDAQDQEERQNFIAENGTYLPETIWP GKIDDFSSLYTLNYNVKNP

YML026C, 1342 bp, exon1: 501-547, intron1: 548-948, exon2:
949-1342 (SEQ ID NO 207)

ATCTGTAAATAATAAGCCCATGAAATATCAATCTCACAATGAAAGAATTGTATAATTCAG
AATGATTTGACGTAAAAGCAAGTCTCATTCAAGAACTGTAAAATCCGTACACACTACTG
AATTTTACATCCATACATTTTTTTGAAATTTTCATGTTTTTTTGAAAAATTGGAAAAGGGC
TAAATTATCCGTCGGGGTGTCTCCTAGCTCGGCTCAACCTAGGCAAATGCGTTTACTGG
GGCCATCCAAGCTCATCCTTCCAGAGATTTCGCCCTTTCAGAGGCAAAGAAGTCTGCTCCGC
AGGCCTCTTGTTCCGGGAGGAGGAGAATTCTTGCGCGGAAACTGGTTGATGCCTGGGCTA
TGGTAATTCTGACACCTTTGCTATCCTAACTGGAAAAGGTCCTTAGTAATAACAATATCA
GGTACTTTTAACATTGTAAAGATATACTATTAGTGAAAAACCGATCTTACGAAAAGCCAA
TAGAGCAGAAAAGTGGTAAAGATGTCTTTAGTTGTACAAGAACAAGGTTCCTTCCAACACA
TTTTACGGTATGTTTACGAGTACAGTGCAGATATGTTGAGAGAGTTTACATTACATGG
GATAATAGCTTAATATTGCGATTGAAAATATGTGAGTGCCTCCGATGGAATAATAAACG
TCACGGGTACCAAATACGAGGCCGAATTAACCTCTACGCTACTATAAAAATTATCACTAG
ATTTTAAAGTAATACACAGTTTATTGGAAAATACAATATATGACTCAATGCGAATTTAAA
AATTTTCAGTCAATACAGCTTGACAAATTCATATTTATCGTCCCTCCATGTTTCGTACGCCA
TTCCAAAATGATGCGCCATGTTGAAAATTTCTCGAAGAACCCTAGCAGTGGTGTGAAATAA

FIG. 1 - 72

ATTACTAACAATAAGATGTACAATTTTTGTGCGCCCATTAACAATCAGTTTGTGTTGAACAC
CAATGTCGATGGTAACATTAATAATTGTTTACGCTTTGACCACTATTAAGGGTGTGGTTCG
TCGTTACTCCAACCTGGTCTGTAGAAGGCTGATGTTGATTGACACAAGAGAGCTGGTGA
ATTGACCCAAGAAGAATTGGAAAGAATTGTCCAAATCATGCAAAACCCAACCTCATTACAA
GATCCCAGCCTGGTCTTAAACCGTCAAAACGACATTACTGATGGTAAGGACTACCACAC
TTTGGCTAACAACGTCAATCCAAGTTGAGAGATGACTTGGAAAGATTAAAGAAGATCAG
AGCCCACCGTGGTATTAGACACTTCTGGGGTTTACGTGTTAGAGGTCAACACACCAAGAC
CACTGGTAGAAGAAGAGCTTAA

YML026C, 146 aa (SEQ ID NO 208)

MSLVVQEQQSFQHILRLNTNVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE
LTQEELERIVQIMQNPTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDRLERLKKIR
AHRGIRHFWGLRVRGQHTKTTGRRRA

YML063W, 1268 bp, CDS: 501-1268 (SEQ ID NO 209)

TATATTATTTTTTCCCTTCTGGGTCTTTTCTTCTTTCTTGTGTTTACCTTTTTTGCTTT
TTCATAAAATAATTTCTCTAGATTTGAAGACAGCATTTTGTACATCCATACACCATACA
CCATACACCATAGCACCAGTACACTATATTTTTATGAATTTACTAAGAATTATTCCTGC
AGGAGCTCCACTGAAAAAAAAGAGCAGCATGGATGTCCGGTAGAAGTGCTACTGAGTAA
ATGGGAAGGACGCGGTAGATCCAGTGTGGAATCAAGGTGGTGCCGGTGTGAAGCCGCCTC
GGCCGGCTGGACTCTCCAGGCCGGAGTGATGATTGCCACGCTGAACGTAACACAGTTTCA
CAATACCAGTGTCTCTATTAGTGAGTTCCAATGTATAGTTAGTAGTGGTATTTTGATATA
TGTGAGTGGTAGCAGATTTGAACCTAGTTAGTTGTATTCGCCCTTTGAGGAAACCAAGCAA
AAAACCGATCTAGACTAATCATGGCTGTTGGTAAGAATAAGAGACTATCCAGAGGTAAGA
AGGGTTTGAAGAAGAAGGTTCGTTGACCCATTTACCAGAAAGGAATGGTTCGATATTAAAG
CCCCATCCACTTTTGAAAACAGAAATGTTGGTAAGACTTTAGTTAAACAAGTCCACTGGTT
TGAAGAATGCTTCCGATGCTTTGAAGGGTAGAGTTGTGCAAGTTTGTGTTGGCTGACTTGC
AAGGTTCTGAAGACCATTCTTTTCAAGAAAGGTCAAGTTGAGAGTCGATGAAGTTCAAGGTA
AGAACTTGTGTTGACCAACTTCCACGGTATGGACTTCACTACCGACAAATTGAGATCAATGG
TCAGAAAATGGCAAATTTGATCGAAGCTAATGTTACCGTTAAGACTTCCGATGATTACG
TTTTGAGAATCTTTGCTATTGCCTTACCAGAAAGCAAGCTAACCAAGTTAAGAGACACT
CTTACGCTCAATCTTCCCACATCAGAGCTATCAGAAAAGTTATTTCTGAAATCTTGACCA
GAGAAGTTCAAACTCTACTTTGGCTCAATTGACCTCCAAATTGATTCCAGAAGTTATCA
ACAAGGAAATCGAAAATGCTACCAAGGACATCTTCCCACTACAAAACATCCACGTTAGAA
AGGTTAAGTTATTGAAACAACCAAGTTTCGACGTTGGTGCTTTGATGGCTTTGCATGGTG
AAGGTTCCGGTGAAGAAAAGGGTAAGAAGGTTTCTGGTTTCAAGGATGAAGTCTTGAAA
CTGTGTAA

YML063W, 255 aa (SEQ ID NO 210)

MAVGKNKRLSRGKKGLKKKVDPFTRKEWFDIKAPSTFENRNVGKTLVNKSTGLKNASDA
LKGRVVEVCLADLQGSSEHDFRKYKLRVDEVQGNLLTNFHGMDFTTDKLRSMVRKWQTL
IEANVTVKTSDDYVLRIFAIAFTRKQANQVKRHSYAQSSHIRAIRKVI SEILTREVQNST
LAQLTSKLIPEVINKEIENATKDIPLQNIHVRKVLLKQPKFDVGALMALHGEESGEEK
GKKVSGFKDEVLETV

YML128C, 2042 bp, CDS: 501-2042 (SEQ ID NO 211)

TTAATAGGGTTAGCCACCATTTGTCTCGAACATGTTACAGGCTCGGAGCTTGTGGCGGGT
GCCTCGCTTACTGGAGTACCATTTAGCGGTGTGTTTGAAGCTAACGAGTTCATCTTCAAT
CTTTATTTCCACTTCTTTACAAGCTTTCTGCCTTTCTCTATGACGTCTTTCCCAAAACAC
TACCTCTTGACACGACTTGTGTTTTCTGTTTTTCTCTAAGAATATCACTATTTTCACTTT
TTTACCTTTTCCACCATTACGTCGGTAAGCAACAGCATTACGCCGGCCTCACCTTAGAG
GGGAAGAATAAGGGATCTTTGGAAGTGAAGGAAATAAGGGAGAGGGAGGAAACAAGGAG
GCGGTGAAAGGGGATCGACAGGGTATTTAAAGCCACTCATGGAGTCGTATTCTTAGCATG
ATTAGATTACCGGAGTTTAGAAGAGGATCTGCAATAGAAGAGGAGACAACACAAAAGAA
CTGTTAATTAAGAGAAGAAGATGAAGCAATTCAGTTGGTTAATGCGGTTTCCGCATCAT
TTGTGCTTATTGGCTTAGTGTTGGCCAATTGAGATTCAAGTGTTCGACAAGTGGACGAGG
AAGACCTGGCCGATTATTTACGTGATAATAAGAAGAGCTTGGAAAAGTACGCTACAGACT
CCATTGAGGACTTGAAAACGGAGGCATCGCAGGTATGGGACAAACACGCGCAGCCCAAAC

FIG. 1 - 73

CATGGTGGCAGGTGTGGTCTAGTGACAGCAGTAGCGTGAGCAACAGTAACCCCGGATGGT
TTGGTTTATACTGGTTCTTCGGATCACCCAGTTTCTGACTGGCTCTTTGACACCTGGTCCA
CAGACAGTCTACGTAACCTTCTTGAAGAAAAACGGCGTGGATGTTGACGACGCTAAGGCTT
CCAAGGACTCGCTGGTGAAGACTGCTAAGGAGAACTTCAACAAGATTTCCAAATCTTTGA
AGTCGTCGGGATACCTATCCTTCTAGCTCTTACTTTGATAGCTGGTCAACCAAGATTTGC
AAAAGTGGTTGAATGACAATGGTATCGACTACGACAAGGCAGTTCAAAGCAAGGACGAGC
TAGTTTCAGAAAGTCAAGGAAAACATCTACCGAACTTCAGAAAAGGCAGAACAGCAGCGTC
TGGGTTTGTCTAGAAAGCTTGGATTTGGCTCACCAACAAATATTAGACACATCGGGACAAA
TAAAAGACACTGTATTTGACAAGTGGTCTAGTGATCAGTTAACCAATTGGTTGGAGAGCC
ACAAGGTCAATATTGACAAGAACATGGCCAAGAAACACGACTATTTGGTTAGAATGGCCA
AAGAAAATTTCTGCCAATTTGAAAGATGATATCTACTGGTACCTGGACTATATGAAAAGAG
AGTCTTCTCCATTTTGGACCAAGACCCAGAAATACGTTGGTTCCGTTGGGACTCTTCTA
AAAATTTCTTCACAAAATTTGTACTCCAAGTTTCAGAGGTAAGACTGACAATGTGATCAATG
ATACTTTTTTGGTTGGCCTAGACTCTTGGCCAAAAGGACAAATTGAAAATGTTTTTAGATG
CTCGTGGTATTAAGTACTCAATGCTGTCTACTGAACATCAATTGAGAGAATTAGTCAAAA
AATCCAGAAACGAAAAGTCAAGATCCTGCCAAAAGACTACCAAAAATACTTTGACAACA
GTAAGTGGTCTTTGGATGACATAAAGGGTTGGTTTGTCTGACAAAAAGGACGACTTCCAAG
ATTCTCAGACTTACTCCACAATTATGCAGGATTTTGACAAGGTTTCCAAAACACAAATG
ATGCTAAGGACCAAAATCGCTAAGACCTGGTCAAATACCTTTTCAGAGCTGGTCTCAAGAAG
ACCTATTGCAGTACCTAAAATCATTCCGGTGTTCGGTTAAACAGACTTCTACGAAGGACG
ACTTAATCAACTTGGCCAAGCAGAATACGCAATGGTTGTTTCGGCACTGTTAAGGAGCCTG
CTTACAAGAGGTACCTACATAACGTTAAAAGTGGTCGAAAAGCATATTAGGGTTCAACT
AA

YML128C, 513 aa (SEQ ID NO 212)

MKQFKLVNAVSAFVLIGLVLANSDSVFDKWTQEDLADYLRDNKKSLEKYATDSIEDLKT
EASQVWDKHAQPKPWWQVWSSDSSSVSNSNPWFYGTGSSDHPVSDWLFDTWSTDLSRNF
LKKNVGDVDDAKASKDSLVTAKENFNKISKSLKSSGYPPSSSYFDSWSTKDLQNLNDN
GIDYDKAVQSKDELQKVKENIYRTSEKAEQQLGLLESLLDLAHQQILDTSQIKDITVFD
KWSSDQLTNWLESHKVNIDKNMAKKHDYLVMAKENSANLKDDIYWYLDYMKRESSPFLT
KTPEYVGSVWDSSKNFLTNLYSKFRGKTNDVINDTFLVGLDSWPKDKLKMFLDARGIKYS
MLSTEHLRELVLKSRNEKLKILPKDYQKYFDNSNWSLDDIKGWFADKKDDFQDSQTYST
IMQDFDKVSKNTNDAKDQIAKTWSNTFQSWSQEDLLQYLKSFVVPVKQTSTKDDLINLAK
QNTQWLFGTVKEPAYKRYLHNVKNWSKSILGFN

YML130C, 2192 bp, CDS: 501-2192 (SEQ ID NO 213)

ACGAGATCATTTTCTTATCTATCTATTGAGTAATGCTTACTTTTCATATTTTCAATGAAC
AATAGGATATGTAGGAGAATTGATATATTTACTGCGTATCAGAGAAAAGGCTCTACTGACA
TTTTTGGCAAAATGTATTCTACACAAATCGAGAATACCACAGACAATGGTACAAGACATA
CACAAAGAGAAGACTGTTCTAATTAAACAAATAATATTGAGCTACCTGCTAAGTATGTCC
TTTTCCCTTTGTCTTTGGTTTCTCTTATAGAAGACCCTGGAAATTTTTCGCATTTTTC
GGCTTTGGGCGTTAGTAAGAACAAAAAGAAAAGAGAACAAAAAGAAACGATACGGA
GTACGTGTCATAAAAACTTGTTCATCATCCTTGAAGCTAAGTATAAAGAGCTTGAAAAG
GTTTACCACTTAACTGGTTATACTATTTCAAGAGTGTAACATTTTATTGCATATACCA
CAGTAACGTGCAGGTAAAACATGAGATTAAGAACCAGCCATTGCCACACTGTGCCCTCACGG
CTTTTACATCTGCAACTTCAACAATAGCTACATCGCCACCGACCAAAACACAAATGCCT
TTAATGACACTCACTTTTGTAAAGTTCGACAGGAATGATCACGTTAGTCCAGTTGTAACG
TAACATTCATGAATTAATGCCATAAATGAAAACATTAGAGATGATCTTTTCGGCGTTAT
TAAAATCTGATTTCTTCAATACTTTTCGGCTGGATTTATACAAGCAATGTTTCAATTTGGG
ACGCCAACGATGGTCTGTGCTTAAACCGCGCTTGCTCTGTTGATGTCGTAGAGGACTGGG
ATACACTGCCTGAGTACTGGCAGCCTGAGACTTGGGTAGTTTCAATAATGATACAATGA
AGGAAGCGGATGATAGCGATGACGAATGTAAGTTCTTAGATCAACTATGTCAAACAGTA
AAAAACCTGTAGATATCGAAGACACCATCAACTACTGTGATGTAAATGACTTTAACGGTA
AAAACGCCGTTCTGATTGATTTAACAGCAAATCCGGAACGATTTACAGGTTATGGTGGTA
AGCAAGCTGGTCAAATTTGGTCTACTATCTACCAAGACAAGTGTTTTACAATTGGCGAAA
CTGGTGAATCATTGGCCAAAGATGCATTTTATAGACTTGTATCCGGTTTCCATGCCTCTA
TCGGTACTCACTTATCAAAGGAATATTTGAACACGAAAAGTGGTAAATGGGAGCCCAATC
TGGATTTGTTTATGGCAAGAATCGGGAACCTTCTGATAGAGTGACAAACATGTATTTCA

FIG. 1 - 74

ATTATGCTGTTGTAGCTAAGGCTCTCTGGAAAATTCAACCATATTTACCAGAATTTTCAT
TCTGTGATCTAGTCAATAAAGAAATCAAAAACAAAATGGATAACGTTATTTCCCAGCTGG
ACACAAAAATTTTAAACGAAGACTTAGTTTTTGGCAACGACCTAAGTTTGACTTTGAAGG
ACGAATTCAGATCTCGCTTCAAGAAATGTCACGAAGATTATGGATTGTGTGCAATGTGATA
GATGTAGATTGTGGGGCAAAATTCAAACTACCGGTTACGCAACTGCCTTGAAAATTTTGT
TTGAAATCAACGACGCTGATGAATTCACCAACAACATATTGTTGGTAAGTTAACCAAAT
ATGAGTTGATTGCACTATTACAGACTTTTCGGTAGATTATCTGAATCTATTGAATCTGTTA
ACATGTTTCGAAAAATGTACGGGAAAAGGTTAAACGGTTCTGAAAACAGGTTAAGCTCAT
TCTTCCAAAATAACTTCTTCAACATTTTGAAGGAGGCAGGCAAATCGATTTCGTTACACCA
TAGAGAACATCAATTCCACTAAAGAAGGAAAAGAAAAGACTAACAATTCTCAATCACATG
TATTTGATGATTTAAAAATGCCCAAAGCAGAAATAGTTCCAAGGCCCTCTAACGGTACAG
TAAATAAATGGAAGAAAGCTTGGAACTGAAGTTAACAACGTTTGAAGCATTACAGAT
TTATTTATAGAAGCTATTGATTACCCAGGAACATCTGGGAATTATCTTTGATGAAGG
TATACAAATTTTGAATAAATTCATCGGTTGCTGATTACGTTAGTGAGGAGACACGAG
AGCCTATTTCTATAAGCTAGATATACAATAA

YML130C, 563 aa (SEQ ID NO 214)

MRLRTAIATLCLTAFTSATSNNSYIATDQTONAFNDTHFCKVDRNDHVSPSCNVTFNELN
AINENIRDDL SALLKSDFFKYFRDLKYQCSFWDANDGLCLNRACSVDDVWDWDTLPEYW
QPEILGSFNNDTMKEADDSDECKFLDQLCQTSKKPVDIEDTINYCDVNDFNKGNAVLID
LTANPERFTGYGGKQAGQIWSTIYQDNCFTIGETGESLAKDAFYRLVSGFHASIGTHLSK
EYLNTKTGKWEPNLDLFMARIGNFPDRVTNMYFNYAVVAKALWKIOPYLPEFSFCDLVNK
EIKNKMDNVI SLDLTKIFNEDLVFANDLSLTLKDEFRSRFKNVTKIMDCVQCDCRLWGK
IQTTGYATALKILFEINDADEFKQHIYVGLTKYELIALLOTFGRLESIESVNMFEKMY
GKRLNGSENRLSSFFQNNFFNILKEAGKSIRYTIENINSTKEGKKKTNNQS HVFDDLM
PKAEIVPRPSNGTVNKKWKAWNTEVNNVLEAFRFIYRSYLDLPRNIWELSLMKVYKFWNK
FIGVADYVSEETREPI SYKLDIQ

YMR022W, 998 bp, CDS: 501-998 (SEQ ID NO 215)

AACAGTATTGGCTGTTGATTCATTGCGCTGCAGCAGTCACCTTCAATTTGTGCACCATTT
TCGTATTCTGTACTTTGCGATGTAGAGTCTACTAAAATAGCGTCTCTGATAGCCATGGGT
GAAGGTCTTCTCTAGTTCTCACCTTAATTAGCATTCGGTGAGAATGCCTGCATGTTGAA
GAGCGATGCCCTCTGATGCACGATGCACACGCATATTTGTTCCCATTAATATTATCATC
TCTGATAGAGCTTGAAGAACTTACCAGACTGTTTCAAGTTTAAAACAAGGCGCCTCATCG
CATCTACCTCAGGAAGATGCAGCAGCTTATTGTCTCGAGATCCTTCTTATAACTCCTTTT
CGCCATTACCCGAAAACGAGATTACAGCCTCTAAACCAAGAGCTCGAAAAGCGCCAAAGT
AAACTTGGCGTTTAGCGTACGAAGGAGATTATCTTAAAGGAACCTCCCTAGTAATAGT
GTAATTTGGAAGGGCATAGCATGTGCGAAAACCGCTCAGAAACGCTCCTCAAGGAGCTTC
AACAGTTAATTAAAGATTCTCCACCTGGTATAGTGGCTGGTCCCAAATCGGAGAATAACA
TATTCATTTGGGACTGCCTAATTCAAGGGCTCCAGATACGCCATACGCTGATGGTGT
TTAATGCTAAGCTAGAGTTTCTTAAAGACTATCCGTTATCTCCACCTAAACTTACTTTCA
CACCAGCATACTACATCCAAATATTTATCCAAATGGGGAAGTGTGCATATCCATTCTAC
ACTCCCTGGTGATGATCCTAACATGTACGAATTAGCGGAAGAAAGATGGTCGCCAGTGC
AAAGTGTAAGAAAAATCTATTAAAGTGTATGAGCATGTTGAGTGAGCCCAATATCGAAA
GTGGTGCCAACATTGATGCTTGCATCTTGTGGAGAGATAATAGACCTGAATTTGAGAGAC
AGGTAAAGTTATCCATTTTGAATCATTAGGATTCTGA

YMR022W, 165 aa (SEQ ID NO 216)

MSKTAQKRLKELQQLIKDSPPGIVAGPKSENNIFIWDCLIQGPDPYADGVFNALKEF
PKDYPLSPPKLTFTPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVEKIL
LSVMSMLSEPNIESGANIDACILWRDNRPEFERQVKLSILKSLGF

YMR118C, 1091 bp, CDS: 501-1091 (SEQ ID NO 217)

GTCTTCCGCTTTATATGTTTCGTTATCTATCACATTATCAAATGACTTTGTGCCACTG
TGTTTTGACAAAATTACTGTAATATAATAGTATTTACATGTTTGTACCAGAAGTAC
TTGCATCGCATCCAGTTCTCATGCAATATAGTTGTATACCATGTGCTTGAAAGGAACCAG
AGTAAACACTTCTACCAGTATTTCTTTACGGTTCGGATCAAACCATCACTCATTCGGTC
ATTCTTACCGTACGATAAACCAAATTACAAGGAAAAGTATCCCTAATTAGAGATCACTGC

FIG. 1 - 75

ATCCGTAATAGTTTTTTTTCTATTTTGGACTTTTGTAAAAAAGGGATTAGGGATACGTTG
CTCATAAAAAATTGACGAAGATTTTAGATAATGGCAAATAAAAAATGAAATAGTATCAAT
ATACCGAAAAATTAAATCACACTCAATGCGACTGTGATAGCTGATAAGTGGAGCTCAGAAA
TATTCAGAAGCGTAAGAATAATGAAAGCAACCATTCAAAGAGTAACATCTGTATTTGGAG
TTCCCGGAGCATCTGTATTCGTGCCAAGAATCAGCACACCATTTATTTTGCATAATTATA
TCTCTAATGGCAGAATGGACCTTTTTTCCAAAGAATTCCACAATGGCCGCGTATCCAAAT
CTGATCTTTGGTCAAGCAACAAGGAAGAGGAGCTCTTAGTATCTCAAAGGAAAAAAGAC
CGATCTCTCCTCATTTAACTGTTTACGAACCTGAAATGAGCTGGTATCTTTCTCTTTTAC
ATCGTATATCTGGCGTTTTACTGGCTCTTGGATTCTATGCTTTCACAAATFACTTTGGGTG
TGACGCAATAATGGGAATGGATACGACTTTTCAGGATCTAAACAAGTGGTATCAGGAAA
AGATGCCCTAAGTGGTCCCAATGGGTGGCCAAAGGCTCTGCAGCATATCTGTTTGCATTCC
ATTTTGGTAACGGTATAAGGCATCTCATCTGGGATATGGGCTACGAATTGACCAACCGTG
GGGTTATAAAAACCGGATCAATCGTTTTAGCCGGCACACTCGTCTTAGGAACGTATTTAC
TGGCTCAGTAA

YMR118C, 196 aa (SEQ ID NO 218)

MKATIQRVTSVFGVPRASVFPRISTPFILHNYISNGRMDLFSKEFHNGRVSKSDLWSSN
KEEELLVSQRKKRPISPHLTVYEPMSWYLLSSLHRISGVLLALGFYAFTITLGVTTIMGM
DTTFQDLNKWYHEKMPKWSQWVAKGSAAYLFAFHFGNGIRHLIWDMGYELTNRGVIKTGS
IVLAGTLVLGTYLLAQ

YMR143W, 1121 bp, exon1: 501-524, intron1: 525-713, exon2:
714-1121 (SEQ ID NO 219)

CCGCTTAGCGCAAACCTATCGTGAACCTCGCTGCAACAACCTGAGAGGGCAAGGATATACATA
AAAATAGCCTACAAATTCTGAACCTGTAAAGGAAGCCTCATAAATAAAGGTAGATAGTA
AAGTATACAAGAGAAGAATCCCAAGATGTCACTGTCCCAAGTGTTCAGATATGTTTTCA
GTTCTGCAGAAATGATGTTTGATAGTATCGATAATTGGAGTGAGATCAAGAGAAAAAATG
AATATGTCAGCCAACCAAGTTCTGAGTAGGCAGTAAATGAGTACGCATAGTGTATTTATC
CAAAGGAAAGAATGTTATTTTTACAAGCCGAATTGAGATCCAATTAGGCAATGTTTTGG
GGAGAGTATTTTGACAAGATTGGTTAAACTACTACGGTCAGTTCCGTAACCACTACGATT
GTACACATAAGGAAACAACCTGTAAAGATAAACAATAAGGGCTTCCAATGCCATTGTAAGA
TATCATATTTCCCTAAACAATAAGTGTACAGCGAATATAAAGCCAGCGTCAGTGTCTTCCCTGG
AAGGTTGCGCAACTAAAGAAGTTGAAATTTAAATGGCAAGCGCTACATTTTTCATCCATT
TCACTCATCAGATGTCCAAGATTTTCGAAAAATAAATATTTCTCATTTTTCTCTCAATGAA
ATAATTGTTACTAACATTGAATTTCTCTCGTAACCTAATTGCATTACTTCTTTAGACTTTTG
GTAAGAAGAAATCAGCTACTGCTGTTGCCCATGTCAAGGCCGTAAGGGTTTGATCAAGG
TTAATGGTTCTCCAATCACTTTGGTTGAACCAGAAATCTTAAGATTCAAGGTTTACGAAC
CATTATTGTTAGTTGGTTTGGACAAATTTCTCCAACATCGATATTAGAGTTAGAGTTACTG
GTGGTGGTCATGTTTCCCAAGTTTACGCCATCAGACAAGCTATTGCTAAAGGTTTAGTTG
CTTACCATCAAAAAATATGTCGATGAACAATCCAAGAACGAATTGAAGAAGGCTTTCACTT
CTTACGACAGAACCTTGTTGATTGCTGATTCTAGAAGACCAGAACCAGAAAGAAATTCGGTG
GTAAGGGTGCTCGTTCCAGATTCCAAAAATCTTACCGTTAA

YMR143W, 143 aa (SEQ ID NO 220)

MYSEYKASTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIAGLVAYHQKYVDEQSKNELKKAFTSYDRLLIAD
SRPEPKKFGGKGARSRFQKSYR

YMR174C, 707 bp, CDS: 501-707 (SEQ ID NO 221)

GTCCCATCATTCTTTACACCTCGTACTGTATTTCATGATCATCTATCCATTTTACATACCG
CTCCCTTTAAGATACGTTTATTCGTAACCTCCCATTTACCAATCACTATGAGCCGTCACG
TTTCCAAAAAACCCTAAACATATGATGCAAACCTCCAATGAGACTCAACGTAACATGCAA
GTAAATACAGAAGGTTAAGAGATAGTTGTCTTAAAGGGGTACCGAAAGCATTTAGGGGAG
GCTTAAGGGAGGGTGCCGATCCTATGAAGTATTAATACGTAATGCCAAAGGAATTGTTG
AACATCTGAAGTGGATAGATTAATCGTACAGTAATCGTACAGTACTATGTCTTACTGATG
TCGGGAATCTCAGGGGCGACCGCCCCCGGCTAGAATTATCTATATAACGGTAAAAAGAAT
AAAACCTCTATTCTAGTTCTCGCCATTTACCTTGACTTTAATGAACCAATAAAAGAAATTT
CTACAACCAAGACATCCAGAATGAATACAGACCAACAAAAAGTGAGCGAAATATTTTCAGA

FIG. 1 - 76

GCTCAAAGGAAAAATTGCAGGGCGATGCAAAGGTAGTGAGTGACGCTTTTAAAGAAAATGG
CTAGTCAAGACAAGGACGGCAAGACTACCGATGCTGATGAAAGTGAAAAACACAACATATC
AAGAGCAATACAACAAGCTCAAAGGGGCGGGGCATAAGAAGGAGTAG

YMR174C, 68 aa (SEQ ID NO 222)
MNTDQQKVSEIFQSSKEKLGDAKVVSDAFKKMASQDKDGKTTDADESEKHNYQEYQYNKL
KGAGHKKE

YMR191W, 1877 bp, CDS: 501-1877 (SEQ ID NO 223)
GGTTCGATACAACACTTGTGCTGGCTGGTATATCAACCATGGGTACGTCAGCATATTGAT
TCGATGTGGCAGTGTACGAGAGCCATTCTGTATCGTTTCGACAAAGTTTGCATGACTTCAT
GTTGTTTCGTAGCAGTATTCGTTGGTCCAGATGCAGGAATGCTGGTTATAAAGTTTGTGTG
TTCTGGTCCACATTTCATCTTTGGATGGCGTTGTTGGTGGCGAATTGTCTTAGGCCTTT
TGTTCCGGATGTGCTTTTGGATAGCCTGGAATACGAAATCTTTGTCTTCTGTAAAGTCG
CCGTTTCCTTTAACCATTTGTGCTCCCTTCTTAAGTTATGTGACGGCTTCGTCACCATT
CCGCCCTGTGTGTACGTGTATGATTTTTTAAATATATACAACAATAATCTGTATTTTTTC
CTTTCCCTCTAGCCAATGACTCCAAGCTGGCTGATAAAAAACAACTAAACGGTAAAGCCAC
AAATCCGAAATGTATACCAATGATCACCCAGCCTGCTAAGTGCCCTCTATTGATCCGTA
TATCAGCTTTTAGATCAGGCTCGAGTTTCTTGTATATGTGCATTGCAAAAGCATAAACA
AATCCTGGCAGCCGAAGCCGGGCAATCCACTTCGAAACGCACGGCTGAACATATATAAATA
TAAAGGACATGTGGAGAGAAGCTTCTCTTCCCTTCACATTTTCGATTTTCATGATCTAAAGT
GGTTCTTTTACAATAGAAGAGCACCAACACGAAATATGGCTGTCCGTGGTAATAACTGGA
GCATGTGGCTGCGAATGTCACGGGTCCACCTCAGGCAGATCACGAAGTCTCTGGACCGAA
CGCTGATCAGTTTGAGCCATGGGAATTTTCCCAACCAATATAATCGCAATATTTTGTCA
CTTGGTGGGAAGAGCCTATTTGAGGCTTCTACAGCTTTTAGGAGGGCAAGTGGTTTAAACGG
TATCTCCTCTCACGAGGAGAGGAATCGCAAGGTTTGACCATTTTCAGACCTGTTCCTCAATG
TCAGTAAATTTGCTTCTTTTCCCAAGAGTGCCCAAGGAGCCCCAAGGGCCTTTTACCA
ACTGGAATATGACTACATCAAAGAGATTATTAGGGCAGAGAGCTTATTCGACTTCCAGTA
TCAAATTTACCCAAGAAGCCGTGAATAACATGACTATATCTTTGAGGTGTTTTTCAACT
CACTAGGCGGATTAAATCAGTGCTCCCACTCTAATTCCTGCAAGCTTATCAGAATGCGT
CTAATGTTACCTCTAAACAGGATCACGTCCAACAGTTGCCCTTAAGAAGTTCATCTCAA
AGGATATCAATTTCAATTCGTAATTTAGAATTTTAAAGATAATGAAGACCCAGAATGAAG
TCGTTGATGAAACAAGCGCATATTACATGGAAAAACCAGGTTCTATATTGAATTTACCA
TTTCAGAATTTAACGTTAATGGGACATTCTCCGCACCTTTGTCAATTTTAGATCCTTCTT
TGTTAGCGGATTTGGATGAAATGATTAGAAATTACAAATACGAATTAATAATCAATATACA
GTAGTGTGACATGATCTTGCAGAAATATGGATCATTGCCGATAACTTTTCATCGAAATA
AGATTGCAATACATTTTCCAACTCAACTGTGGTGGAAACAGAAAACTAATTGCAAGGTC
TGAATATTGCTACGGGTGTTATTTACGCAGATACGTCTCCCGATATCAGTCTAGAAGGTA
CAAATTTGAATGCTCTGGTTAATGTTGACAATTCAGGAAGCGTATGGTCTTTTGTAAAGG
AGCCCTCGTTTCCCTCTAGGAGCGCTTTTTCACCTATTTTATCAGATGCATCCTATGATA
CTTATGAATTGGTCTAG

YMR191W, 458 aa (SEQ ID NO 224)
MITQPAKCPLLIRISAFRSGSSFLLYVHCKSINKSWQPKGNPLRNARLNYINIKDMWRE
ASLP SHFAFHD LKWF FHNRRAPTRNMAVGGNNWSMWLRMSRVHLRQITKSLDRTLISLH
GNF SHQYNRNIFVTW WKS LFEASTAFRRASGLTVSPLTRRG IARFDHFRPVPNVSKFASF
PRVPKGAPRGLFTNWNMTTSKRLLGQRAYSTSSIKFTQEAVNMTISLRCPFNSLGLNQ
CSHSNSCKAYQNASNVT SKQDHVQPVALKKLSQK DINFIRNLELFKIMKTQNEVVDETS
YYMEKPGSYIEFTISEFNVNGTF SAPLSFLDPSLLADLDEMIRNYKYLKSIYSSVDMIL
QNYGSLPITFHRNKIRIHF PNSTVVETEKL IAGLN IATGV IYADTSPDISLEGTNLNALV
NVDNSGSVWSFVKEPSFPSR SAFSPILSDASYDTYELV

YMR230W, 1228 bp, exon1: 501-552, intron1: 553-962, exon2:
963-1228 (SEQ ID NO 225)
ATCAAATATTGATCGAGTTCATATAAAGCTAAAGAGTAGGAAATATACCATCAATGGTGA
GCACTTATTTT TTTTGGATTTAGATGTGAGACATACTAAAAAAGTTGCTATCAAGCC
TATAATTTGGCTACGTTGCTTCCGGTGT TTTTCAATTGATTTAAGTTACAACACTCAA
TCTGGGTAATTTGATCTTTT TTAATAATTATTTTAGTGACATATAGTTCTTAGAGTTCCG

FIG. 1 - 77

AGATTTATTTTGTTCATTTTTTGGATCGGCGTCTTATAAAATCAAGACATAATACATCCGC
ACATCGCGCATGTGTGGGTGTATATGCCCTTTTCACGATTTTAAAGTTGCGTCTCAAAAT
AGTTTCCGAGTTGGAAGCCTGAGTTTTCAAAACAATATAGGAATTAAGGTATACGTCT
TTGGATACATGTTATTTGAAATGGGGTAGAACTAGCACAACTGAAACCAAGAAAACACAG
ATCATAACTAACCGTTCAAGATGTTGATGCCAAAGCAAGAAAGAAACAAAATTCACCAAT
ACTTGTTCAGGTATGTTTGCATTTTTTAGGTGAAATATGCAGTGATATGCTCCGAAAT
GGATAGCAAAGATGATAAATGAAAAACAATTAAATTGAACTTGAATATCATTTAAAGTG
GTAGAAAACCGATTGTTTCAAAAAGATCTTTGTGGACAAGTACGGCAGTGCATGAATCCG
AAAGAAAAGTGCAACCTAAGCAGAATTCATTATTTACGCGTCCATTTTATAATGTTT
GAACTTTTGAGTCCTTATAGAAATGCTAATATTATGATCAAAGCGATTATATCATTTACT
TTACAGTTTCCGGAGTTTCCGTATTATTGCAAAAGGACCACAAACAATTGAAATCATGAT
ATCGTAAGAAATATTATTACTAACAAGGAAGATCATTGAATTACGATCGCATATCGAAAT
AGAAGGTGTTGTCGTCGCTAAGAAGGATTTCAACCAAGCTAAGCACGAAGAAATTGATAC
CAAGAACTTGATGTTATCAAGGCTTTGCAATCCTTGACTTCTAAGGGTTACGTTAAGAC
TCAATTCTCATGGCAATACTACTATTACACTTTGACTGAAGAAGGTGTTGAATACTTGAG
AGAATACTTGAACCTGCCTGAACACATTGTCCCAGGTACCTACATTCAAGAAAGAAACCC
ATCCCAAAGACCTCAAAGAAGATACTAA

YMR230W, 105 aa (SEQ ID NO 226)

MLMPKQERNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS
WQYYYYTLTEEGVEYLREYLNLPHEHIVPGTYIQERNPSQRPQRRY

YNL054W, 3998 bp, CDS: 501-3998 (SEQ ID NO 227)

CCCTTCGCTAAATCATTAAGAGGTCATTCATGAAGTTAATTCAGCACCAAGTTGGACTG
TTAGACACGAGATACACATTGCAGTCCAAATGTGCAGATTTTTCAGATAAATGTCGTCGC
ACAAGACTGCCCCCTCCCGTCCTCAGACAGACACAAAATTAGATTTTACGTTTACATAAAG
ATGTACATAACTTGAAAAACGTTAATCCCTCTTAAATTTAGACCTTGTAAGTCTTCCTG
GCCACTCTTTGTGATATATTGTAGTGCAATATATTGATTTCGTTCTTCTTATTCTTTGTT
CTTAGGCATTTCCGCTTTAGAAAATTCGTTGGGTGGTTTCTGCGACGGGTATCCCCCTCG
ATTTTGCATAATGATCTTCAATTCTACAATAAAATCAAGTAGATACAGGAAAATATTCC
ATAAATTATAGTGTAATTCGCCCTGTATACACCTTATCGTTTCATCTCAGGCAAGTTAA
GCATTTGGGAAACGTGCTAGATGACAGAAGAAGATAGAAAGCTCAGTGTAGAGACAGAAA
CAGTTGAGGCACCCGTGGCAAATAATCTTTATTGTGCAATAACAGTAATGTAGTAGCAC
CTAATCCTTCTATTCCCTCTGCCTCCACATCTACCTCTCCGCTACACAGGGAAATAGTTG
ATGATTCTGTGCTACTGCTAACACCACCAGCAACGTTGTACAGCATAATTTGCCACCA
TAGATAACAATTTAATGGATTCCGATGCCACGTACATAATCAAGATCATTGGCATTCAG
ACATAAACAGGCAGGAACATCAATGTCAACGAGTGATATCCCAACAGATTTACATTTAG
AACATATCGGCTCTGTTTCATCACTAATAATAATAGTAACAATGCCCTAATCAACCACA
ACCTCTGTCTCATCTCATCTTTCCAATCCGTCATCTTCATTACGAAACAAGAAGAGCTCTT
TGTGGTAGCTTCTAACCCTGCGTTTGCTTCAGATGTTGAACTCTCGAAGAAGAAACCTG
CCGTCATCTCCAATAATATGCCTACAAGTAACATTGCCCTTTATCAAACAGCGAGATCGG
CGAATATTATGGTCCATCATCAACTTCCGCATCTAAAGCGTTCAGAAAGGCTTCGGCCT
TCTCCAATAACACGGCACCCAGCACTAGTAATAACATCGGCTCGAATACACCTCCAGCTC
CTCTTTTACCTCTACCTTCACCTATCACAAACAAAATAAGCCAAAATAATAGAGAGGCCCA
CAATGCACGTCACTAATTCAAGAGAAATACTTTTAGGTGAAAACCTGTTAGATGATACAA
AGGCGAAGAATGCTCCCGCAATTCAACCACACACGATAATGGTCCAGTAGCAAAATGATG
GGCTGCGTATACCGAATCACTCGAACGCAGATGATAATGAAAATAACAACAAAATGAAGA
AGAATAAAAACATTAATAGTGGGAAAAATGAACGTAATGATGACACCAGCAAAATATGCA
CTACATCTACTAAAACAGCGCCTTCAACCGCACCTTTGGGCAGTACAGACAATACTCAGG
CTCTCACTGCTAGTGCTCCAGCAGTAATGCTGACAATCACAATAATAACAAGAAGAAAA
CCAGCAGCAACAACAACGGCAATAACAGTAATAGTGCATCCAATAAAACCAATGCCGATA
TCAAGAATTCTAACGCCGACTTGAGCGCTTCTACCTCTAACAATAATGCAATAAATGACG
ACTCACATGAGAGTAATTCAGAAAAACCAACAAAGGCGGATTTTTCGCTGCAAGGCTGG
CTACAGCTGTAGGTGAAAATGAAATTAGTGATTCTGAGGAAACATTTGTTTATGAATCGG
CAGCTAATTCGACTAAAAACCTAATATTTCTGACTCCTCCAGCCAGCAGCAGCAGCAGC
AACAGCAACCTCCAAAACAACAGCAACAGCAACAAAATCATGGAATAACCTCAAAGATAA
GCGCCCATTGCTAACAATAACAAAAAATTATTAAGCCGACTGAAAAATTCAAGACATA
TTAGCACTGGTGCCATATTGAATAACACAATCGCGACTATAAGCACAAATCCGAACCTGA

FIG. 1 - 78

ATTCTAATGTGATGCAGAACAAATAACAATCTGATGTCGGGACACAATCACCTGGACGAGT
TGAGCAGTATAAAACAGGAGCCACCGCATCAATTGCAGCAGCAGCAACCACCAATGGATG
TACAATCGGTAGATTTCGTATACCTCTGACAACCCAGACAGCAATGTTATTGCCAAGTCGC
CTGATAAGAGGTCAAGCTTAGTATCCCTATCTAAAGTTTCTCCACATTTACTTTTCATCCA
CATCAAGCAACGGTAACACAATATCGTGTCCCAATGTTGCCACAAATTCGAGGAATTGG
AACCAACAATGATATTTCAACGAAGAAATCTCTTTTCCAATTCTACTTTGAGACATTCCT
CTGCTAATAGAAATTCTAATTATGGTGACAACAAAAGGCCTCTTAGAACAACAGTGTCAA
AGATATTTGATTCAAACCCTAATGGAGCTCCTTTACGGAGATACTCTGGGGTACCGGATC
ACGTTAATCTAGAAGATTACATCGAACAGCCGCATAATTATCCAACAATGCAAAATAGTG
TGAAAAGGATGAATTTTATAACAGCAGGAACAATAAGTTTCCCCATGGTTTAACTTTT
ATGGTGATAACAATGTTATTGAAGAGGAAAAATAATGGTGACTCGTCTAATGTAATCGAC
CGCAACACATAACCTTCAGCATGAGTTTATTCCAGAAGATAACGAAAGTGATGAAAACG
ATATTCACTCCATGTTTATTATAATCATAGAACGATTTAGAAAACAAACCGCTAATAT
CCGATTATGGTGAAGATGAAGACGTAGATGATTATGATCGCCCAATGCTACTTTCAACA
GTTACTATGGCTCAGCATCCAACACGCACGAACTTCCATTACATGGAAGGATGCCTTCAA
GATCAAATAATGATTACTACGATTTTATGGTTGGCAACAATACTGGCAATAACAACCAAT
TGAATGAATATACCCCTTAAGAATGAAACGTGGTCAAAGACACCTATCAAGAACAAACA
ATAGCATAATGAATGGTAGCATCCATATGAATGGTAACGATGACGTTACCCATTCCAATA
TCAATAATAACGATATTGTTGGTTACTCACCGCACAACTTTTACTCAAGGAAGTCCCCAT
TTGTGAAAGTAAAGAATTTTCTTTATCTTGCATTTGTTATATCATCACTATTGATGACAG
GATTCATTCTGGGATTTTATTGGCCACTAATAAAGAACTACAAGATGTAGACGTGGTAG
TGATGGATAATGTGATTTCAAGTTTCGGACGAGTTGATCTTCGACATCAAGTAAGTGCTT
TTAATCCAGGATTCTTCAGTATAAGCGTTTCCCAAGTCGATTTGGACATTTTGGCAAAAA
GTTCTTACCTGAAGTGCGATTCTAATGGTGAAGTGTACAGTAATGGAACAGGAACGGAAAA
TTTTACAAAATAACGACAAATCTTTCGTTAGTTGAAGAGAGTGCTAATAATGATATTAGTG
GTGGGAACATAGAGACGGTATTACTAGGAACCGCTAAAAAACTAGAGACACCATTAAAGT
TCCAGGGCGGCGCATTTAATAGGAACACGATGTGTCAAGTCTCGAGTGTCAAGCTTTTAA
GTCTTGGGTCTCGTGAAGCCAAGCACGAAACGACGATGATGACGATGATGATGGCGACG
ATGGTGACGATGAAAACAATACTAATGAAAGACAATACAAAAGCAAACCAATGCTAGAG
ATGACAAAGAAGATGATACTAAAAAATGGAAGCTACTAATCAAGCATGATTACGAATTGA
TAGTCCGTGGAAGCATGAAGTATGAGGTGCCCTTTTTCATAACGCAAAAATCTACGGCTA
TTCAAAAGGATTCCATGGTCCATCTCGGTAAGAAGTGA

YNL054W, 1165 aa (SEQ ID NO 228)

MTEEDRKLTVETETVEAPVANLLLSNNSNVVAPNPSIPSASTSTSPHLHREIVDDSVATA
NTTSNVVQHNLPITIDNNLMDS DATSHNQDHWSDINRAGTSMSTSDIPTDLHLEHIGSVS
STNNNSLINHNPLSSHLSNPSSSLRNKSSLLVASNPAFASDVLSKKKPAVISNNM
PTSNIALYQTARSANIHGSPSSTSASKAFRKASAFSNNTPSTSNNIGSNTPPAPLLPLPS
LSQQNKPKIIERPTMHVTNSREILLGENLLDDTKAKNAPANSTTHDNGPVANDGLRIPNH
SNADDNENNNKMKKNKNINSGKNERNDTTSKICTTSTKTAPSTAPLGSTDNTQALTASVS
SSNADNHNNNKKKTSNNNGNNSNSASNKTNADIKNSNADLSASTSNNNAINDDSHESNS
EKPTKADFFAARLATAVGENEISDSEETFVYESAANSTKNLIFPDSSSQQQQQQPPKQ
QQQQQNHGITSKISAPLLNNNNKLLSRLKNSRHI STGAILNNTIATISTNPNLNSNVMQN
NNNLMSGHNHLDELSSIKQEPHQLQQQQPPMDVQSVDSYTSNPDNSNVIKSPDKRSSL
VSLSKVSPHLLSSTSSNGNTISCPNVATNSQELEPNNDISTKKSLSNSTLRHSSANRNSN
YGDNKRPLRTTVSKIFDSNPNGAPLRRYSGVPDHNLEDYIEQPHNYPTMQNSVKKDEFY
NSRNNKFPHGLNFYGDNNVIEENNGDSSNVNRPQHTNLQHEFIPEDNESDENDIHSMFY
YNHKNLLETKPLISDYGEDEDVDDYDRPNATFNSYYSASNTHLPLHGRMPRSRNNNDY
DFMVGNNNTGNNNQLNEYTPLRMKRGQRHLSRTNNSIMNGSIHMNGNDDVTHSNINNNNDIV
GYSPHNFYSRKSPFVKVKNFLYLAFVISSLLMTGFI LGFLLATNKELQDQDVVVMDNVIS
SSELI FIDITVS AFNPGFFSISVSQVDLDIFAKSSYLKCD SNGDCTVMEQERKILQITTN
LSLVEESANNDISGGNIETVLLGTAKKLETP LKFQGGAFNRNYDVS VSVKLLSPGSREA
KHENDDDDDDGDDGDDENNTNERQYKSKPNARDDKEDDTKKWKLLIKHDYELIVRGS MK
YEVPPFNTQKSTAIQKDSMVHPGKK

YNL067W, 1076 bp, CDS: 501-1076 (SEQ ID NO 229)

GACGACTATTGATGCCAGGCAAATTTTGGATTTACTGCTCCTCTTTTAAAGAAGACAAGTG
TGTGATATCGTAGCGGTAGGAACCAATTTTGCAATCGATTTACTTACAGCCAAGAAAAATC

FIG. 1 - 79

TATTTTCATGTTTAGCATTGCCATTTCTTCTGTGTACACGTTGTGCTTGCCAGGAAC
TAGGAGACGTATACAAGCATCAATGTTACGAATGTACGATCCCGTTTGCATCTGATGT
GTAAACTCATGTGGTGCCTGGTGTGTTTCCAAGACTGCACTATTAAGTGGGAATTTT
TTTTTCTTCTAGTGAATTTTTTTTTTAAAGCGACGCACAGGAAAAGTGAAAATTATTTAA
ACGGACGGCAAACATGAAAAAAAATTAACCAACCATATTTCTATTTCCCTTTCCCTTTAC
CTATTCTCTTTTTGAAATAGTTCATTTTCTCTCTCTGAAACGACAATAAACCAAACCTCTA
GCCTCCAATAGTCACTAAAGATGAAGTACATTCAAACCGAACAACAAATTGAAATCCAG
AAGGTGTTACTGTGACGATTAGTCCAGAATCGTCAAGGTTGTGGTCCAAGAGGTACTT
TGACCAAGAACTTGAAGCATATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA
AGGTTGCTGTTTACAACGGTGACAGAAAGCACGTTGCCGCTTTGAGAACCCTTAAATCTT
TGGTTGACAACATGATCACTGGTGTCAACCAAGGTTACAAGTACAAGATGAGATACGTCT
ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCTAAATTCATTGAAG
TCAGAACTTTTTGGGTGACAAGAAGATCAGAAACGTCCCAGTTAGAGATGGTGTACTA
TCGAATTCTCTACTAACGTAAAGGACGAAATCGTCTTATCTGGTAACTCTGTTGAAGACG
TTTCCCAAAATGCCGCTGACTTGCAACAAATCTGTCTGTGTTAGAAACAAGGATATCCGTA
AGTTTTTGGATGGTATCTACGTTTCCCAACAAGGGTTTCATTGTGCAAGACATGTAA

YNL067W, 191 aa (SEQ ID NO 230)

MKYIQTEQQIEIPEGVTVSISRIKVKVVGPRGTLTKNLKHIDVTFKVNQLIKVAHVHNG
DRKHVAALRTVKSLVDNMITGVTKGYKYMRYVYAHFPINVNIVEKDGAKFIEVRNFLGD
KKIRNVPVRDGVTFSTNVKDEIVLSGNSVEDVSQNAADLQQICRVNRKDIRKFLDGIY
VSHKGFIVEDM

YNL075W, 1373 bp, CDS: 501-1373 (SEQ ID NO 231)

TCGATGGATATCCCATCCAAGAACAGGAATACTGGGTTTTTGAAGACCAGAATGGAGATC
TCTGAGGAAGAAAAGATGGTACGTACAATATCACGGCTTGACAATACGAGTATTGCAAC
AGTAATGGAAATGGTAATGATGACACCTCTAATCAGAGAACGGAAGCACTGGGGCGTAAG
ACGAGTAATGGAGGGCGAATATGATTACTAAGTTAAATAAATCAGATACAGTATTTAAAG
TTCTTTCAAAAAAAGATAATGTATATATTTTACTATCTACGCAGTGAAAGAGTTCCTTC
TAATGACACACTATTCACTTCGGGTAACGGATATTGTGTACTGAAAAATATAAAAAATTT
TATCCCGGAAATGCGATGAGATGAAAATGCATGAAGTAGCGTATATATTGATTGCATGAG
GTTGGACTTGAAAGGGCATATATACTCGGTTTTATCATTGATTCAAGTGTTCCTCATAAAT
AATAAAACAGTTAAATCGAAATGCTAAGAAGACAAGCCCGTGAAAGGAGAGAATATCTAT
ACAGAAAAGCGCAAGAATTACAAGATTCTCAACTGCAACAAAAACGTCAAATAATTAAAC
AAGCGCTAGCTCAGGGGAAGCCATTGCCAAAGGAACTAGCAGAAGATGAGAGTTTACAAA
AGGATTTTCAGATATGACCAAAGTTTAAAGGAGAGCGAAGAAGCAGATGATCTACAGGTTG
ATGATGAATATGCTGCCACAAGTGGTATAATGGATCCAAGAATCATCGTCACAACATCTC
GTGACCCAAGCACTCGTCTCTCGCAATTTGCCAAAGAAATTAAGTCTATTTCCAAATG
CTGTCAGGCTGAACAGAGGTAATTATGTGATGCGCAATCTAGTGGATGCTTGTAATAAATG
CCGGTACTACAGATTTGGTGGTATTACATGAACATAGAGGTGTTCCAACCTCTTTGACCA
TATCACATTTTCCACATGGACCCACTGCACAGTTTAGTTTACACAATGTTGTTATGAGAC
ATGATATTATAAATGCTGGTAACCAAAGCGAAGTGAATCCACATCTAATATTTGATAACT
TTACTACCGCTTTAGGGAAAAGAGTAGTCTGTATTTTAAAGCACTTGTTCAATGCGGGGC
CCAAAAAGATTCCGAAAGAGTAATCACTTTTGCGAATAGGGGTGATTTTCATTAGCGTTA
GACAGCATGTATATGTGAGAACAAGAGAGGGAGTAGAGATTGCCGAAGTTGGTCCTAGAT
TTGAGATGAGGTTGTTTGAAGTGAAGTTGGGAACCTTAGAAAAATAAGGACGCTGATGTTG
AGTGGCAGTTGAGAAGATTCTATAAGGACTGCCAATAAAAAAGACTATTTGTGA

YNL075W, 290 aa (SEQ ID NO 232)

MLRRQARERREYLYRKAQELQDSQLQOKRQIIKQALAQQKPLPKELAEDESLQKDFRYDQ
SLKESEEADDLQVDDEYAATSGIMDPRIIVTTSRDPSTRLSQFAKEIKLLFPNAVRLNRG
NYVMPNLVDACKKSGTTDLVVLHEHRGVPTSLTISHFPHGPTAQFSLHNVMRHDIIINAG
NQSEVNPFLIFDNFTTALGKRVCILKHLFNAGPKKDSERVITFANRGDFISVRQHVYVR
TREGVEIAEVGPRFEMRLFELRLGTLENKDADVEWQLRRFIRTANKKDYL

YNL096C, 1418 bp, exon1: 501-644, intron1: 645-989, exon2:
990-1418 (SEQ ID NO 233)

AAACACCTACTTATAGACACGACCAAACCTTCCACAACCTTTCATCAGAGAGAAATGTTG

FIG. 1 - 80

ATCAAGTTGAATGCGTGAAAGTAGCAATTCGAAACAACAACCTACCTGTCATTCTGCATAG
TAGTAGTTACGAAAGGCACAGAAAAATAACAAAAAAGTCAATTTTCTACGGT
CTCCATCCGTACCTCTTTAAATCCGTACATTATTGTTTTGCTTAATTTCAATATTTCCGA
AAAAGCGAGCGCCCTGGTAAATGTGGTTCAAGCCTGCGAGCCTTTGCTTGGTAACTCAC
CAAATGCAATTCAGTCACGTTCCACACAGTTTGGGTTTCCAGCCTGGCTTTAGGGAAGAA
TGGGCTCACTAGGCGTTTCAATAACGCGGAGGGGAAATACCAAATGCTATTGATTATGG
TTAAATATGTGTTATTTGACTTTGTATATACAAACAGAAGAGAAACCAACACTAAAG
ACTAGACACATAACTGACCAATGTCTCTGTCCAATCCAAGATCTTATCCCAAGCTCCAA
GTGAGTTGGAATTACAAGTCGCCAAGACCTTCATCGATCTAGAAAGCTCCTCTCCAGAAC
TAAAGGCTGACTTGAGACCATTGCAAATCAAATCTATCAGAGAAATATGTTAAAGTTAT
ATAATTTGGAAGCAGCAACATTGTGATTTCTTCTAAAGGGTTCTTTGCAGTAATTTTTT
CAAAAAGAGTGATTTTGAGCAGTATCTGTATGAAATTTTCATGTGTTTCGAGAAATAG
TAATTCGAGAGCTGTCAATACCATGAACGTTGCGATGAGCCTTTGAACTATAAAGGCCCT
CCTTGGTCAGTACCAATATCGATGAATAAAATAGAAGCACGCGAAAAAGACCTTACCCCA
AGGAGAAGAATCACAAACCCTTTTTTGTATGAATGAACCAATTCAGTTACTAATTTTAT
TTCAACGCTGCTTGATTCTTATTGTTTAGATTGATGTCACCGGTGGTAAGAAAGCACTAG
TCCTTTTTGTCCCAGTTCCAGCTTTGTCTGCATACCATAAGGTCCAAACCAAATTGACCC
GTGAATTTGAAAAGAAATTCCTTGACCGTCATGTTATTTTCTTGGCTGAAAGAAGAATCT
TGCCAAAACCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACTTTGA
CTGCTGTTTACGACAAGGTTTGGGAAGACATGGTTTTCCCAACTGAAATTTGTCGGTAAAA
GAGTTAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTTGTTAGACTCCAAGGATG
TTCAACAAATCGACTACAAGTTGGAATCTTTCCAAGCTGTCTACAACAAGTTGACTGGCA
AACAAATTGTTTTTGAAATTTCCAAGCCAGACCAACTAA

YNL096C, 190 aa (SEQ ID NO 234)

MSSVQSKILSQAPSELELQVAKTFIDLESSPELKADLRPLQIKSIREIDVTGGKKALVL
FVPVPALSAYHKVQTKLTRELEKKFPDRHVIFLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKVLEDMVPFTEIVGKRVRYLVGGNKIQKVLLDSKDVQQIDYKLESFQAVYNKLTGKQ
IVFEIPSQTN

YNL162W, 1333 bp, exon1: 501-504, intron1: 505-986, exon2:
987-1333 (SEQ ID NO 235)

TTCATCACCATATAGACTAATGCGTTTTTGGAAACGCCAAACCGCAGTGACAAATAGCAAA
TATGTAGCTGTATATCGGCATATAATAACAGTTTTCTACCAAATGCTGTCTTACATTCA
GAGATCTTACATCCTTACATCTAAAAGTAAACCTAGACATTTACTTCGAGTTATACTTTT
TTTTTATTTATCTATTTTTTCTCTTGGCGACATTTAACACCTGAATTCGCTAACGCCA
GGACTGATCTGCCAGGGAAGGGAGCTTTGTCTAGTGCCAATAGGCCGGACCGTAGGAA
GGTTACAGCAGCTGGCCCGCAGAGTGATTGGGTACAGGAAATAGCGCAACCTTCTCTTT
TGCCCCGGGAAAGGCGGTTCAATCTACCTTCGAAGGGCTAGTACATGAGCGCGAAGGAGGC
AGATAATAGCACCATTAAGTGGTCCAAATGCATCTTGAAATCTAATCCTTAATAGAGGAA
ACAACAATTATCAGTAAAAATGGGTATGTTATAACCATAATTCCTAATGGTGAATAAAA
TCAGGACCAATAAAGAAAAGCTAATTTGATTTTTATTGTCAATGAAATTTCAATATCGTC
ATGAATGCATAAACAGACACACCTAGCAACTGTATAATCTGCGCCTAAAAAGGGCGTATA
CACAAAATAAACGATGCGCAATAAAAGTTTCAGCAGTCAGCAATGAAACCGAGATATGCA
GCAACAGAGTATCATATGCATGGAGGATCCTTTCTGTTTTTCTGATAATATGCTCTGAAA
AAGCTCCAAACAGCAGTAGCCTATTTGTGAAGCTCAAAAAGGCTTCTATTTCCCTCG
CTATCTTCAGATTGTGCAGTGATATCTTTGAGGAAGGAAACGTAGAGGGGATAAGTTGG
ATACTGTTATTTCTTTTCAATATGCTAGATTTTGCTTACCACCTTACTGATTTTTTCTA
ATAATAAACTTTTTTTACTAACATTAGTACGATGTCTCATCTATTTCTTCTATTTAGTTAA
CGTTCCAAAGACCAGAAAGACCTACTGTAAGGGTAAGACCTGTGCTAAGCACACTCAACA
CAAGGTTACTCAATACAAAGCTGGTAAGGCTTCCTTGTGTTGCCCCAAGGTAAGAGACGTTA
TGACCGTAACAATCTGGTTTCGGTGGTCAAACCAAGCCTGTTTTCCACAAGAAAGCTAA
GACTACCAAGAAGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACCAGAGCCCAATT
GACCTTGAAGAGATGCAAGCACTTCGAATTTGGTGGTGAAGAAGCAAAAGGGTCAAGC
TTTGCAATTCTGA

FIG. 1 - 81

YNL162W, 116 aa (SEQ ID NO 236)
MVRCLIIYFFYLVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGF
GGQTKPVFHHKAKTTKKVVLRLCEVKCKTRAQLTLKRCKHFELGGEKKQKGQALQF

YNL178W, 1223 bp, CDS: 501-1223 (SEQ ID NO 237)
GGTCCACGTCAGTTCCACACAATAACATTTACGTAGTGTTACGCGAAGCAGTTACATCT
CAACTAACATAATTGCTGGTGAGCCTACAACACTGCATGCGTAAACGTC AACGGGATTAC
GTTAGTATTTTTGGCCGCCGGTAAATTCCTTGTTTTTTTTCTTGATTTCACCTCTTTT
CATGTTCCCTTTGGAATAATCTAATTCCTCATGATTAAATGAGACTGTTTTTGTTCCTG
AACATCCATACCTTTCCTGTATAATATTCCTTGCTGTAAAGTTTGTTTTTTTATGAAAAA
AACATTTTTCTTTCTTGAGATGAGGCGCCGCGAGCCTTCTCCCATGGGCAGTGGTAAAT
TTTCCAAATCAATGCAGCTCTTTGAAATACAACAGCATTTTTTCATACATTTTAAGCAATT
TCTAGTTTGTAGATATTGTTAGATTAGTTTTTTGAACATTGTTTTGATAACTGAAAATAAA
ACAGCAAACAACTACAAAAATGGTCGCTTTAATCTCTAAGAAAAGAAAGCTAGTCGCTG
ACGGTGTCTTCTACGCTGAATTGAACGAATTCCTTACCAGAGAATTAGCTGAAGAAGGTT
ACTCCGGTGTGTAAGTCCGTGTCACTCCAACCAAGACCGAAGTTATCATCAGAGCTACCA
GAACCTCAAGATGTTTTGGGTGAAAACGGTAGAAGAATCAACGAATTAACCTTGTGGTTC
AAAAGAGATTCAAGTACGCTCCAGGTACTATTGTCTTATATGCTGAAAGAGTTCAAGACC
GTGGTTTGTCCGCTGTGCTCAAGCTGAATCTATGAAATCAAATTTGTTGAACGGTTTGG
CTATCAGAAGAGCTGCTTACGGTGTGCTCAGATACGTTATGGAATCTGGTGCTAAGGGTT
GTGAAGTTGTTGTTTCCGGTAAACTAAGAGCTGCCAGAGCTAAGGCTATGAAATTTGCTG
ACGGTTTCTTGATTCACTCTGGTCAACCAGTCAACGACTTCATTGACACTGCTACTAGAC
ACGCTTTGATGAGACAAGGTGTTTTGGGTATCAAGGTTAAGATTATGAGAGACCCAGCTA
AGAGCAGAAGCTGGTCCAAAGGCTTTGCCAGATGCTGTCAACCATCATTGAACCAAAGAAG
AAGAACCAATTCTTGCTCCATCTGTCAAGGACTACAGACCAGCTGAAGAACTGAAGCTC
AAGCTGAACCAGTTGAAGCTTAG

YNL178W, 240 aa (SEQ ID NO 238)
MVALISKRRKLVDGVFYAELNEFFTRELAEEGYSGVEVRVTPTKTEVIIRATRTQDVLG
ENGRINELTLLVQKRFKYAPGTIVLYAERVQDRGLSAVAQAESMKFKLLNGLAIRRAAY
GVVRYVMESGAKGCEVVVSGKLRAARAKAMKFADGFLIHSGQPVNDFIDTATRHVLMRQG
VLGIKVKIMRDPKASRTGPKALPDAVTIIEPKEEEPILAPSVKDYRPAEETEAQAEPEVA

YNL182C, 2168 bp, CDS: 501-2168 (SEQ ID NO 239)
CTTTGATAAATTAATACGGTAAGATACCGTGTAACCTATTATAATAACTGCCACGCTTAT
AGCATGTACGCTATACATTTACGTGCTGAGCTCCTAGGAAAGCTCATGAGCAGCCACTGT
ATCGTGAGCATAACTACAACAAAGAAATACACAGCGTCACATAGAGGGTTTTTGAGAGGA
GAAGTTGAAATAGGACTTGATCTTGGGGGAGGGGATTTGAAAGCACCCATTCAAGAGT
ATGTGTCTGTAATTGAAGTGTTAGCGCGCGATTCACCTGTAATAAGAGTGATGATTTGAT
AGCGCCATTCTACATCATATGGCAAATGTTGAAAACTGTACGCGCGAACTAAAATTTTT
TTTTACATCCCACTAAATGAAAATTTTAAATCGATGCCCATTCCAAATATGCTTATTCGA
AGGACGGCTCTGACAAGGGCATATGCGTTAAGATTGATTGTTCAATATTCATAAAACAGG
ATCTTTCAAGGGACGATAAAATGGATGAGCAAGTTATTTTTACAACAAATACCTCAGGAA
CAATAGCTTCTGTACACTCATTGTAACAGATAAATTTGAGGCAATGCTCCACTCAATCAA
GAAATAGCTGTGTTCAAGTAGGAAATAAATACCTTTTTTATTGCTCAAGCACAAAAAGCAT
TAATCAATGTCTACAATCTGTCAGGTTCTTTCAAAGAGAATCTGTTGAACAGCGCTTAC
CATTACCTGAAATCCTAAAATGTCTGGAAGTAGTTGAAAATGATGGTGTGCAGTATGATA
GAATTCAAGGTGTCAATCATAATTTACCAGACTTCAATCTTCCGTACCTTTTACTTGGCT
CCACCGAATCGGGTAAATTTGTACATATGGGAGTTAAATTCAGGGATTTTATTGAACGTGA
AGCCTATGGCTCATTACCAAAGTATACCAAGATTAAAGTCCATTTTAAACGGCAAGTATA
TTATTACTTCTGGTAACGATTCGAGAGTTATTATATGGCAAACTGTTGACTTGGTATCAG
CGTCCAATGATGATCCTAAGCCTTTATGTATCCTTACGATCATACTCTACCCGTGACAG
ATTTCCAAGTTTCTTCTAGTCAAGGAAAATTTTATCATGTACTGATACGAAACTCTTCA
CAGTATCTCAAGATGCTACCATTAGATGCTATGATTTGAGTTTAATAGGCAGCAAAAAGA
AGCAGAAGGCAAACGAAAATGACGTTAGTATTGGTAAGACCCCAGTATTGCTTGCGACAT
TTACAACCTCCTTATTCTATCAAATCCATTGTACTGGATCCTGCTGACAGAGCATGCTATA
TTGGTACTGCGGAAGGTTGTTTTTCATTGAATTTATTTTATAAACTAAAGGGTAATGCTA
TCGTTAATCTGCTACAGTCCGCCGGAGTAAACACAGTTCAAAAAGGTAGGGTTTTTTCCC

FIG. 1 - 82

TAGTGCAACGTAACCTCACTAAGTGGCGGCGAAAATGAAGATTTGGATGCACTATATGCAA
 TGGGCCAACTTGTCTGTGAGAATGTCTAAATTCAAATGTGTCATGCCTAGAAATATCAA
 TGGATGGTACATTATTATTGATCGGTGATACGGAGGGGAAAGTTTCTATTGCGGAAATTT
 ACTCAAAACAAATCATTAGAAGTATCCAACTTTAACTACATCACAGGATTACAGTTGGAG
 AAGTGACCAATCTCTTAACCAACCCTTACAGACTCGAACGTGGAAATTTACTTTTTGAAG
 GAGAATCCAAAGGCAAACAACCTAGTAATAATAATGCTCACAATTTTATGAAGATACCAA
 ACTTACAAAGAGTTATCTTTGATGGTAAAAACAAAGGCCATTTACACGATATTTGGTATC
 AGATAGGAGAACCAGAAGCAGAGACAGATCCTAAGCTCGCATTACCCTTAACGACTTTA
 ATGCCTATTTGGAGCAGGTCAAACGCAAGAATCGATATTTTCACATATCGGTAAGGTGT
 CAAGCAATGTAAAGTGATTGACAATAAAATCGACGCCACTTCATCTTTAGACAGCAATG
 CCGCTAAAGATGAGGAAATTACAGAAGTAAAGACCAACATAGAAGCATTAACTCATGCCT
 ACAAGGAGTTACGTGACATGCACGAAAAGCTGTACGAGGAACACCAACAGATGCTTGACA
 AGCAATAA

YNL182C, 555 aa (SEQ ID NO 240)

MDEQVIFTTNTSGTIAVHSFEQINLRQCSTQSRNSCVQVGNKYLFIAQAQKALINVYNL
 SGSFKRESVEQRLPLPEILKCLEVVENDGVQYDRIQGVNHNLPDFNLPYLLLGSTESGKL
 YIWELNSGILLNVKPMHYQSITKIKSILNGKYIITSGNDSRVIIWQTVDLVSASNDPDK
 PLCILHDHDTLPVTDQVSSSQGKFLSCTDTKLFVTSQDATIRCYDLISLIGSKKKQKANEN
 DVSIGKTPVLLATFTTPYSIKSIVLDPADRACYIGTAEGCFSLNLFYKLGNAIVNLLQS
 AGVNTVQKGRVFSLVQRNSLTGGENEDLDALYAMQQLVCENVLNSNVSCLEISMDGTTTTL
 IGDTEGKVSIAEYISKQIIRTIQTLTTSQDSVGEVTNLLTNPYRLERGNLLFEGESKQKQ
 PSNNNGHNFMKIPNLQRFVFDGKNKGHLHDIWYQIGEPEAETDPNLALPLNDFNAYLEQV
 KTQESIFSHIGKVSSNVKVIDNKIDATSSLDNAKDEEITELKTNIETALHAYKELRDM
 HEKLYEEHQMLDKQ

YNL190W, 1115 bp, CDS: 501-1115 (SEQ ID NO 241)

AATGCGCTCCCGTACGTACGTGGCTGTTGCTGAAACGAGACAATTTCTCAATTCGTTTGT
 TTGTGTACTGTATTTGTTATCTTTACTATATATATGTTGTTAAGTTTCTTTTACCAATTA
 GTGCTCACTTCTCTCGTCTTTTATTAGGTGTGTGTGTTGTGCGTAATTTTCGTTTCGCTG
 ATTACTTTATATAGTGTAGTTTGTCTTGAATGTAATAAAGACTTCTGTTTTATTTTGT
 TTGTTATTTAGAAACAGTCTATCTGGTTTAACTTAAACGAGTGAGCTTAAGATAATCTGA
 CTACAAGAAAACCAAGCTTCTATTACTTTGTTTCTTTCTCTTTTCTTTTTTGAATAAAA
 GAATTTTCTTTAAGGAGTAACCTAAGCATTTAGCTGCACATTAAACACTTTTTTTTTTA
 CTTCTAACTCACACACTTTTGGGAAGAACATTTATTTTTTCGACCTTCTTTCCCAAATACC
 CAGCGCTTTATAATTGAAATATGAAGTTCTCTTCTGTTACTGCTATTACTCTAGCCACCG
 TTGCCACCGTTGCCACTGCTAAGAAGGGTGAACATGATTTCACTACCCTTTAACTTTGT
 CACTCGGACGGTAGTTTAACTACTACCACCTCTACTCATACCCTCACAAGTATGGTAAGT
 TCAACAAGACTTCCAAGTCCAAGACCCCAACCACACTGGTACTCACAAGTACGGTAAGT
 TCAACAAGACCTCCAAGTCTAAGACCCCAACCATAACCGGTACTCACAAGTATGGTAAGT
 TCAACAAGACTTCCAAGTCCAAGACTCCAACCATAACCGGTACTCACAAGTACGGTAAGT
 TCAACAAGACCTCCAAGTCTAAGACCCCAACCATAACCGGTACTCACAAGTATGGTAAGT
 TCAACAAAACCAACATGACACTACCCTTATGGTCTCTGGTGAAAAGGCCCGTAAGAACA
 ATGCCGCCCCCTGGTCCATCTAATTTCAACTCCATAAAATTGTTTGGTGTACCCTGGTA
 GTGCTGCCGTAGCCGGTGCCCTTATTACTATTATAA

YNL190W, 204 aa (SEQ ID NO 242)

MKFSSVTAITLATVATVATAKKGEHDFTTTLTSSDGLSTTTTSTHTTHKYGKFNKTSKS
 KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKS
 KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTKHDTTTYGPGEKARKNNAAPGPS
 NFNSIKLFGVTAGSAAVAGALLL

YNL208W, 1115 bp, CDS: 501-1115 (SEQ ID NO 243)

GGTTATACATATATATATATTTTTCATTTTAAATGTCTTAGCTTTGTATCTTAGATGAA
 GTTTTATCTGTATATCAGATCAAGATATCATACAATCATAAATCAATTATTCTTCT
 GTTTCCCTCTTGAGGCATCAAACGAGTGTGTTGACTGATACACACCAACATACTAAGGCA
 ACTTTTCTGGCTGCCCAAAGCTGTGGCACGTATGAACTGCTTTTCGGCTGCATAAAACA

FIG. 1 - 83

ACCATGTGGAGTTTTACTGTATTTCGCATTTGCCCCGCTAGCATTCTTCGTTTCATGCTA
AAAATGAGGCGTGGGCTAATATTTCAGTATTAATAATTCGGCACCCGCACAGCCCATAACC
GGAAAAGGGGCTGGCTGTTGGGCTTGGCAAAAACCTCAATCTGAGCAGTCATTTATAAAG
AAAGACTTTAATTTGTCTTGCTAAACACTTGTAAGCCTTCCAAATATAGATCACTTAAGA
CAATCTAACAAGTGTCCAAAATGTCTGCAAACGAATTCTACTCAAGTGGCCAAACAAGGTC
AATATAACCAGCAAAAACAACCAAGAAAGAACTGGTGCTCCAAACAACGGTCAATATGGTG
CCGACAATGGTAACCCCAACGGTGAACGTGGTTTATTTCCACTATTGTAGGTGGCAGTG
CCGTGCGTACGCTGGATCTAAGGTGTGCAACAACCATTTCTAAGTTGAGTGGTGTGCTGG
GCGCCATAGGTGGTGCAATTCCTTGCCAACAAGATATCTGATGAGCGTAAAGAGCATAAGC
ACAAGAGCAATACGGCAACTCAAACCTTCGGAGGTGCTCCTCAAGGTGGACACAACAACC
ATCACCGTCAGACAATAACAACAATAACGGTGGATTGGCGGTCCAGGCGGCCCTGGCGG
TCAAGGTTTTCGGAAGACAAGGCCCAAGGATTTGGAGGTCCTGGTCCACAAGAGTTTGG
TGGTCCAGGTGGCCAAGGATTCGGTGGTCCAAATCCTCAAGAATTCGGCGGCCAGGTGGC
CAAGGATTCGGTGGTCCAAACCCTCAGGAATTCGGGGCCAAGGTCGTCAAGGATTCAAT
GGCGTTTCACGTTGGTGAATGGCTCAACAGAGTGA

YNL208W, 204 aa (SEQ ID NO 244)

MSANEFYSSGQQGQYNQNNQERTGAPNNGQYAGDNGNPNGERGLFSTIVGGSAGAYAGS
KVSNNHSLSGVLGAIGGAFLANKISDERKEHKQEQYGNSTFGGAPQGGHNNHHRQTIT
TITVDLAVQAALAVKVSSEDKAHKDLEVLVHKSLLVQVAKDSVVQILKNSAARWPRIIRWSK
PSGIRGPRSSRIQWRFTLVNGSTE

YNL210W, 1313 bp, CDS: 501-1313 (SEQ ID NO 245)

TCATAACGGGTTCTTTTCAAAAAACCGTAAAAATTTGAGGTCACACCAACTAAATACAAA
TTGTTTCATCACGGTGACTATATCAAGAACTTCGTAAGGAAACATTTAGAAAACCTCAATA
TAGTAAAGTTTTTCATCAGCAATCTTATCTGAGTAATATTATCTACGATCTAAATATAGGAT
GATCTGCCGATTTAGGAATCGTACTGTAGATTGCTCTTGGCGACAGATATAGTGAAATAC
CTTTTACAAAGTGGATACAGGTTGCCTATCACTACCGCCATTTCACTAGCAAGTAGAGTA
TTGAGAAAACGGTAAACTTTGAAAGTTGCAGATGCAGAATATATATCTGGTTTTGTAGTT
CTATCCGCTAAACGGGACGATCGCATTTTAGCCGCCGACAGTGTTAATATAAGTAATGAA
CTTGGGTTAATTTGATTACGCGTCACAGCTACTAATAAAATAAGACCGAGAGTTTTAATC
AGCTAGTGCATACCAAAAACATGAGTAACCAACACAGCCCTCAGCCATTTTGTTTGGACA
CCAAATTTGGTGAACCTATTAGAAGAGCTCCAGGAGGGAAGCAATTCAACAATAAAAACA
TATTCCTCGGAAAAAGCATTATATTTGAAGCTCGCTCTTGATTATTTCTTTCTCAGAAAGA
ATTTACTAGAGTTTTTGGCTCCACCTTGACAAGATAAAAGGAGTCATTAGACCAAACCTATG
ACACTATATATATTTTTGTGCCTGTTGGAGGTGGATCTCCTCAATCTGGTATTTACCGACA
ATATATTTGGAATATGTTTGGCCAGGTTGTTTCAAGGGAGGACTTGAGGGTTTTTAATA
ATACTTTTTACACATATCACGATAACCGCTACGTATTCTCCAAGAAGACTTTTCTCAAT
TGTTCAAAAAAATCAAAACTAAGGCTTCTGTACTATGTTTACAGTTGAGGAAATTTTTC
TGACAAACCAAGAAATTTTACCTCAAAACTCAACAGTGGCAGAACTGCAAAAGAGCACTA
ATAAAGTACAGACAAATGGGCCGCAACGGCACGATTTTCATAGTCACTCTAGAAATAAAAC
TGAACAAAACACAAATCACTTTCCTCATTGGAGCTAAAGGAACGAGAATTGAAAGCTTGA
GGGAAAAATCAGGCGCCAGCATAAAAATAATACCTATTAGTGATAAAATGACTGCACATG
AAAGGAACCAACCCTGAATCTGTTCAACAAACAATACTAATTTCCGGGTGACTTATACCTCA
TTGCATTAGCCGTCACCAGTATAGAGTCTGCATTAATTACTTTGGATTTATAG

YNL210W, 270 aa (SEQ ID NO 246)

MSNQHSPQPFCLDTKLVLLEELQEGKQFNNKNIFPEKALYLKLALDYSFFRKNLLEFCV
HLDKIKGVIRPNYDTIYILCLLEVLLNLVFTDNILEICLPRFVSREDLRVFNNTFYTYH
DNRLRILQEDFSQLFKKIKTKASVLCFTVEEIFLTNQEILPQNSTVAELQKSTNKVQTNQ
PQRHDFIVTLEIKLNKTQITFLIGAKGTRESLREKSGASIKIIPISDKMTAHERNHPE
VQQTILISGDLYSIALAVTSIESALITLDL

YOL031C, 1766 bp, CDS: 501-1766 (SEQ ID NO 247)

AGTTTTTTTTTCTCGAGAAATTTGTGAACAAAAGAAAGCAAAGACACAGAAGATGATAAGAG
AGAGAAACAACGAAGAAAGAACAACAATGTTGGGGTTCACCCGAGAGATATTGACATACT
GACCTTAGAAAAGGCATTACTGAGGCTACTGACTAAAGCGCGTTACATAAATGCATAGTA
TATTTCTTGTTGTATACGCAGCGGCCAACTAGTGGCAGCAAGAATGTAATGAACGATTCA

FIG. 1 - 84

TCTGCAGGTTTGGAGGCCGCAACTAGATCAAAACGTAAATAGCGGGTGAAGTGTCTGGA
CGTTAGAAGTAACGTCCGCAGATCGAAGCTAAACACGAGATTAGATTTCCGGTAACGGAA
TTGTGATAATTAAGAAAGACCAGACTATGTGAAAAGGCCACGTAAATGATAGAGCACACA
TTAGCAACTATAATAGACTAGTTTTCGCATCGCTGGAAGTTCTCGATATTGAATATCACT
TCCAAGAACGCAAACTTAGAATGGTCCGGATTCTTCCCATAATTTTGAGCGCCCTATCTT
CGAAATTAGTGGCGAGTACAATATTGCATTCATCCATACACTCAGTGCCATCTGGAGGCG
AAATCATATCTGCAGAAGATCTTAAAGAACTTGAAATTTTCAGGGAATTCGATCTGCGTTG
ATAATCGTTGCTATCCTAAGATATTTGAACCAAGACACGATTGGCAGCCCATACTGCCAG
GTCAAGAACTCCCCGGTGGTTTGGACATTAGAATAAACATGGACACAGGTTTAAAGAGG
CAAACTAAATGATGAGAAGAATGTCGGTGATAATGGTAGCCATGAGTTAATTGTATCTT
CAGAAGACATGAAAGCATCGCTTGGTGACTATGAATTTTCCAGTGATTTCAAAGAAATGA
GAAACATCATAGATTCTAACCCGACTTTATCTTTCACAGGACATTGCCAGATTGGAGGATA
GTTTTGATAGAATAATGGAATTTGCGCATGATTACAAGCACGGCTACAAAATTATTACCC
ATGAATTCGCCCTCTTGGCCAACTTAGTCTCAATGAAAATTTGCCGTTAACATTGAGAG
AGCTCAGTACTAGAGTCATTACCAGCTGCTTGAGAAACAATCCTCCTGTAGTCGAGTTCA
TTAATGAAAGTTTTCAAAATTTTAAAAGCAAAATCATGGCCGCTCTGTCAAATTTGAATG
ATTCTAACACAGATCCTCTAATATCCTAATAAAAAGATACTTGTCCATTTTAAACGAAT
TACCTGTACATCCGAAGATCTTCCATATATCTTACGGTTGTTTTACAAAATGTATATG
AAAGAAACAACAAGGACAAACAGTTACAAATAAAAGTCTGGAGTTGATCAGCAAAATTT
TGAAGGCCGACATGTACGAAAATGACGATACAAATCTAATTTTGTTCAAAAGAAATGCTG
AGAATTGGTTCGTCAAATCTGCAAGAGTGGGCAAACGAGTTCCAAGAGATGGTCCAGAACA
AAAGTATAGATGAACACATACAAGAAGCTTTTTTGACACCCTTTACAACCTGAAGAAAA
TTTTTCAAAGTGACATCACGATCAACAAAGGGTTTTTGAATTGGTTAGCGCAACAATGTA
AAGCCAGGCAATCTAACTTGGACAATGGGCTCCAAGAGAGAGATACTGAACAAGACTCAT
TTGATAAGAACTTATCGACAGCAGACACTTGATCTTTGGCAACCCCATGGCTCATAGAA
TAAAAAATTTTCAGAGATGAACTCTGA

YOL031C, 421 aa (SEQ ID NO 248)

MVRILPIILSALSSKLVASTILHSSIHSVPSGGEIISAEDLKELEISGNSICVDNRCYPK
IFEPRHWDQPIPLPGQELPGGLDIRINMDTGLKEAKLNDEKNVGDNGSHELIVSSEDMKAS
PGDYEFSSDFKEMRNIIDSNTPLSSQDIARLEDSFDRIMEFAHDYKHGYKIIITHEFALLA
NLSLNENLPLTLRELSTRVITSLRNNPPVVEFINESFPNFKSKIMAALSNLNDSNHRSS
NILIKRYLSILNELPVTSEDLPYISTVVLQNVYERNNKDKQLQIKVLELISKILKADMYE
NDDTNLILFKRNAENWSSNLQEWANEFQEMVQNKSIDELHTRTFDLYNLKKIFKSDIT
INKGFLNWLAAQQCKARQSNLDNGLQERDTEQDSFDKKLIDSRHLIFGNPMAHRIKNFRDE
L

YOL048C, 821 bp, CDS: 501-821 (SEQ ID NO 249)

TAAGTACATGATTTTTGTTTGCATTGATATGACTTGTTTTATGACTAACATATTTAATTT
TTATTTGTTAACCGTAGGGGTTTTATGAAGTGCTGACGAATCCTGTTTATTGGAAGCATA
TTTTACTGTTTGGCGTTTGCTATGCCCTGATTTTTGTCACTATTGCTGGTCTCTTTATG
TCACACTTGTACCGCTTTTAGTGACATGGGCCATACTGTTATTAGGGCCTCTTGGTGTGA
TACTGGTTCATATTCAATGGATTTTACAAACGAATGCTCTTGACTGCCTTTGTTTGTAGAA
CACTGGTCTTGACCCATATTACGAATCAGATATTTGATATATCTTTGGTGTGCAAGACC
AAGATGAATTTCTAAACGAGGTGAAGGTATTGCCTAAACCACAAAAGCCACATAGAAAAA
TCGATGAACCTGATGCGGTGAGAAATTTCAACACAATAAAGGGAAGTCGGATTTTAAAGA
TTCCCAGATTACTATTGAGAATGTTTTTAAAGTCTCCAATTTTACTTCACTAACATTAC
TGTCGCTAATTCCTATTGTAGGACCAATCTTGGCAAATCACTAATGGCCCCAAAAAGAA
CCTTTACCTATTTGCAGAGGTACTTTTTACTAAAGGGATTGAGTAAGAAACAGGCCAAAG
ATTTTCAGTACGAGCATTACGCAAGTTTCATATGTTTCGGTATGTCTGCCGGTCTACTAG
AGTTAATACCCTTCTTACAATAGTCACCATATCTAGCAACACTGTTGGTGCAGCTAAAT
GGTGTACTTCGCTACTAAAGGGTGAAAGAAAGAAGGAATGA

YOL048C, 106 aa (SEQ ID NO 250)

MFFKVSNFTSLTLLSLPIVGPILANQLMAPKRTFTYLQRYFLLKGFSSKKQAKDFQYEHY
ASFICFGMSAGLLELIPFFTIVTISSTNTVGAAKWCTSLKGERKKE

FIG. 1 - 85

YOR010C, 1256 bp, CDS: 501-1256 (SEQ ID NO 251)
ACATTTCCCAAAAAAGACATTTCTGTCCAAAAGTAGAAGGCAAGAAAACCTTGGAGGAAT
CATAGGCAAAGAAAAGAAAAGAAGTTTCATCTTTAAACTACCTTTCAAGCCTTTATTC
GTTCCCTCGTAAAGGACACACGAAAAAATAAACAGTACCTTGCAGAAGGAGTGCAGAGTT
AGGTCGCAGGGAATCCTTGAAAGCCAAGAGTTTTCCTCGTAATGATCTCCCAAAGCAA
CCATCAACATTGTGGTGCAAAGTTTAGTGTAAGATGTTCTACTGAACTATCTTAATAGCT
GAGCATCATGTGAGTAAACGAGTAAGCAAGAAAACAACAAAGTAATGTTCAACTTTTCGTA
ACTACGGAATAATATATAAGTAGTTAACGAAATTCGAACAATGAGAGCTCTCACATAT
CATCTTCTTTTCCAGTTTAGCCATTATCAGCACAAATAACAAAACACACTCGTACACTC
GCTTCAACTATAACAAAAAATGGCTTACATCAAGATCGCTTTATTAGCTGCTATCGCTG
CTTTGGCTTCTGCCAAACTCAGGAAGAAATTGACGAATTGAACGTTATTTTGAATGACG
TTAAGTCCAACCTGCAAGAATATATTAGTTTGGCTGAAGATTCTTCATCTGGATTTTCCT
TAAGCAGTCTGCCATCTGGTGTGTTTAGACATCGGTTTAGCTTTGGCTTCCGCCACTGATG
ACTCCTACACTACTTTGTACTCTGAGGTTGACTTTGCTGCTGTTAGCAAGATGTTGACCA
TGGTTCATGGTATTCTTCCAGGCTTCTACCAGAATTGGAATCCTTGTTAGGAACCTTCTA
CCACCGCTGCCTCTTCTACTGAAGCTTCTTCTGCTGCTACTTCTTCCGCTGTTGCTTCCT
CCAGTGAAACTACTTCTTCTGCGCTGCTTCTCCAGTGAAGCTACTTCTTCTGCGCTCG
CTTCTTCCAGTGAAGCTTCTTCTTCTGCTGCTACTTCTTCTGCTGCTGCTTCTTCCAGTG
AGGCTACTCTTCCACCGTCGCTTCTTCTACCAAGGCTGCCTCTTCCACTAAGGCTTCTT
CCTCTGCTGTTTCTTCCAGCTGTTGCTTCTTCCACCAAGCCTCCGCCATTCTCTCAAATCA
GTGATGGTCAAGTTCAAGCCACTAGCACTGTTTCCGAACAACTGAAAACGGTGCTGCCA
AGGCTGTCATCGGTATGGGTGCTGGTGTGTCATGGCCGCTGCCGCCATGTTATTATAA

YOR010C, 251 aa (SEQ ID NO 252)
MAYIKIALLAIAALASAQTQEEIDELNVILNDVKSNNLQEYISLAEDSSSGFSLSSLP
VLDIGLALASATDDSYTLYSEVDFAAVSKMLTMVPWYSSRLLELESLLGTSTTAASST
EASSAATSSAVASSSETTSSAVASSSEATSSAVASSSEASSAATSSAVASSSEATSSSTV
ASSTKAASSTKASSAVSSAVASSTKASAIQISDGQVQATSTVSEQTENGAAKAVIGMG
AGVMAAAAML

YOR019W, 2693 bp, CDS: 501-2693 (SEQ ID NO 253)
CATTGATCTCGAGCAGCTGCTCTTTTCTCTCAATGAATTACGTTATGTTAATCACA
CAAGCATCAGTTTTTCATCGCAAAGAAAATATTTAGAGTTCTTGCAATTCAGATGTACC
TCAATTAATAACTCAATCACCTCCTATGTTCTTGCTGGTAGTACTGCTTTTGTCTTAATT
ACTGCTGAATCAGCCTTCTAGAAGACCGTTCTGTTTCAGCCGCTCGCCCCCTTTTCAAAGC
TTGCGCGGCTGAGTTTATGAGGGGCGGCTTTTGTGTAATGGCAATCTACCATTATTAG
TAGCAATATGATTTGCAGATAGATACATATATATCCTTCTGGGTTCATGTCCTCGTTACCA
TCCACACTAATGCATAGGACCAGAAAGAAAGGACATCGAATCCAACACGTATTAATAA
GGACTCCTCATTAATAAAGGCTTTTAATATTCAACTTGCTATAGATCAGCACCCTTTTGG
CAAGTCAACCTTAAATTATTATGATTTCTGTTTGCCCAAAAATGACTTGCAAAAATGCT
ACAGAAGCCTCACATTCGATGTTCCAGGACAACAATTCGAAGAGAGAAATGAACAAAACC
TTAAAAACGGGCCAAAAAGAAAGGCAGTTTCCAACCATCTGTTGCCCTTGTACACAGTGC
CTTCCACCGCTGGTTATTTCTTCTATAGACGACAGCAGGGAAGGATTCAAAGGTGTACCTG
TTCCCAACTATTACACGATGGAAGAGTGCTATGACGATGAAACAGACTCTTTTTCGCCAA
ATTTGCAATATTATTGAGAGATACATTCCAATCATCACCTTTTCTGAATACTAGAAAAG
AGAACAAATCTGAATCCAGTAGTTTTCGAATGAGATCCTCAAAGTTGTTGGAAAAGAATT
CTGACATCAAAAAATATTCTTGGTATCCAAGAAATGGAAAAATAGTGAGGAGAGACTATC
CAAGCACGCCAGTAATTGTCAACGAAACGTTGATGATAAACAGGTTTGAAAAGAACTGGA
TAAAGTTATGGCGCCAAAGAAACTACAAATAAATGAAAGGCTGAATGACAAAAAAAAT
GGTTTACTTACCCAGAACTTATCTTCTGAAAGAGCGTATTAAACCGTTATATAGAGGAG
ATGATAGTGACCATGTACAAAAGAACAAAAAGAAAGCATAAAATACTTCAACAAAAGG
TCGGATATCCCAATAACCTAAGACAATAGTTTGTACATTAAACGGAAAAAACATACGT
GGGTTGCCCTAGACTGGACAGTCTACAAGTTTGCACGAAATCTTGATCACATTGTTGTCA
TAACTACACTGCCAAAAATGATTTCTAACAGGAAAAAACTGCAAAAGATGATACAGAAT
GGGCACCGGGATATCAAAAAGAAAGTAATAGATCAAAAATTAAACGACATTTTGTATTATA
TTTACAGCTAGTAAAGTGGTCAAAATATCCGTCAAAATTACTTTAGAAATAATTGTAG
GCAAAATTAAAAAAGTCTGGTAGATGTCAATATGTCCATACTCCAGATTTCTTAGTTT
TTGCTACTTTAAAGCACGAGCGAAATGAGAATCTTATTACATATAAATCCAAAAGCTGA

FIG. 1 - 86

CAGATGTCCTTCTGTTAGTTATCCGATTCCCACATTTGTTGTTCCCTCGAAACGAATGT
ATTCGTTTCGAACGAATCTACAAAGAGAAGTAAATGAACATTATGTCTCAAAAAATCATA
TGAAGCACGAACACACTGACGTTGAGAGCATGAGCAGTTCAATGTTCAAAAAAATACAA
TATCAGATATTTCTTACATATTTCCGCTAGATTTCGTACGCCGAAGATTTCAAAAGGCAAG
GCTACATCAAAAAGCAGTTCAACACCTCTAATGATTCCATTCCAAGAAAATTGACCGGTC
TCGCCCAGCATTCAAGAAGGAAGATCACGGGTGATATAGAAAAATTACAAGACGATGAGA
AAGATAGAGAATGTACTAAGGAAAACTTTTGTGTTGAAGAAAATTGATATCATAATTAGAG
AGTCATTGAAGTCTTCTTTAGCGATAGAGACGTTGCCTGGTAAAAATGTATCGCAGTCCA
GTCACGGTGACCAAATTTCCAGCTTTAAGAATGCTTTGATAGGCAATGGGTGCAAAAAACA
CAAAGTTTAGAAAATCTTTAATACCATATTTCTTCTCAGAGGAACAAAATACCACAACAA
CTATTAAACTCAGTAGCTCGCTACGTCCCAATCAAGTTTGCAACCTCTGTAAAAACACA
AAGATGGAAGAGCCGCCCTTGGCAAAGCCAGAAATCTGCCTGATATAAGGCACAGTATTT
CCTTCGACAAAGAAAATTCCTTTGATCCATCTGATAAAAGCAGTAGTGTGATAATAGCA
TTCTTTTGGAGAAAGTTAAAGTGCCGGTGCCTTAAGAAAAGTCAAACTAATGACTCCT
CAAGTAGTGACGGGTCAAAGAAAAGCTCGTCTAGTTTGTAGTACTGTGAACACCTTCACGT
GGGGTGGAGTTGGGATTTTAAAGGTGTTTAAAGTGGAAGTTCTCTGGAAATAAATCAT
CCAGTAGAAGGAATAGTAGCAGTGGCGATGTTTGTGAAAGTGATGATCGTAACGACAAGA
AAAAGAAGAAGAAAAAAGAAGAAATCATTGTTCTTATTCGGCAAAATATGA

YOR019W, 730 aa (SEQ ID NO 254)

MISVCPQNDLQKCYRSLTFDVPQGQFEERNEQNLKKRAKKKGSFQPSVAFDTPVSTAGYS
SIDDSREGFKGVFPVFNYYTMEECYDDETSFSPNLQYYLRDTFQSSPFLNTRKENKSESS
SFPMRSSKLEKNSDIKKYFLVSKNGKIVRRDYPSTPVIVNETLMINRFKNWIKLRQR
KLQINERLNDKKKWFYTYPELIFSEERIKPLYRGDDSAPECTKEQKRKHILQOKVGYPNNP
KTIVCHINGKKHTWVALDWTFVYKFARNLDHIVVITTLPKMISNRKKTAKDDTEWAPGYQK
EVIDQKLNDIFDYILQLVKVKISVKITLEIIVGKIKKSLVDVINVHTPDLVLATLKHE
RNENLITYKSKKLTDFVPVSYPIPTFVVP SKRMYSFELNLQREVNEHYVSKNHMKHEHTD
VESMSSSMFKKNTISDISHSISVDSYAEDFKRQGYIKKQFNTSNDISPRKLTGLAQHSRR
KITGDIKLODDEKRECTKEKLLKKIDII IRESLKSSLAIEITLPKNVSQSSHGDQIS
SFKNALIGNGSKNTKFRKSLIPYSSSEEQNTTTIKLSSSPTSQIKFATSVKHKDGRAAL
GKARNLPDIRHSISFDKENSFDPSDKSSSVDNSIPLRKVKSAGALRKVKTNDSSSSAGSK
KSSSSFSVTNTFTGGGVGIFKVKSGSSSGNKSSSRNSSSGDVFESDDRNDKKKKKKK
KKSFLFLFGKI

YOR027W, 2270 bp, CDS: 501-2270 (SEQ ID NO 255)

AATTTTCCCCCGTCATAAGTTCTTATACACGGCTGGCTCTGATGGCATAATTTTCATGCT
GGAACCTACAAACCCGCAAGAAAATAAAAAATTTCCGCAAATTTAACGAAGACAGCGTGG
TTAAAATTGCTTGTTCGGACAATATTTCTATGTCTGGCAACTTCTGATGATACTTTCAAGA
CAAACGCCGAATTGACCAAACTATTGAACATAACGCAAGTTCAATATACATAATATTTG
ACTATGAGAACTGATATCTTCGTGAAGATTCGTGTAGTATGATAGAACATTCCAGAAAAA
AAATTCAGATTCATCGCTCTCTCTTCGCTTCTCCTCCTTTAAGGAATAAAGAAAAATCA
CATACATAGATTAAGTAAATAGGATCTGCTAGAAAAATTATATATAGATCAATCATCTTA
TTAAGGTATCTTGTTTAAGCCCAAAGTCTGCTCCCAAATTCCTCACTGTAGCTACTAAA
ACAACCTATACGCAAGAAAGATGTCATTGACAGCCGATGAATACAAACAACAAGGTAACG
CTGCATTTACCGCTAAGGATTACGATAAAGCGATAGAGCTCTTCACTAAAGCTATTGAAG
TTTCTGAAACTCCAAACCATGTTTTATATTCTAACAGGTCCGCTGTTATACTTCTTTAA
AGAAATTTAGTGACGCATTGAATGATGCTAATGAATGTGTCAAAATCAATCCATCTTGGT
CTAAGGGTTATAATAGACTCGGTGCCGCCCACTTAGGTCTTGGCGATCTCGACGAAGCTG
AAAGCAACTACAAAAAGCCTTGGAGTTGGATGCCAGTAACAAGGCCGCCAAGAAGGAT
TGGATCAGGTTTCATCGTACCCAACAGGCAAGACAGGCACAGCCTGATTTAGGGTTGACAC
AGTTGTTTGTGCTGACCCAAATTTAATTGAAAATTTAAAGAAGAACCCAAAACTAGCGAAA
TGATGAAGGACCTCAATTAGTGGCTAAACTGATTGGGTACAAAACAAATCCGCAAGCTA
TTGGCCAAGATCTGTTTACTGATCCAAGATTAATGACCATCATGGCTACATTGATGGGG
TTGATTTAAACATGGATGATATAAACCAATCAAACTCCATGCCAAAGGAACCGGAAACCA
GTAAAAGCACTGAACAAAAAGAGATGCTGAACCACAAAGCGATTCCACTACGAGCAAGG
AAAATTCCTCTAAAGCACACAGAAAGAAGAAAGTAAGGAATCCGAGCCAATGGAAGTTG
ATGAAGATGACTCTAAAATGAGGCCGACAAGGAAAAGGCCGAAGGTAACAAGTTTACA
AGGCACGTCAATTCGATGAAGCTATAGAGCACTACAACAAGCGTGGGAACTGCATAAAG

FIG. 1 - 87

ATATTACCTATTTAAACAACCGTGCTGCTGCTGAATACGAAAAAGGCGAATACGAGACAG
CTATTTCTACCTTGAATGATGCTGTTGAGCAAGGTAGAGAAATGAGAGCGGATTACAAGG
TCATTTCCAAATCATTGCGCGTATTGGTAATGCCTATCACAAATTGGGTGACTTGAAGA
AACTATAGAATACTACCAAAAATCATTGACCGAACATCGTACTGCTGACATTTTGACCA
AGTTAAGGAATGCTGAAAAAGAATTGAAGAAAGCTGAGGCGGAGGCGTATGTTAACCTTG
AAAAGGCGGAGGAAGCCCGTCTTGAAGGTAAGGAATATTTTACCAAGAGTGATTGGCCGA
ATGCTGTTAAGGCTTACACTGAAATGATCAAAAGGGCACCTGAAGATGCTAGAGGATATT
CTAATAGAGCTGCTGCACTAGCGAAGTTAATGTCTTTCCCTGAAGCTATCGCAGATTGTA
ACAAAGCCATTGAAAAAGATCCAAATTTCTGTGAGAGCTTATATCAGAAAGGCCACCGCAC
AAATTGCTGTTAAAGAATATGCTTCCGCTTTGGAAACACTAGATGCGGCCAGAACCAGAG
ATGCTGAAGTGAATAATGGTTCTAGTGCAAGGGAAATTGATCAACTGTACTACAAGGCAA
GCCAACAAAGATTCCAACCTGGTACCAGTAACGAAACCCAGAAGAAACCTATCAAAGGG
CCATGAAAGATCCTGAAGTGGCTGCGATCATGCAAGATCCTGTTATGCAAAGTATTTTGC
AGCAGGCCCAACAGAATCCCGCTGCTTTACAAGAACACATGAAAAATCCAGAAGTATTCA
AAAAGATTACAGACGTTGATCGCTGCTGGTATCATCCGGACTGGCCGCTAA

YOR027W, 589 aa (SEQ ID NO 256)

MSLTADEYKQQGNAAFTAKDYDKAIELFTKAIEVSETPNHVLYSNRSACYTSLKKFSDAL
NDANECVKINPSWSKGYNRLGAAHLGLGDLDEAESNYKKALELDASNKAAKEGLDQVHRT
QQARQAQPDGLTLQFADPNLIENLKKNPKTSEMMKDPQLVAKLIGYKQNPQAIGQDLFT
DPRMLTIMATLMGVLDLNMDDINQSNMPEKETSKSTEQKKDAEPQSDSTTSKENS SKAP
QKEESKESEPEMEVDEDDSKIEADKEKAEGNKFYKARQFDEALEHYNKAWELHKDI TYLNN
RAAAEYKEGEYETAISTLNDAVEQGREMRADYKVISKSFARIGNAYHKLGLDKKTI EYYQ
KSLTEHRTADILTKLRNAEKELKKAEEAYVNPEKAEERLEGKEYFTKSDWPNVAVKAYT
EMIKRAPEDARGYSNRAAALAKLMSFPEAIADCNKAIEKDPNFVRAYIRKATAQIAVKEY
ASALETLDAAARTKDAEVNNGSSAREIDQLYYKASQORFQPGTSNETPEETYQRAMKDPEV
AAIMQDPVMQSILQQAQQNPAALQEHMKNPEVFKKIQTILIAAGIIRTGR

YOR031W, 710 bp, CDS: 501-710 (SEQ ID NO 257)

CTGCAGAAGTACAGCTGCCTTTATTTCTTGTGGTCATTTATTGCTTTTATTTTCAAGTCA
GATATACAAGAAAAATCAAATCCCATCGTCAACGTCACGTATAAACGATTAATTTACAGTA
ATACCATACTCTACCAACATTATTTTAGTCCGACGTTTCAGTCTGTAGGTGTTCCAAATC
CTTCTGGCATTGACTTCTGTGCAGAAACCTTCAAATGAGTTCACCTTTACGTCAGATC
GCATAACAACCGGTCAATATTTTTTTCTTTTGCTAAACCCCTACTGCAAGCACTTTTA
AGAAAAAGAACAAATAATGCGTCTTTATTGCTGTGTGGAAGTGATTTTTGTCTTTCCGAC
AAAAAAGGATAGGGATGCGAGAGGGCTGTGAAGTAGTGATCAAGCGGGGCTATATAAG
AAGGCGGCACATCGTCCCCCTAAGAATAGCGAAGCGATATTACACTGAACACTACAATG
TCAAATAGTACTCAATAAATATGACTGTAAAAATATGTGACTGTGAAGGCGAATGTTGTA
AGGACTCTTGTCAATTGTGGGAGCACCTGCCTTCCAAGCTGTTCTGGCGGTGAAAAGTGCA
AATGTGATCACAGCACCGGAAGCCCTCAATGTAAGAGTTGTGGTGAAAAATGCAATGCG
AAACCACGTGCACTTGTGAAAAGAGTAAATGCAATTGTGAAAAATGTTAG

YOR031W, 69 aa (SEQ ID NO 258)

MTVKICDCEGECKDSCHCGSTCLPSCSGGEKCKCDHSTGSPQCKSCGEKCKCETTCTCE
KSKCNCEK

YOR096W, 1474 bp, exon1: 501-644, intron1: 645-1045, exon2:
1046-1474 (SEQ ID NO 259)

AAACCCATACACAATGAACCTTATCACACCCAAACATATGATATGGTATTAAAAAATGAA
AAAAATTCATTATTCTTTAGCGTAATTATTGAAGAAAAACAGTGC GCGCGGTAATTTTT
TGTCACCTCAGTAAGTACGAGAGAAGCCGAATGTACTCCCCCGGCTAGCTGGAGACCATGGC
TCTGCCTAGGATTTCTCTTATGCTTTCTTTTACCAATCACTTTGTTCCGGCGAGGCCCG
CGAAGCTCGCTTTCTTTTACGCTAGCAATCATGTTCTTGCCAGCGTCGTAGACTACTGTA
TGGCAGTTGCTGCACTTGCCATGAATATCCTAGTGAAGCCTCTATGCAATAATCCAGTTA
CTGCGTTAGAATCCTGGTAAAATGTCTAATCTTATTACATTACAGCAACGTATTAGATTT
TGATTGAAAATTAGTCTTGGCACTTGGTATATATCTTATTTTAAAGAAAGCTGAAAGGAA
GAAAGATCATCACGAACAACATGTCTGCTCCACAAGCCAAGATTTTGTCTCAAGCTCCAA
CTGAATTGGAATTACAAGTTGCTCAAGCTTTCTGTTGAATTGGAAAAATCTTCTCCAGAAT

FIG. 1 - 88

TGAAAGCTGAGTTGAGACCTTTGCAATTCAAGTCCATCAGAGAAGTATGTTATTAATTTG
AATCTAAACTTAAGAATAATGGAGAGTAACAAAGGAAAAAGTGTGAACGGGACGATACC
AGAATGTTTCAATCTAGAAAAGTATAAAAGATAAGGACTAGGACTCAAATGTATTTGGCT
GACTATCGCCTGAACCTTGATGCTAAGCAAATACCATATCTTCAAGAAAAAGCCTACTCC
AGTGTTTAAGAAGAAGGGAACGATTTACTAGATCATGCTATACGCAGTAAGGTTCTGATA
GTTAATTACAATCGGTCCAAGTTCTAAGCGGTGTCGTCCATGCATATATCATTTACAAGT
TACTGGCGTCAACTCTTCAAATATTTCAAATATCACCTAATCAAACCTTACTAACATTTTC
CTTTTTTGTTCCTTCTTTTATAGATCGACGTTGCTGGTGGTAAGAAGGCTTTGGCCAT
TTTTGTTCAGTCCCATCTTTGGCTGGTTTCCACAAGGTTCAAACCTAAGTTGACCCGTGA
ATTGGAAGAAATFCCAAGACCGTCATGTCATCTTCTTGGCTGAAAGAAGAATCTTGCC
AAAGCCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACCTTGACTGC
TGTTTCATGACAAGATCTTGAAGACTTAGTCTTCCCAACTGAAATCGTTGGTAAGAGAGT
TAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTTGTTAGACTCAAAGGATGTCCA
ACAAATCGACTACAAATGGAATCTTTCCAAGCTGTTTACAACAAATTGACTGGTAAGCA
AATTGTTTTCGAAATCCAAGTGAAACTCATTAG

YOR096W, 190 aa (SEQ ID NO 260)

MSAPQAKILSQAPTELELQVAQAFVELENSSELPKAE LRPLQFKSIREIDVAGGKKALAI
FVPVPSLAGFHKVQTKLTRELEKKFQDRHVI FLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKILEDLVFPTEIVGKRVRYLVGGNKIQKVL LDSKD VQIDYKLESFQAVYNKLTGKQ
IVFEIPSETH

YOR248W, 803 bp, CDS: 501-803 (SEQ ID NO 261)

ACCCATTTTACAAATTTTTTTTGTCTATTTGAGCCATAGTACCCATTAATAGGTCCTCGTCC
ATTCCCTTGTTTTTTTTATTGTTTCAATTACACTACATAATTAAAAATCACATCACCTT
TCACTCTCACCTTAGTCGTTCTTTATCAACCAAAAATAAAAAATGCTTCAATCCGTTGT
CTTTTTCGCTCTTTTAACCTTCGCAAGTTCTGTGTCAGCGATTTATTCAAACAATACTGT
TTCTACAACCTACCACTTTAGCGGCCAGCTACTCCTTGGTGGCCCAAGAGACTACCATATC
GTACGCCGACGACACCACTACCTTTTTTGTCACTCAACGGTCTACTCCACGAGCTGGTT
CACCTCAACTTCAGCCACCATTACCAATGCGGCCTCCTCCTCCTTGTCCACCTCTTCGGC
TCTTGATCTGTAAACCCAGAAATCCACCCATGAAATTACCTCCACCTCGACTATCACGTC
CACTTTGCTGCTAACCCCTCATGACTCCACTACTTTGTCTCCATCATCTACTGCAGCAAG
TGTCAGTGACGAAGATTCAAACAACAAAGATGCAAAGGTCAAGTCCTTTGAACAGGCTTC
AACTTTCAATGGTTGCGTCCCAATCACAAAGTTTGTCACTGTACCAATGAGCCCGTTAC
CCAGTACGTTACAGTCACCCCAAATACGACTACACAATACGTTACTGTACCCGGTGCACC
TTCTGTTACCACTACCTCTCCAGGTAACGTACAATGGTACAACACCACTTCGATTACTAA
TTCGACCAGTTGGTGAATTATGA

YOR248W, 100 aa (SEQ ID NO 262)

MTPLLCLHLLQQVSVTKIQTTKMQRSSPLNRLQLPMVASQSQSLSLSPMSPLPSTLQSP
QIRLHNTLLSPVHLLPLPLQVTYNGTTPRLLLIRPVGEL

YOR293W, 1255 bp, exon1: 501-552, intron1: 553-989, exon2:
990-1255 (SEQ ID NO 263)

AACTTTTCGAAATATATACTCTGAGTTCTTGCTCCCCGTTTTGTACGATGTTCTTAATGCA
AACACACGTCCTTTAAAGATCCCCTGATAGGTTTCATTAAAGGCAACTTCCATACACGTT
GAAGTGCCAATTTTTTCCCTACATCCAAGCATCTGGGTTTGTATGGGTGTTACACCGGT
TTTTCTTTTTTATTTCAGAGAAGTACAATTTTAGGCGGGTTTCAAATTTCCCTGTGTG
CGAGAAACGCTCCGGTACGCCCTAGGCTCACTCCGGTCTTCTCCCCATTTCTATCAGCGC
GATAGGCATACTGTGGGAGAGCGGCCTAGGGAGACCGGTGGGAAGCACCGTATCTAGTA
ACGCACGCTCTTTTGCAAAAATATCCATTAATTGCATGTAACCTAGATTAACTGGTAT
TAAGATTTTCGAAATTTGGGCTGGATTATTAAGGTGAGTAGCAAAGTTTAGCAAGAACA
GTACGAACTAAGTAGCCAAGATGTTGATGCCAAAGGAAGACAGAAACAAGATCCACCAAT
ACTTATTCCAAGGTATGTTTGAATAAATTTTCAAGAAAGCATGAAGATACACGGAAAGTC
AAGCGAGGGAAGTTATGCGTATACACAGTAGCGGTAGTGTGCATTACATACACGATGTT
TCAAACACACAGATGGATACCATGCATATGAGGTTAAAGGATTTCTTATGAATATATTAG
TGGATTACATAGAAGAAATTACAAGGAACCGTGTGACGACATTTTCGAAAGGACAGCACA
AGGCCATCGACCTCGAGACGTATGAAATATGGTATACGTCCTATATTTGGGCAAGAAAA

FIG. 1 - 89

CGGTAAACTGTTTTACGCGGAGATCCAACTTTTGATCCTTACCGAGTACCACGAATCAT
CTATATGATCTTTTTACTAACTTATCTTCAATTTCAACGGAGAGATGTAAACATCATTCT
CTCCTATGATAATTTCTTTTTTTATACAGAAGGTGTTGTTGTCGCCAAGAAGGATTTCAA
CCAAGCCAAGCACGAAGAAATTGACACCAAGAACTTGTATGTCATTAAGGCTTTACAATC
CTTGACTTCTAAGGGTTACGTCAAGACTCAATTCTCATGGCAATACTACTACTACACCTT
GACTGAAGAAGGTGTTGAATACTTGAGAGAATACTTGAACCTTGCCAGAACACATTGTTCC
AGGTACCTACATTCAAGAAAGAAACCAACTCAAAGACCACAAAGAAGATATTAA

YOR293W, 105 aa (SEQ ID NO 264)

MLMPKEDRNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS
WQYYYYTLTEEGVEYLREYLNLP EHVPGTYIQERNPTQRPQRRY

YOR312C, 1432 bp, exon1: 501-507, intron1: 508-914, exon2:
915-1432 (SEQ ID NO 265)

TATTTACAAGCTAGATAAAAAAAAAAATCAAATAGCAAGCTATTCTGTTCATATCTTAAGGT
GCTGATTGTTTGTAGGCACGAAGTAAACAAGCTCTTCCCCAAAACAATAAATACGGTTTT
CGGACTGTTTACCCGTACATTTTACGTTTCCGACGGCGCGATGCTATCTTTGAATTTTT
ATCTCTTTCAGGTAACCCCATGACCAAGTAGGGCGGCTTACTACCGAAGAGAAAAATGTCC
GCGGCTTAGACAGTTACTTCCCAGGCCAGGGCCAGGCCACACGGACAGAGCGAGATTCCA
AGTTGTTCCGCATAGTCTGTCTAGCTCTTTCTCAATTTTCCGCCAGATTCTGTCTAATTT
CTTTCCGCTCGAGTTGGCAACAGTACGAAGAAGTAACTCTAATAGATAGATATAACCGTT
TTTGAGGGCATTATTTTTTGCAGAAAGATAATAGAAGAGAACCGTAACAAAGGAATCAAGCA
AAGAAAAAGTATGTAATAGAATGTATTGTATGCTTGTGGAATGAATGTCAATGTAGCTAT
TTTATATGGTGAGCTCAAATTGAATGAACATATCGTGGAATTTAAAAATACTGAAGAATA
CCCAATAAGTCAATGCAACCTGTGAATGTGTTTTTCTGAAATACGCCGAATACTGAATACG
ATTATTACCATAAATTGCTTCTAGAAGGAAGGCGGTGTACCATTTAATACTGATGATATG
GTTAATATCATTTGAGAAGTCTTCACATGAGGACTATAGAATACTACCATCCAGGAATTATA
GAGGAAATTAAGTGAATCAGAGATCTATTTTGAACATTCATTTACATGTAATTGTCTGC
AATAAAGCAATATTTTTTGAAATATGCAAGTTTACTAACAAGATAAATTCTTTTTTTGATT
TTTATCTTTAACAGTGGCTCATTTCAAAGAATACCAAGTCAATTGGTTCGTCGTTTACCAAC
TGAATCCGTTCCAGAACCAAAGTTGTTTCAAGATGAGAATTTTTGCTTCAAATGAAGTCAT
CGCAAGTCTCGTTACTGGTATTTCTTGAATAAATTGCACAAGGTTAAGAAGGCTTCTGG
TGAAATTGTTTCCATCAACCAAATCAACGAAGCTCACCAACCAAGGTCAAGAAGCTTCGG
TGTTTGGGTAGATACGATTCCAGATCTGGTACTCACAACATGTACAAGGAAATCAGAGA
CGTATCCAGAGTTGCTGCCGTCGAAACCTTATACCAAGACATGGCTGCTAGACACAGAGC
TAGATTTAGATCTATTCACATCTTGAAGGTTGCTGAAATTGAAAAGACTGCTGATGTCAA
GAGACAATACGTCAAGCAATTCTTGACCAAGGATTTAAAATTCCCATTACCTCACAGAGT
CCAAAAATCTACCAAGACTTTCTCTTACAAGAGACCATCAACCTTCTACTAA

YOR312C, 174 aa (SEQ ID NO 266)

MYLAHFKEYQVIGRRRLPTESVPEPKLFRMRIFASNEVIAKSRYWYFLOKLHKVKKASGEI
VSINQINEAHPTKVKNFGVWVRYDSRSGTHNMYKEIRDVSRVAAVETLYQDMAARHRARF
RSIHILKVAEIEKTADVQRQYVKQFLTKDLKFLPHRVQKSTKTF SYKRPSTFY

YOR369C, 932 bp, CDS: 501-932 (SEQ ID NO 267)

CTTCTTACAAGTTAATGAATAGTATATATATGTAAAAAAATTTCTGCTTCATGTATATA
CGCACCTCGTTATTGAGGTATTGCGAATGTAGCAGTTGAATAAGCAAAGACGAGGTTTGT
ACATCTTGGCATATTAAATGGTTATTTTCGGGGTTTGTTCGGCTCAACGGTGATATAAAA
AGAAATCCAGTACTGTTTACCATTGTGCATCCGTACATTTGATTTGTTTACAACATCTTC
ACATTTCCATTGTGGAATCATTTTATTTTTTTCAGAATACCTTACCCGCAAGCAAACCTTT
CAAGCAAACCTTACAATTTGCAAAATTTTCATCGAATTCTCCGACGACATATTATAAAAGT
TATGTCATCTCTTATCACAACAGGTCTATAAGTGTTCCCTGTTCAATTGTTTTCCTCAAT
TCAAAACTCTTCACGGAGCAGTTTAATTATCTTACTGTGCAAGAAGTCAAAAACCTAGACT
ATATATTATTGAGAAGAAAAATGTCTGACGTTGAAGAAGTCGTTGAAGTTCAAGAAGAAA
CTGTTGTTGAACAAACTGCCGAAGTTACTATCGAAGATGCTTTGAAGGTTGTTTGTAGAA
CCGCTTTGGTTACCGATGGTCTAGCTAGAGGTTTGAGAGAATCTACCAAGGCTTTAACCA
GAGGTGAAGCTTTATTGGTTGTTTTGGTCAGCTCTGTTACTGAAGCTAACATTATCAAGT
TGTTTGAAGGTTTGGCTAACGACCCAGAAAACAAGGTTCCATTGATCAAGGTTGCTGATG

FIG. 1 - 90

CTAAGCAATTAGGTGAATGGGCTGGTTTGGGTAAGATCGACCGTGAAGGTAACGCCAGAA
AGGTTGTCCGTGCCCTCCGTTGTTGTTGTCAAGAACTGGGGTGCTGAAACTGATGAATTGT
CCATGATCATGGAACACTTCTCCCAACAATAA

YOR369C, 143 aa (SEQ ID NO 268)

MSDVEEVVEVQEETVVEQTAEVTTIEDALKVVLRALTALVHDGLARGLRESTKALTRGEALLV
VLVSSVTEANI IKLVEGLANDPENKVPLIKVADAKQLGEWAGLGKIDREGNARKVVGASV
VVVKNWGAETDELSMIMEHFSQQ

YPL047W, 800 bp, CDS: 501-800 (SEQ ID NO 269)

GGTTAGGGGCCAAGATTACGTTCCAGCTTTTCGATGTCGCACCAGATTGGGAATCTTACGA
CTATGCAAAAGTTGGATCCAACTAACGACGACGACAAAGAATTCATCAATAACATGTGGGC
CTGGGATAAGCCAGTTTCCGTCATGGCGAACCAGGAAATTTGTTGACGGTAAGGTCTT
AAAATAATCTCTTCGTACTATCCTTCATGTCGCCCTTTTATTATAAAGTATGCTAGGTAGT
TTTATCTATATCTTATTTATGACGCAATATAGGGTAACAGAGTTTTTCTGCTCTGAAACT
TCCGCAGAAAAAAATCAAGTTTTCTTTTCGTATCTTGGATTATTGTTATATAATAGAT
GCATGTATTATATGTATAGCAGTGATTGCTTATTTTCTTGATTCTGAGGAATCGAAGAA
GTAACCTTAGCGTTTCTTCCGTTGAGCAGAGCAGTATAATAATCCTTCAAATCTTTAGGT
TACGGGGTTTTCTGTTGCGATGACCGAAGAACTATTACTATAGATTCTATTTCAAATG
GGATACTGAATAACCTGTTAACCACATTGATCCAGGACATTGTAGCTCGGGAAACCACTC
AACAACAATTGCTGAAGACAAGATATCCGGATCTTCGCAGTTATTATTTTCGACCCGAACG
GATCTCTCGATATTAATGGACTACAGAAGCAACAAGAGTCCCTCTCAGTATATTCACTGTG
AGAATTGTGGCAGGGATGTGTCCGCAACAGACTAGCAGCTCATTTACAGAGATGTTTGA
GTAGGGGTGCTAGACGTTGA

YPL047W, 99 aa (SEQ ID NO 270)

MTEETITIDSISNGILNNLLTTLIQDIVARETTQQQLLKTRYPDLSYYFDPNGSLDING
LQKQOESSQYIHCENCGRDVSANRLAAHLQRCLSRGARR

YPL090C, 1605 bp, exon1: 501-506, intron1: 507-900, exon2:
901-1605 (SEQ ID NO 271)

GTAAGCAGAAGCCGGAAGAAGACAAGAGGTTTCATTTCAGAGAAAACATCCGTACATTCGAG
TTCTCATTGAACCCATACATTTCAACTATTTTACATAGTTTCGTTTTTCATGTGTAAAT
TGTCATCGACGCGCCGGAGCATCGGAAAGTTGGAACGTGCGCGATTGCACCAATCCCACT
GGGGCCGTGCATTCTGTAGGCAGGAAGCCACTGGACACTCTGCCCCGTTCCCACTTGAAG
ATTGGCGTAATTTCCACGCTCCTCTATCGATTCTAGCGGAAAGTTATCTCTCTGGTAAG
CGTTGGAGGAATGCCGCTACCTAGGTAAAGTCTACTGGGTGGGAATTCAGTACCGACGTC
TAGGAACATCATGATGCTGCAGTTTCTTTGAAATTTTCATATACAGTGTTACCAAGGATAA
AGTGGTTAATGCTTATTCGTCAATTGAATTTTATATTTGCTTAAGAGAAGTGACAAAAGA
GTGAAGACAGACTATACATCATGAAGGTATGATTTATGATACTATTATTGAGGGGCAACA
GAGAACTTTATATGTGGAATAATGGCATGAAAGTTTGAAAGTGAGAAAGAACTAAACAGA
ACCAGACGTCGTAAAGATTTTAGAAATTTTATGGAAGAAGCAGGAAGACTACCATAT
ACTAATTGATGCGTTTGTGGCGTTATTTTAAACAAACAGAGCGGGTTTACATATACTGT
TACTACAAACCGTGAAATTGAAGCAGTTTCATATACTTGGAGTATAGTCAATAAAAGACAA
GCTTTTTTCATCTTCCACTTAATAATTTCTCTAGAGTAATAAACTTCACCTATTCAAACA
TTAATTTTGCAATAGTATACTAACAATTTTCTTAATAACCTGTTGAAATTTAAATAG
TTGAACATTTCTTACCCAGTTAACGGGTCTCAAAAGACCTTCGAAATTGATGATGAACAC
CGTATTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAGTCGATGGTGAAGCCGTTGGT
GACGAATTCAAGGGTTACGTCTTCAAGATCTCTGGTGGTAACGACAAACAAGGTTTCCCA
ATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTGTTGACCAAGAAGCTTTCT
TGTTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAGTCCGTCAGAGGTGCCATTGTT
GGTCCAGATTTGGCTGTCTTGGCTTTGGTCAATTGTCAAGAAGGGTGAGCAAGAATTGGAA
GGTCTAAGTACACTACTGTTCCAAAGAGATTGGGTCCAAAGAGAGCTAACAACATCAGA
AAGTTCTTCGGTTTTGTCCAAGGAAGATGACGTTTCGTGATTTTCGTATCAGAAGAGAAGTC
ACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAAAGATTGGTTACTCCTCAA
AGATTGCAAAGAAAGAGACACCAAGAGCTTTGAAGGTCAGAAACGCTCAAGCTCAAAGA
GAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTGTCTGAAAGAAAGGCTGAG
AAGGCTGAAATCAGAAAGAGAAGAGCTTCTTTTGAAGGCTTAA

FIG. 1 - 91

YPL090C, 236 aa (SEQ ID NO 272)

MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEV DGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPD L AVLALVIVKKGEGE
LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVT KGEKTYTKAPKIQRLVT
PQRLQRKRHQ RALKVRNAQAQREAAAEYAQLLAKRLSERKA EKA EIRKRRASSLKA

YPL137C, 4331 bp, CDS: 501-4331 (SEQ ID NO 273)

GTCTCAGTGATGCAATCATCATGGCACGGGCATTAATTAAGGTTAAGGAACCACTTCTCT
ACGCCATACTCCAAACAATAACAATATTAGACCTAGCCAATTGATACCCATGAGCGTGCA
GTCATTGCCATGGATTATTCATCTCTTTTCGCTGTTCTCTTTCTTTTCAAGTTTGTCATC
ATCATGCCTTCACCTTTTGCTTTCCATCTTTCTTTTGCTGCAAAATAAAGGGAAGAGGG
GTAAAAACGCAAGGAAGAACAAGAAGAAGAGGGTAGTGCAAGAAAAAGAAAAGAAGAAAA
AAAAAAAAAAGTAATCTTGATACCGTGAGCAATAAGCTAACGGAAAGCGTAAGAAAGAA
GAGCGTGTTTTGGGAAATAACACCACAGCATAAAGCTAAAATTCAGTTTATATAATCTAT
AGTAGTCCTATAGAAATTGCGAATAACGGAAACAATAGTCCACCAAAGCAAGCATAGGGA
GTGGAGATAGCATCTAGGTTATGATAACTAACACCGAGTTCGATGTGCCCCGTAGATTGGT
TGTATAAAGGTAAGAGTAGACGGAAGACAAATACGAAGCCATCGAGGCCTTCTACGTCGC
CAGCCTCCTCTTCATCTACGTCCTCTTCGAAAAACGGAGACAATAGCAGAGTGGTAACA
GGTCTAGCAATGATAAGCCTCGTGCGAGGTCGTCATCTGTATCCAATGCAGCACTTTGTA
ATACTGAGAAACCAGATTTGAAGAGGAACGATGGTAATACCTCTGCATCAGACACTGATA
ACATACCGCTACTTACTCCTATTAATAGCGGTAACCGGAGCGATTCCGCTGACATTGATA
ATCCGGCTACCGTAGACGCCATAGACCTTATAGATAATGATGACAACGGCTCAAGTACTC
AATTTGTAAGGAAAAACGTTCCACTTCTATATCCAATGCTGTGGTCTCGTCCAAACCAA
GACTGGCCAGTTCTGCCATAAACGCCACCGCATCTTCTTCTGTGGCAAGGGAAGCACC
CGCCAAATTTCTACCATCTAATGCTACTCTCAAGAGAAGCAACTCGACTAGTGGAGAAA
AGACTAAAAGGTCGATTTTGGATCTTTGTTTGTAGCAAAACGGTCTACCTCTTCTCAGCTT
CCACTGCCAAGAAACCATTACCTGTTGTTAATACTAGCACGACTGAGAATGAGTCTGGTG
GCATTAAAGCAGTTGCGACTCCTGATCCACGGGTGAAGGAGATATCATACCAATGAGAG
GAGTGGCACCAACAGCTAGCAAGCCACAGACACCTATACTCCCTCCCTGCACCTGCGAG
TAAAAGACCTATCTACAGTTTCATTGAAAAGGGTCTCGTTTGCCGTCGATAAATTCGAAT
CCGATCCTCCCCAACAACTTCCCTTCAAGAACCCCAAAAAAGGGAACATCCTTATCCCTG
ATGACATGATAAGCGAGGTTCCCTTCTATTCTCGTGGGTATTTCCAGTAGCAACCAATCGG
CCAAGTCAACCAATTCACATTAAGGGACCGTTGTACACTAAGAAGTCTAAAGAATATA
TACTCGCCCTGGAAAATCAAAAGTTGGCTTTAAGGGAGGCTGCTAAGCATCAGCAAGAAG
CTCATTTTGTCTGCTAATAGAATAGCCTTTGAAGTAGCCAATTTTAAGACTGCTTCGGATG
CAGGCGGTAAGCTTACTGAAAAGTCATCAGAAGGCACCATTACGAAGCAAAGAGAAGAGG
TGTCACCTCCAAATGTTGAAGCTGATCGGGAGCTTGAGAATAATAAACTTGCAGAAAACC
TCTCAAAAGCCGGCATTGATAAGCCCATTCATATGCATGAGCACTATTTCAAGGAACCTG
ATCAAGATAAGTACCAAGACGGTCATTCTATTGAAAATAACGAAGTTACGCTGGATGTTA
TTTACACAAGATGCTGCCATTTAAGGGAAATTTTACCCATTCCGCTTACCTTAAGACAAG
TAAAGGACAAGACAGCTCCCTTGCAAATATTGAAGTTTTTGAACCCTAAGCCTACCTTGA
TCGATATTCTTTCTTTGTGATTTCATCACCATTGCTCCCATTCACACGATTGTTTTTCG
ACAATGTAGCTTTAAACCAGGATATGTTTCAGAATAATTATTTCTGCTTTGGTAAACTCCA
CAGTTTGGACAAATTGAGTTTAAGAAATGTACGAATCGACCAAGATGGATGGAAATTAC
TATGTAAGTTTCTTTTGCTAAACAAATCACTGAACAAGCTCGACATTTCCCAAACGAAAA
TCAAATCTGACCTTGCTGAATCACTATATCGCCATAACATGGATTGGAACCTGTTTACTG
ACGCTTTGTCTCAGAGATCTCACAACCTATAGAAGAATTGTTATTCAATGGTATTCAAT
TTAGCAAAATTCCTTACTCATGCTTTGCACGTTTACTGACATCCTTTGCTACCCAAAAAA
ACTTTCCAGAATCGGGCATCAGGCTTGGTTTAGCAGGTGCCACTACTTCCAATATCTCTC
AGGATTGTCTGAAATTTATCTTCAATTGGATGTCTCAATATAACGTCCAGGGTGTGGATC
TAGCGTTTAATGATCTGTCCACTATGATTAAGCCAATGGTTGGTAAACTATCTGCTCTAT
CATATGATAACTTAAGATATTTTCAATTTGAACAGCACTAATATTTGACTTCTTATGATT
TAGCTTTGCTCTTGAATATCTTTCTAAGTTGCCTAACTTGATTTTTTTGGATTGTAGTA
ATTTGTGCGCAATGCTTTCCTGACATTTTACCCTACATGTACAAGTATTTACCAAGATTTT
CGAACCTGAAGAGGATACATTTGGATAGCAATAATTTGACATTAAAGGAACTAGCTGTCTG
TTTGTAATATTTTGAATTAAGTGCAATCGCTCTCGCATGTGTCAATGACTAATCAAACG
TTGAAAACCTTCTATCTAATGAACGGCACAGATTCTCCCGTTCAACAACTAACACAGACG
GCGACTTGGATAGTTTCGAGCACATTGGACGTTAAGGGCCAATTTGCTAAAAATAGTTTTT

FIG. 1 - 92

CATCCACACTTTACGCATTTGCTAGAGACTCTCCAAACTTGATTGGTTTAGATTTTGACT
ATGATTTGATATCAGAAGAGATTCAATCAAGAATAGCACTGTGCTTGATGAGAAATATGA
AACCGACCATGGATTTCGACTTTCCAGTTAGATGAATTGGATTTCGCAAGATGATTTGCTAT
TCGATGGCTCTTTAGTAACATATGACCGCTGAAAGTGTTTTAGAAAACTGAACTTGTTAA
GCGATAAGAGTACAAAGGTCAAAAAAGACACCAGGAAGAGATATTTGCTGAAAAAATATA
TTGAAAAGTTCCATATCTTGCACCATAATGTTTCAGCATACAATAGATACTATGTTTCGAAA
AAAGGAAATCAGGTGAATTGCCATTGCAAGAAAAAGAAAACCTTGTAAGATTACTCCTTT
TGGAACAAAACCTTATGCAATATACTAGAATTGTTTTTCGCATAATCCGAATCTGAATGATG
TCCTTGGATCCAGCAGGGATGATTTCGAAGGAAAGTGTTGACTCCAGCGAAGATTCAAAAT
TACCAGCATTTGAAGCACGTTGAATCCGGATACCATGTTCCCGAAGAAAAAATACAACCTG
AGAATGATGTAATTACAGCAAGACCACATTTAATGGCCACCGATTCTGGTAAAACTATTG
ACGTTTTTCACAGGCAAACCATTTGGTGTTCAGCATACATCATCTAGTACTTCTGTAGGTT
GTAAAAAGCAGGAAGAAGAAGGTGAACATACATAAATGGGGTTTCTTTCGTTTCAGCAGC
AGAGGTCCTTTATACCCTGAAAATGAATCAACAAGGCAGACACCTTTTGCATCAGGTGATA
CGCCTATCAACACAGAAACAGCTGGTAAGTCAACTTCATCTCCTTCAGTTTCAACTTCTA
ACAATGAACTGCTACCACCTAGTTTATTTAGCCCAGCTAATCCTAAGATTTTACCAAAAA
TTCCATCCGGTGCTGCTTTAAGATCGGCAATCATGAAGGCTAAAGGTATTGATTCTATCG
ATGATTTGATTTCAGAACGTTAATCCAAACATAGAATTGGAGAACATTTATGGTGAAT
CCATTCGAAATAGCGCTTCGACATTTACACCAGGCGTGGATTCTGATGTATCTGCGCCCA
ATACCGATAAAGGATCCGTAGAAACATTGCCTGCAGTCTCAACTGACGACCCAAATTGTG
AAGTCAAAGTCACTGCTACCTATGACAAACTATTAAATAATTTGTCGATGGAGAGGTCAA
TCAGACTTTGA

YPL137C, 1276 aa (SEQ ID NO 274)

MITNTEFDVPVDWLYKGKSRRTNTKPSRPSTSPASSSSSTSSSKNGDNSTSGNRSSNDKPF
RARSSSVSNAALCNTEKPDLRNDGNTSASDTDNIPLLTPINSGNRSDSADIDNPATVDA
IDLIDNDNGSSSTQFVRKKRSTISINAVVSSKPRLASSAINATASSSVGKGHPPISSPS
NATLKRNSNSTSGEKTORSIFGSLFSKRSTSSSASTAKKPLPVNTSTTENESGGIKAVAT
PDPRVKEISSPMRGVAPTASKEPQTPILPSPALAVKDLSTVSLKRVSFVDFKESDPPQQL
PSRTPFKGNILIPDDMISEVPSISVGISSNQSAKSTNSNIKGLYTKSKKEYILALENQ
KLALREAAKHQQEAHFAANRIAFEVANFKTASDAGGKLTEKSSEGTITKQREEVSPNVE
ADRELENNKLAENLSKAGIDKPIHMEHYFKEPDQDKYQDGHSENNNEVTLVDVIYTRCCH
LREILPFPSTLRQVKDKTAPLQILKFLNPKPTLIDILSFCDFITIAPIHTIVFDNVALNQ
DMFRIIISALVNSTVLDKLSLRNVRIDQDGWKLCKFLLLNKSINLKLIDISQTKIKSDLA
SLYRHNMDWNLFDTVLSQRSHKPIEELLFNGIQFSKIPYSCFARLLTSFATQKNFPESGI
RLGLAGATTSNISQDCLKFIFNWMSSQYNVQGVDLAFNDLSTMIKPMVGLSALSYDNLRY
FILNSTNISTSYDLALLKYLKLPNLIFLDLSNLQCFDILPYMYKYLPRFPNLKRIH
LDSNNLTLKELAVVCNLIKCKSLSHVSMTNQNVENFYLMNGTDSVPVQQTNTDGLDSSS
TLDVKGQFAKNSFSSTLYAFARDSPNLIGLDFDYDLISEEIQSRIALCLMRNMKRTMDST
FQDELDSQDDLLFDGSLVTMTAESVLEKLNLLSDKSTKVKKDTTKRYLLKKYIEKFHIL
HHNVQHTIDTMFEKRKSGELPLQEKENLVRLLLLEQNLNILELFSHNPNLNDVLGSSRD
DSKESVDSSSEDSKLPALKHVESGYHVPKEKIQPENDVITARPHLMATDSGKTIDVFTGKP
LVFKHTSSSTSVGCKKQEEEEGELHKWFFVQQQRSLYPENESTRQTPPFASGDTPIINTET
AGKSTSSPSVSTSNNETATTSLSFSPANPKILPKIPSGAVLRSAIMKAKGIDSIDDLIQNV
NSNNIELENIYGESIQNSASTFTPGVDSVDSAPNTDKGSVETLPAVSTDDPNCEVKVTAT
YDKLLNNLSMERSIRL

YPL159C, 1262 bp, CDS: 501-1262 (SEQ ID NO 275)

AAACAAAGCGATTTGAGTATTACGTTAAGATCTCCATTTGCTATGCTAAATCCTGCCTAC
TCAACAGCATTATATCGCTACCAACAGGTGTGGTCAAGAGGTCAATTGACTCTTCCTGTC
GGTATGAAAATTTAAAAATATATAATAACATAAGTTTGCAATCATTAATATTAATATAAA
TCAACGTATCAACCAATAAGAACCATAATCATAATAATTGTTTACCTTAATGGCGATATCG
CCTTTTATCACCATCGACGATAACAAACGCCTATTCTGTCTACCGTTTCTTTTTTTCGCT
CGCAATATCAGAATCGTTTATCCCAAAGGGTAGTTATAGCAACTATTTAAATAACTTAGA
TGTTTCTTTAACTTATTCCGTCATACGTACACAAACACCCGCTAGATATAGCACTCCTTG
CTGTGCAACATTATAAAGGTGCTTTTAAACTACTAATCGTATATTTCAGCAGGTGAGAAC
GCAAGTCGGACGATAAACTATGTTGAAGCTAGCTCGTCCATTTATTCGCTTTTATCAA
GGAACAATGCCATTTCTTCAGGAATAGTTCTCACTTCTAGAAGATTTTCAGTCTTCCTTTA

FIG. 1 - 93

CGTTCTTAAGTAACCAGTCTTTACTATCTAAAAATCAAATGAAATCCAAAAGAAAAAGG
GCAGTAAAAAGGCAGCGTACCATCGTCAACCCCGGAACACGAACATACTGCACCACTTA
TAAAGCAAAACAAGACAATCACAAGAAAGAACATAGCGATGTGAGAGGTTCTCATTTAA
AAAAGAAAAGAAGCGATTTTTTCGTGGCTACCAAGAGTACCATCCACCTCACATTTAAAGC
AGAGTGACATGACCACAAATGTACTCTATTCTGGATATAGACCCCTTATTCATCAATCCCA
ATGACCCGAAGCTAAAGGAAGACACCGGAAGTACGTTATACGAATTTGCGATGAAGCTTG
AAGATTTAAATGAACCTCTATCACCATGGATTTCCCTCTGCCACTGGACTTGAATTCCTTT
CAGAGTGGGAGAAATATACCTAGTGAACCTACTGAAAAATTTGAAGCCTTTTCATCCACCTA
AGGAAAAATCAATGAACACAAATGAGCTTATTCATGTAAGTGCTAAGAGAAATACATTAG
TTGACAATAAAACAAGTGAGACGCTTCAGCGGAAAATGGATGAATTTTCAAAGAGAAGAG
GAAAGGGGAGAAAAAAGTCAGTAGTGACGTTGCTCCAAATGAAGAAAAAAGCTTGAGGGAT
GA

YPL159C, 253 aa (SEQ ID NO 276)

MLKLARPFIPPLSRNNAISSGIVLTSRRFQSSFTFLSNQSLLSKNQMKSKRKKGSKKAAY
HRQPEHEHTAPLIKQNKTTITKKEHSDVRGSHLKKRSDFSWLPRVPSTSHLKQSDMTTN
VLYSGYRPLFINPNDPKLKEDTGSTLYEFAMKLEDLNEPLSPWISSATGLEFFSEWENIP
SELLKLNLPFHPPEKSMNTNELIHVSAKRNTLVDNKTSETLQRKMDEFKRRRGKRKKS
VVTLLQMKKKLEG

YPL175W, 1940 bp, exon1: 501-514, intron1: 515-568, exon2:
569-1940 (SEQ ID NO 277)

ACGTTATTTTCAAACACATACGAAATCGCTGGACTTTTCTCACTAAAGGCTTCCGGAGCC
TGCGGTTCTTCCATCCCATCTCTTCCACATATACCGGGGGTCTGATGGCATTCCCTATA
GCTTGCTCAAAGTCCTGCGAGTTTAGCTCATCTTGTGAGTTATTTGCTGGTCTTCAACA
TTCGGAAGAGTAGTGTAGCCCTAGTATTCACCATATCCTTTGTATACTCATATGCGAAC
TTGTCTAATACAATGTATACCAAAAATAACAGCTTGAAAAAATCTCAGGGTCTTTTCAT
TGAATAATCTCATTCTGCTATTTTAAAGTTTTCGTTTGCAACCCGAGACTGTCGAGCTAG
AAAATTTTCATTGATACGATTTAAAAAATAATCGATGCCAGTAATAGCCTCAAAAACTTAT
GCAAAAATACGAGATACTATAAACTACAGCTTAGCTAACTCTAACATTATTATATAAAAC
AATGGGCTTCAATATAGCGTATGTCTAGCTCACAGCATGTGTTCCAAATACATTAAAGAA
GATCTCTTTTGTGTTGATACTAACCAGTAAAGTTGAGAGTTATAACAATGAAAATAGGA
TGCTGTGCGACTTTTTTTATCCACAGTTAGGTGGAGTCGAATTCATATATATCATTTAT
CGCAGAACTAATCGATTTGGGCCATTCTGTCTGTCATTATACTACGCTTACAAAGATC
GAGTCGGCGTACGACATCTTACCAACGGTCTAAAGGTCTATCACGTACCATTTTTTGTGA
TTTTTCAGAGAAACCACTTTCCCACTGTTTTTTCAACATTTCCAATAATAAGGAATATTC
TTCTCAGAGAGCAGATCCAAATTGTTTCTATCTCATGGTAGCGCTTCCACGTTTCGCTCAG
AGGGAATTCTTCATGCTAATACTATGGGATTGAGAACTGTGTTACCGGACCATTCACTCT
ACGGTTTTTAATAACTTAACGTCGATTTGGGTGAATAAGTTGCTAACATTTACCTTGACAA
ACATAGATCGGGTTATATGTGTTTCTAATACATGCAAAGAAAATATGATTGTTAGAACAG
AATTAAGTCCTGATATAATCTCAGTAATTTCCCAACGCAAGTGGTGAGCGAAGATTTCAAAC
CAAGGGATCCTACTGGTGGCACCAAGAGAAAACAAAGTAGGGATAAGATAGTGATCGTGG
TCATCGGAAGGCTCTTTCCAAACAAAGGGTCCGATTTACTTACTCGCATAATTCCGAAAG
TTTGTTTCCTCACATGAAGATGTCGAATTTATAGTAGCGGGCGATGGTCCAAAGTTCATAG
ATTTTCAAACAAATGATTGAAAGTCATAGACTACAAAACGTTGTGCAACTCTTAGGCTCTG
TTCCACATGAGAAAGTCAGGGATGTATTATGTCAAGGTGACATATATTTACACGCTAGTT
TAACAGAAGCATTTGGTACAATTTCTAGTTGAGGCCGCATCTTGTAATTTGCTAATTTGTAA
CGACACAAGTCGGAGGAATTTCCGAAAGTGTACCAATGAGATGACTGTTTATGCAGAAC
AGACATCCGTTTCTGACCTTGTTCAAGCAACAAATAAAGCTATCAATATCATAAGAAGTA
AAGCTTTGGACACTTCTCTTTTCATGATAGCGTGTCTAAAATGTACGACTGGATGGACG
TAGCCAAAAGGACAGTAGAGATATATACTAATATATCTTCTACTTCTTCCGCTGATGATA
AAGATTGGATGAAAATGGTAGCAAATCTTTACAAAAGAGATGGAATCTGGGCTAAACATC
TTTATCTGTTATGTGGAATTGTAGAGTACATGCTTTTTTTTCTCTTAGAGTGGCTATACC
CCAGGGATGAAATCGATCTAGCTCCAAAATGGCCCAAGAAAACAGTGTCTAACGAGACGA
AGGAAGCAAGAGAACTTAA

YPL175W, 461 aa (SEQ ID NO 278)

MSSSHKVESYNNENRMLCDFYPQLGGVEFHLYHLSQKLIDLGHVSVIIITHAYKDRVGV

FIG. 1 - 94

HLTNGLKVYHVPFFVIFRETTFPTVFSTFPIIRNILLREQIQIVHSHGSASTFAHEGILH
ANIMGLRTVFTDHSLYGFNNLTSIWVKNLLTFTLTNIDRVICVSNTCKENMIVRTELSPD
IISVIPNAVVSEDFKPRDPTGGTKRKQSRDKIVIVVIGRLFPNKGSDLLTRIIPKVCSSH
EDVEFIVAGDGPKFIDFQQMIESHRLQKRVQLLGSVPHEKVRDVLCOGDIYLHASLTEAF
GTILVEAASCNLLIVTTQVGGIPEVLPNEMTVYAEQTSVSDLVQATNKAINIIRSKALDT
SSFHDSVSKMYDWM DVAKRTVEIYTNISSTSSADDKDWKMWANLYKRDGIWAKHLYLLC
GIVEYMLFFLEWLYPRDEIDLAPKWPKKTVSNETKEARET

YPL180W, 2900 bp, CDS: 501-2900 (SEQ ID NO 279)

CTCAATGGGAATTGAGTGAAGATCAGTCTGATCGAGAGGAATTTGTACGATTTCGTGGAAA
ACCAGCATTTTCGTAGAAAAAGTTGATACGATTTACAACGGTTATAATGAAAGCTATCAA
TGATGGACGACCTGACTAGAGAGTTACTACTATGGGAGAAAAAATATTCAAATAACACTA
ATGCCATTCAATAAACGCAAAACACTGCAATATTATTCTCAACCAAAGTATAACTGTAAT
GAGGCGAACAACACATCTATACATATATATACATCTATATGGATATAAAAAAGACTAAT
TCAACGTTGTTTATCAACCGAGCTTACTCTTGTACGGGTAACCGCAAGGATAGCTAGT
TGCGGATGGTATAGCGATTTGGCTGGCAGCATGATTAAGGAATCCAAACATCTAATGGAC
TAGCACATTCTATCGATTTACGGGTCAGGTAACATAGATATTGGGATATATCATATATC
CTTACTGAGTAATAATTATGGTTCATCGAGGAAGGACTTTGAAGTCAGACACTGATG
TAACATCTCTTAATGCGTCAACAGTATCACACCAGTCAAAGCCATTTAGACAGTTTTCGA
CTAGGTCGAGAGCAAAGAGTAACGCAAGCTTCAAAGGTTTGCGTAGAGTTTAAACACATG
ATGGCACCCCTGGATAATGATTATTTTAATAAGCACACGTTTCTCAGAAATGCAAGAGTT
CTGATGCACTTTTCAGAAAGCGAACGATTAGTGGGTTGAATATGACAGCTTTAAACAAGAG
TAAAGTCCAATCAAGGAAAAAGATCAGCATCCTTTCATAGTCCGGTGCATAATACCGTGC
TCAGTCCAAAGAACAGCAGTCATTCTAATACTGGAAGTCTGCTGGTTTCGGCTGAAACAC
GAAGAAGTAAAAAGTACCCAATCTGTTCTGAGTCTTCGAGATGCGCAAGAATCTAAAAAGA
GTGAATCTACTACTGACGAGGAGGTGGAATGTTTTTCGGAAGACAACATTGAAGATGGAA
AGGTGAATAATGATAAAGTAATAGCCGAGCATGTTATGCCTGAAGAAAAAAGAATGTGC
AGCAATTAAATCAGAAATGAATTACAATCCCCGGATTCAATAGATGAACAAGAAGAAGATA
AATCAGGTACTGATGGAAAGGAAATCATAGAGCTGTATCCTTACCATTACCTCATTTAT
CTTCCAATAACTATTTTCGGAGAATCAAGCCATTCTATAGAATCATCAGAAAGATGGAGAAA
CATCTCCAAGCTCAATTGAAACAAAACCTGAATGCAACAAGTGAATCAATGAAGAGGGGC
AATCAAAGGTGACGAAGGAAGCTGATATTGATGACTTGTCCAGCCATTCTCAAAATTTGA
GGGCTCATTTGGTTAAAGCGGGCGATAATATATCAGAAGCACCATATGATAAAGAAAAAA
AAATTTCTTGATGTTGGTAATACCTTAGCTGCACATAAAAGTAATCAAAAACCAAGTCATT
CAGATGAACAGCTTTGATCAGGAAGATCACATTGATGCCCCTAGGAGTAATTCATCAAGAA
AAAGCGACTCGAGCTTTATGTCCTCTTAGGAGACAAAGTTCTAAACAACACAAATTTAA
ACGAAGAAGAAGATCTAATCAAGCCTGATGATATTTCTTCCGCTGGTACCAAGGATATTG
AAGGGCATAGCTTACTGGAAAATTATGCGCCTAATATGATTCTCTCCAGTCGACTGGAG
TTGAACGTAGATTGAAAATTCATCATCCATCCAAAATTCGCTTGGGAATGAAATTCATG
ACTCGGGTGAGCATATGGCTTCAGGTGATACTTTTAATGAACTGGATGATGGCAAATTCG
GCAAGAGCAAGAAAAATGGTGGAAGATCTCAACTTGGCCAAAATATACCGAACTCTCAGT
CTACTTTCCCAACCATTTGCTAATCGGTAGTAAAGATAATAATGTACCACAGCACAACT
TTTCGACCTCCATATCGAGTTTAAACCAATAATTTGAGGAGAGCTGCTCCTGAAAGCTTCC
ATGGTTCAAGAATGAATAATATTTTCAAGAAGGTAATCAGAACTACTTCTGAGAT
CCAACGATCTCAACAAAAATTCGTCAGCCCCGGCCTCTCATTGTCCAACGAACATATTA
CATCTAGTACGAACTCCGCTAGCGATGCAACAGACAATCCAACCTCAGGTGCCAAATTTA
ATAGCTTCGCCCAGTTCTTAAATCAGATGGGATTGATGCAGAAATCAAGAACACAAAGAA
AATTATGGTTGCAGAGGGAGAATTTCTATTATGGACTTAAGTTACAAAAATGACGGTAGTG
ACTCTATCTTTATGGCAGGAAACATTGATGCGAAAAGGGAGTTTGAGAGAAATATCCCATG
AATACTCTAATGTAAAAAGATTTTACAACCCATTAGATGAAGCATTGTTGAGAGTACAAC
CTATAATAACGGGAAATGCAATAATATCAGGAAAAAAGCCATAACGATGCTCAGTCAA
TCGCACATTCTAGCAGTGATACAGATCATAGGATGAGGACGATTTGCTCTTTACTAACT
ATGACAAAAAATTTGATGATCTTTATCCACATCTTGCAAGTGCAAGATTCAGGCAGTGT
TGTCCGGTATATGAAAAGCGAAAGTTACTTTATTAACAAGGATGTTAATCCAATCAACA
AGAATAGGACAACGAGTACAAACCCACAGCGTTGGCCACACTGCTTCACAGAAATGCACGTA
ACTTGCTGAGGGGCCCCGATGGGTTCCAGCACGACTTTGCACCACCAACGCGTCATTAAC
CTCTGCAGCCGACTACGAGGGCAGTGAATCGCAGGATGGAAAATGTGGGCTACATGCATA
CACAGCCACAACAAAGGTGA

FIG. 1 - 95

YPL180W, 799 aa (SEQ ID NO 280)
MVHRGRTLKSDTDVTSINASTVSHQSKPFRQFSTRSRAKSNASFKGLRRVLTHDGTLDND
YFNKHNVSQCKSSDALFRKRTISGLNMTALTRVKSNOGKRSASFHSPVHNTLLSPKNSS
HSNTGTAGFGLKPRRSKSTQSVLSLRDAQESKKSESTDEEVECFSEDNIEDGKVNNNDKV
IAEHVMPEEKKNVQQLNQNELQSPDSIDEQEEDKSGTDGKENHRAVSLPLPHLSSNNYFG
ESSHSIEHQDKGETSPSSIEKLNATSVINEEGQSKVTKEADIDDLSSHSONLRASLVKA
GDNISEAPYDKEKKILDVGNTLAAHKSNOQKPSHSDEQFDQEDHIDAPRSNSSRKSDSSFM
SLRRQSSKQHKLLNEEEDLIKPD DISSAGTKDIEGHSLENYAPNMILSQSTGVERRFEN
SSSIQNSLGNIEHDSGEHMASGDTFNELDGKLRKSKKNNGRSQLGQNI PNSSQSTFTPTIA
NIGSKDNVNPQHNFSTSISSLTNNLRRAPESFHGSRMNNIFHKKGNQNL LRSNDLNKN
SAAPASPLSNEHITSSTNSGSDANRQSNNGAKFNSFAQFLKSDGIDAESRTQRKLWLQRE
NSIMDLSSQNDGSDSIFMAGNIDAKREFERISHEYSNVKRFYNPLDEALLRVQPIITGNA
NNIRKKSHNDAQSIAHSSSDTDHKDEDDLFTNYDKKFDDLYPHLASAKIQAVLSGIWKS
ESYLFNKDVNPINKNRTTSTNHSVGHTASQARNLLRGPMGSSTTLHHQRVINSLOPTTR
AVNRRMENVGVMHTQPQQR

YPL218W, 1212 bp, exon1: 501-528, intron1: 529-667, exon2:
668-1212 (SEQ ID NO 281)

TGATACAAGACAGGCATTAGGAAACACATGAGTTTTGCATATGTATTATGCAGGTTTCATT
TGTTCCCTTCCCTTATTTCTTTTCATAGTATTTATTTTATTTATTTATTTTATTTT
GGATTTTATTTTATTTCTTTTAAATGCTAAGAAAGTAATCCGCATAATTAAACGTGTG
CTGGCCTCGATAGGTACCTATAGTATACAGAAGCTTACGAAAAGCTCCTGCAGGATGGCA
CTTCTAAAATTCGCGCTCAACATGGCCGTATTGTACATTATATCGTTCTATCATTATATC
GTATACGCCCCGATTACCCGACAACCTCCGTCTGCAACGCGTTGACCAGAAAACCTCGAACA
AGAGATCGCATAAAAAACCAAAAGGAAACGAATTACTTGTCAAATAGTTATTGTAATGGA
TCCTCTAGAAAGGCAAACAGTAGATTTATTTCTTCTTTCTAGAAACATCATTATAACT
AACAATATATAATTGGAATAATGGCTGGTTGGGATATTTTGGTTGGTGTATGTTATCAC
CCTGTTACGTTTTCGGATACTTAGTTTATTTTCAATGTGGTAAACATTGAATGTTTTCA
GCTTAAGATCTATTTTTTTTTTTCTAGAAGAAATTGCGTCTTTACTAACTTTATTTTAC
TGACAGTCAGAGATGTGTTGGCTTCCCTTGGTCTGTGGAACAAACATGGTAAACTACTT
TTCTTGGGTTTGGATAATGCCGGTAAGACCACATTGCTACATATGTTAAAGAACGATAGA
TTGGCAACCTTACAACCAACATGGCATCCAACCTCTGAAGAACTGGCTATTGGTAAACATT
AAGTTTACAACCTTTCGATTGGGTGGTTCATATTCAAGCTCGTCGTTTATGGAAGGATTAT
TTCCCAGAAGTTAATGGTATCGTCTTTTATGTCGATGCTGCTGACCCTGAAAGATTGAT
GAAGCACGTGTGCAATTAGATGCTTTATTTCAACATTGCCGAATTGAAGGACGTTCCCTTT
GTAATTCTTGGTAACAAGATCGATGCTCCAAACGCCGTTTCTGAAGCGGAGCTACGTTCT
GCTTTAGGATTATTGAATACCACTGGCTCTCAAAGAATTGAAGGTCAAAGACCAGTTGAA
GTTTTCATGTGTTCCGTTGTTATGAGAAATGGTTATTTAGAGCGGTTCCAATGGTTATCT
CAATATATTTAA

YPL218W, 190 aa (SEQ ID NO 282)
MAGWDIFGWFRDVLASLGLWNKHGKLLFLGLDNAGKTLLHMLKNDRLATLQPTWHPTSE
ELAIGNIKFTTFDLGGHIQARRLWKDYFPEVNGIVFLVDAADPERFDEARVELDALFNIA
ELKDVFPFVILGNKIDAPNAVSEAE LRSALGLLNTTGSQRIEGQRPVEVFMCSVVMRNGYL
EAFQWLSQYI

YPR102C, 1025 bp, CDS: 501-1025 (SEQ ID NO 283)
TTCTTTACAATTCACCTTGCATTATTGAAGGAGTGCTATTCTTCGTTTTTGCCACCCTTTT
GCTGTTTTCCCTCATATCACATAATACCCGGAGAGGCTCTTTCTGCGACAGCGCAACAT
CCAACCATCCTAAAGGTATGGGTGTACTGACGATGCGATTATTTTATTAAAGTTCTGTCTT
TTTTGTATAAATGAAAAAAGAACGGTGAAATCCATAGAAATACAGAGAGCGACGCAAAACA
GCGCGCAGACTCTACGGGTAATAGACTCACATCCACGTGACCAGTTTCCAATCGAACTTT
TTCACCTTGCAGGGAATTATTGTTTCACTAGCAAAGGTAGCCCACTTACCACTCAGCTAT
GCGAAAGTTTCATTGTTGATACATCTTGATAGTAACCGCAGGCTTCTTTCTTAGTTTCAT
ATTTTATTGTATTTCAACTAATATTATTTTCTTTCAGTGGAAGGGAAGGTGAACCAAGA
ACATACAAACATAGCCAAAGATGTCTGCCAAAGCTCAAACCCCTATGCGTGATTTGAAGA
TCGAAAAGTTGGTCTTAAACATTTCTGTTGGTGAATCTGGTGACAGATTGACCAGAGCCT
CCAAGGTTT TAGAGCAATTATCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTG

FIG. 1 - 96

TCAGAACTTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAACTTCTCTGCTACCGGTAACTTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTTCTATGTCGTCATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACCGTTGGTAACTCCCACAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGATGCTGATGTTTTGGACA
AATAA

YPR102C, 174 aa (SEQ ID NO 284)

MSAKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR
RNEKIAVHVTVRGPKAEIILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKRCCKGTVGNSHKTTKEDTVSWFKQKYDADVLDK

FIG. 1 - 97

YBL051C_homolog_1 1229bp PathoSeq: 1..1229; CDS: <1..>1229 (SEQ ID NO 285)

AGAGAACGTATTGAAGAGGAGAAAAGGGAGAAAAGAGGTCAATTGGAAGAACAACATCGTTCTGCA
TCAAAATGCTTCTATGGCTTCTTTATTGTGCTGCTTCAACTACAGCAGCAACTAAAAATTTGAGT
GTGGCTGGCACAATCCTTCTCATACCACTGAAAGAATGTTTTTAAATTTACCTTTTAAACAATTCC
CTGTTCAATGCCCCACCAGTAGAAATTAATTTTAATGATCTTGAAAGTTTTGGAATTGTACACTCAA
TTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCAGCAAATTTG
AATATTTCTCAACGGAAAATCATATCAATTTTATGTAATTATTTGAATTTATTAGAATTGTTTGAT
AATGGGTTGATAATAATTAGAAGAAAACCAGGATACATTGCTCAGTGATAACTCAACAATCTATT
ATTCCTAATTTCTCAACAGGTGTCTGGGCCAACTCACCCGCAACAACATCAACAGAATCAACTTCAA
CAACAGCAACAGCAACAACATCAACATCAACATCCTTCACATTCATCATCGATGATGAACCTTCAT
CAATTGGGTGGTACATTAGCTGTTCCAGCGCACCTTGAATTATTAAGATCCCAATCGCAATCAGCA
TTACCGTTGCCAAGATTGAGACAGCAAACCTCTACACCAATTCAACAAAATCAACAAGTTCAGCAC
CAAAATCAACCACCACAACAACAACAGCAACAGCATGTTCAACCACAATATAATTATTACAATCAG
CAATCTATTCAAAGCCAACCACATTCTGCGAGACCTTATTCTCAATCATATAATATTTATCAACAA
CAACAGCAACAGCAGCAACAACAAGCTCAACAACAAGCTCAACAACAACAACAACAACAATTAACA
TATCAACAGGGACACCAGTCACAAGTTTCAACACCTACATTGAATTCTTCTAGTGCTGCTGCATTA
CTTAGATCAAGTAGCAGTAGATCATTTGTTGATGTGAGATCCACACCTCCCACAAGTAGTTTGTGCT
CAACAGCAACAACAACAACAACAACAGCAACAGCCGCCACTAACTTCATCAATCCATGATTCT
CCAACACCACATCATCATTTTACCCTTCAACAGCAGCCACCACAACCAATCATTACCTATCCAAT
TACCATCAGGGGGTTGGATCTCAACCAAAAACCTCCATTGGC

YBL051C_homolog_1 409aa (SEQ ID NO 286)

RERIEEKREKRGQLEEQHRSASNASMASLLSAASTTAATKNLSVAGTNPSTTTERMFLNLPFNNS
SFNAPPVEINFNDLEVLLEYTLVLVYRDDITKSTFELAI SPANLNISQRKIIISILCNLYLNLELFD
NGLIIIRKPGYIAQCITQOSIIPNSQQVSGPTHPPQHQQNQLOQQQQQHQHQHPSHSSSMNLH
QLGGTLAVPAHPELLRSQSQSALPLPRLRQQTSTPIQQNQVQHQNPQQQQQHVQPPQYNYNQ
QSIQSQPHSARPYQS YSYNIYQQQQQQQQQQAQQQAQQQQQQQLQYQQGHQSQVSTPTLNSSSAAAL
LRSSSRSFVDVRSTPPTSSFAQQQQQQQQQQQQPPLTSSIHDSPTPHHHLPLQQQPQPNHYLSN
YHQGVGSQPKTPL

YBL051C_homolog_2 2153bp public: 1..2153; CDS: 501..2150 (SEQ ID NO 287)

ATAACAAAAAAGAAGCACGAACTGTGGGCAACAACAACAACAACAACAACAAAAAATTTT
CTGGAAAATCAAATTGAATCCAACCAGCAGCGGCGGCGGCGACAGAAAAATATATTAACAGAAT
ACTTTTTTGTATTCAACTCTCTAACTCTTTCTATTTTTTTTTTTTTTCTATATACACTGTTAAATC
AATCAACAATAGCAGGATATCCATTTCATATACAAATAGATAAACTGTTTAATTAATTAATTAAGT
ATTTGATTTGGGAAAAACAAATTTTATATTTGGAGAATTGAATTTCAATCATTTTTAACAAATTC
AAGCTTTAATTTCCACCTATCAAATTTTCATTATTATTTTGTTCATTATTTTTTTTTTCCCTTTC
TTTCTTTCTTTCTTTCTTTTTTGGAAACAAAGTAATAGCCGATAAAATAAATAATTCACATAGCCCA
ATTCATATTACATTGACTTTTGACAAGAGGTATATATAATGGATTTTAGAAAATTTATCAACTACAC
CGAATCAAATGGGCACTGTAATGCAACGTCGTCCTCTCTATCATCATTATCGTCAGCCTCGGGCT
ATTCTTCTTCCAATTATGGTGGAATCCTACACCCAATCCCAACAATTCCAATACCAATAACAATA
GTAGTGGCAATAGTAATAACAACACTCATGGCAATAACACTCCCAAAATTATCAACTCAAAGATTGA
CAAATAATAGGAATTTACAATCCTTGTGGATAAACCAACCATCTATTGCTCCTTCTAATGTTGTTT
CTTGGGTGGAACAGCAACAACAACAACCCCTTGATCTGTTGGAAAATAATACTAAAACAGACTCCA
GTAATGATGCTTCTGCTACTAATAATAATAATGTTAATGTTAATGTTAATGCCAATGCCAATGTTA
ATGCCAATGCCAATATCCATGCCCAAACCCATGTCAACACAAATGTTAATGCAACACAACAGCAA
CTAGATTAAATGCTTCCACGATTTTAAATACTACACCAAGTATTAATGACACTAATGATAATGCCA
AAAAAATTAATGTTTCCATGATTAGTAATAACAATAACAATAACAGTAACAATAATAACAACAACA
CTAACAATAGTAGTACAGGAAGTTCTAACATTGCAACATGCTTCCTTCTGTTTCTAATGCAACGA
CAATGAATAACAGTAATAGTATCAATAGCACCACAACAATACTACAATTAACGAAGCTGATGATG
ACGAGTTAATTCCTACTGCGATTGTGATTAAAAATATTCCATTGCCATTAAAAAGGAACAATTGT
TAGATGTGATGACAAAAATTAACTTGCCATTACCATATGCCTTTAATTATCATTTTGATAATGGTG

FIG. 2 - 1

TGTTTCGTGGATTAGCATTTCGCAATTTACATCTACAGATGAGACATCAGCAGTAGTAAACCAAT
TGAATGGAAGAGAAAATAGGTGGAAGAAAATTACGTGTTGAATACAAAAAATGCTTCCGGCACAAG
AAAGAGAACGTATTGAAAGAGAGAAAAGGGAGAAAAGAGGTCAATTGGAAGAACAACATCGTTCTG
CATCAAAATGCTTCTTTGGCTTCTTTATTGTGTCAGCTTCAACTACAGCAGCAACTAAAAATTGGA
GTGTGGCTGGCACAATCCTTCTCATACCACTGAAAGAATGTTTTTAAATTTACCTTTTAAACAATT
CCCTGTTCAATGCCCCACCAGTAGAAATTAATTTTAATGATCTTGAAGTTTTGGAATTGTACACTC
AATTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCAGCATAT
TTGAATATTTCTCAACGGAAAATCATATCAATTTATGTAATTATTTGAATTTATTAGAATTGTTTG
ATAATGGGTTGCTACTAATTAGAAAAAAACCAGGATCCATTGCTCAGTGTATAACTCAAAAATCTA
TTATTCTCAATTTCTCAACAGGTGTCTGGGCCAACTACCCGCACCACCATCAAAAGAATCAACTTC
ACCAACAGCAACAGCAACACACATCAACATCAACATCCTTAACATTCATCATCGATGATGAACCTT
CATCAATTGGGTGGTACATTAGCTGTTCCAGCGCACCATGA

YBL051C_homolog_2 550aa (SEQ ID NO 288)

MDFRNLSTFPNQMGTVMQRRPSLSLSSASGYSSSNYGGNPTPNPNNSNTNNNSSGNSNNNTHGNN
TPKLSTQRLTNNRNLQSLWINQPSIAPSNVVPWVEQQQQQLDLSLENNTKTDSNDASATNNNNVN
VNVNANANVNANANIHAQTHVNTNVNANTTATSINASTILNTTPSINDTNDNAKKINVSMISNNNN
NNSNNNNNNNTNNSSGTSSNIANMLPSVSNATTMNNNSNSINSTNNNTINEADDDDELIPTAIVIKNI
PFAIKKEQLLDVMTKLNPLPYAFNYHFDNGVFRGLAFANFTSTDETSAVVNQLNGREIGGRKLRV
EYKKMLPAQERERIEREKREKRGQLEEQHRSASNASLASLLSAASTTAATKNLSVAGTNPSHTTER
MFLNLPFNNSFFNAPVVEINFNDLEVLLEYTLQVLVYRDDITKSTFELAISSPISFEYFSTENHINLC
NYLNLELFDNGLLLIRKKPGSIAQCITQKSIIPNSQQVSGPTHPHHHQKNQLHOOOQOHTSTSTS
LTFIIDDEPSSIGWYISCSSAP

YBL066C_homolog 3254bp PathoSeq: 1..94/2146..3254, public:
95..2145; CDS: 501..3251 (SEQ ID NO 289)

ATAAAAAAGAAATACAAATTAATAAAATTTTCCTTCTGTGAAAAGGCAATTTCCGGGTCTAGTAGTA
AACAAAGCTTAATAATTTCTCCCATTCAAATTTACAACGGACGATGCAGAAAGTAGTTTTCAAATT
CAGTTTCTTTTCTTTTATATATTTTCTTACTTTCTCTTCTTCTTCTTCTTCTGACAGTATATTAATA
AATATTCTTTTAACTTATTTTTCATCAAGAAGGTACTGAAGATATCAATTAACCTCAGTTAAAG
TCCATATTACCAGTTGTGGAATAATCAGAAGAAAAAAGAGAGAAAAATCACGGGAATTAC
GTTCTCAACAGAAAAATAACAATAATTTTTTTTTTATTCAATCCAAGGTATAACAAGAACGTTAGGAA
TAATATAAAATTATCACCAAAGCTGCCATCAACGTGTGTCGACAACCAATCGACTCCTCCCTTAAC
TAGAACCATAGAACCTCAACATTTGTTTCTATAGAAAAATGAAGTTTGAAAAAGGTAAAGTGAGAA
TTTTGCCTTAACCATCCCCACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA
CTAACTGTAACTCAAAAAGAAAATCAGCAGCCAGTACACCTGGAAATGAATTCAGCAACCAACCA
GAAAATCAAATTTCTACAGCTTCAACACCCAACAGTGCTACACCAACATCAGTCGGAACACCTCCAC
AGAAAACCTCCAAACCAACAGGTCATAGGCCAGTGACTTCATGTACTTTTTGTGCTCAACATAAAA
TCAAATGTAATGCTTCAGATAATTATCCAAACCCATGTGAAAGATGTAAAAAATGGGTTTGAAAT
GTGAAATTGACCCGAATTTAGACCTCGCAAAGGGTCACAAATCCAATCATTGAAACTGGATGTTG
ATGAATTGAAGGCAAGATTGAAATGTTGACTAAAAATGAATCTTTGCTCACACAAGCTTTGAATC
AACACAATTTGAACCACGCTTCGCAACAGCAACAACTGTCTGGATCGCAATCTCAACAACAACATC
CTCCAAATCCACAACGTGCATTGTCTATACGTCTGCAAACTCATCACCACAAGTTGCATTTAGCA
ATGCATCGCCAATTCCTTCTGTGACAAGTATTCAACAAAATGCACCGTTGACTCACGAAAATTCCG
ACAATTCTCCATACGCTTTAAATACACCAGAAAACATTGAAGAATTACAACCAATCTCAGAATTTA
TTTTGGGTGACGTTACTTTGCCATTAAACAGGGCCAATGAGTTACACGACAAGTTTATGACCACAC
ATTTACCAATTTTGCCAATAATAATATCTCGATCTGCCACCGAATGTATCATAAATCTCAATTGC
TTTTCTGGGCCGTGATTCTTACCGCAAGCTTATCAGAACCAGAACCAAACTTTATATGTCGTTGG
CATCCTTAATTAACAATTAGCAATTGAAACATGTTGGATTAAAAACCAAGATCAACTCATGTTA
TCCAAGCCTTGATCATACTTTCAATATGGCCGTTACCTAATGAAAAAGTTTGGATGATTGCTCTT
ATAGATTTGTTGGATTGGCAAAGAATTGTCTATTACAATTAGGTCTACATCGTGGTGGAGAATTCA
TTCAAGAATTTAGTCGGAATCAAGTAAGTCTAGGACCTGATGCAGAAAGGTGGAGGACTCGTTCAT
GGTTAGCAGTTTCTTTTGTGAACAGTTTGGTTCATCATTGTTGGGGTTGCCACCTTCAATAAACA
CTACTGATTATTTATTAGAGAATGCTCGTGTGATAAATCGTTGCCATAAAATTTCCGTTGTTTGA

FIG. 2 - 2

TTTCGCTATCTATTTTCCAATGCAAATTAGTTAATATTATGGGTATTAGCGTTACTAGACCAGACG
GTTTATTGGAGCCTCTGAATCGTGCTGGTTCACCTTAGTTTATTGGATAGAGAATTGGAAAGATTAA
GATTTAAACTTCAATTTGAAGAAGGGGGGCCAATTGAAGTATATTATTTGTATATTAAATTGATGA
TCTGCTGCTTTGCCTTTTTACCAGGTACACCTATCGAGGATCAAGTCAAGTATGTCAGTTTTGCAT
ATTTATCAGCAACAAGAATCGTGACAATCGTTTCTAAAATGGTGAATGACATTTTCATTGATTGAAT
TGCCAATATATATCAGACAAGCAGTGACATATAGTGTTCATGTTGTTCAAATTACATTTGTCAA
GATATTTGATTGACAAGTATGTGGATAGTGCTAGACAGCTGATTGTTACTGTGCATCGTTTATTTA
GAAACACGTTGAGTTCCTGGAAAGATTTGCAAAACGATATTTCTCGAACAGCCAAAGTTCTAGAAA
ATTTGAACATGGTGTGTATAATTATCCTGAAATATTTTAAATGATCTGGAAAATGAGGATTCAA
GTATTATCACCAGAATGAGGTCACATTTGACAGCATCTTTATTCTATGATTTGGTTTGGTGTGTAC
ATGAGGCAAGAAGACGATCAGTACTTGATAAGGGGAAAAGACAGGCTCAGCCTAACAGAAAATCT
TGCCCTTGCCATTTTACAACCAAATCACTAAGGATGATTTCAAGACAATTACCACGACATCACCTA
ATGGAACTACTATTACTACATTAGTTCCAACGATCAAGCTATGAATCAAGCAAAACTGAAATCTT
TTGATTCCAGCAAACCACTTGAAATAAATGGTATTCCCTTACCTATGCTTGAAGCTACTGGTTCAA
CAAGAGAAGTTTTAGATTCTTTACCCTCGCAATCTTTACCATCACAAGCACCAACTCTTCAGCAGT
ATCCAATGCAGCAAGATCAACAACAGCAAGAACCATCACAACAACAACAACAAAGCACCCTGCAGC
AACTGCAGCAATACCAACAACAGCAGCAATCGAATCAACAGCAACCACATCTTCAACATCAAAGAC
AGTTTCAACAATCACCACCACCGCAATTTCAATGATTTCTTCAACGCCGCCCTTCAGCAACCAC
CTTTTATTTTGGCAAACCTCACCCTTACCACAACTTATTTGCCAAAAGATTGATGAAATGAATATGT
CACCAGAAGTAAACAAGAAAACCTCTGTTGCTCCATTTGCATCTCAAATCACCAACTTTTTTGATC
AACAAACAAGTGGATGGTTTAATAATGATAACCAAGATGACGACTTTTTGGGTTGGTTTGATGTTA
ATATGATGCAAGAGAAATAA

YBL066C_homolog 917aa (SEQ ID NO 290)

MKFEKGKVRILPKPSPTPTNPQTPLPLPAQTKPVNSKRKSAASTPGNESKSKSRKSNSTASTPNSA
TPTSVGTPPQKTSKPTGHRPVTSCFTCRQHKIKCNASDNYPNPCERCKKMGLKCEIDPEFRPRKGS
QIQSLKSDVDELKAKIEMLTKNESLLTQALNQHNLNHASQQQQSSGSQSQQQHPPNPQRALSYS
NSSPQVAFSNASPIPSVTSIQQNAPLTHENSNDNSPYALNTPENIEELQPISEFILGDVTLPLN
ELHDKFMTTHLPFLPIIISRSATELYHKSQLLFWAVILTASLSEPEPKLYMSLASLIKQLAIETC
IKTPRSTHVIQALIILSIWPLPNEKVLDDCSYRFVGLAKNLSLQLGLHRGGEFIQEF SRNQVSLGP
DAERWRTRSWLAVFFCEQFWSSLLGLPPSINTDYLLLENARVDKSLPKNFRCLISLSIFQCKLVNI
MGISVTRPDGELLEPSNRAGLSLLDRELERLRFKLQFEEGGPIEVYLYIKLMICCFALPGTPIE
DQVKYVSFAYL SATRIVTIVSKMVNDISLIELPIYIRQAVTYSVFMFLKHLHSRYLIDKYVDSARQ
SIVTVHRLFRNTLSSWKDLQNDISRTAKVLENLNMVLYNYPEIFLNDSENESSIIITRMRSHTAS
LFYDLVWCVHEARRRSVLDKGKRQAQPNKKILPLPFYNQITKDDFKITTTSPNGTTITTLVPTDQ
AMNQA KSKSFDSSKPLEINGIPLPMEATGSTREVLDLSLPSQSLPSQAPTLOQYPMQOQDQQQEPS
QQQQKHSSQQYQQYQQQQSNQQPHLQHQRFQQSPFPQFSMISSTPPLQPPFILANSPLPQTY
LPKIDEMNMSPEVKQENSVAPFASQITNFFDQQTSGWFNNDNQDDDFLGWFDVNMMEK

YBL078C_homolog 908bp public: 1..908; exon 1: 417..449, intron 1:
450..533, exon 2: 534..908 (SEQ ID NO 291)

TTATTATTACTATGACACACACTTACTCTCTTCTATGTCTCCGCTTACATCACACATCATACGTTT
GAAAACACCCACCCCTTTTTCTTATCTACAAAAAAAATAACAACTCACATATACTACTAAAC
CTTTTTTTTTTATTTATTTATTTTGTATTTTGTATATTAATCAAATATTATCATCTATATA
TACATCCCCATCGATTCTATCTGACATAATAGTATGTATGATCATAACAGAGGAAAATCACCTTTT
TATTATTACCAAGGTCTCAATGATTAGTGTGGCTAGCGTCTGTTACTACTTACCCCGTGTGTAG
ATAATTGCCACTCAATCTTTAATTGACCATCGACCACAAAATAATATGGAAATAATACTAACAGA
ACTTAGAAACATCACTCATAATGAGATCACAATTCAGAGCAGCATCCTTTTGGTATGTATTACA
TGATTTTTAGTCCCTCTGAATCTTCTTCCGATCATCATATACTAACATTTTCGTGGGTGTATTCTT
TAATAGAAAAGAGACAAGCCGAGGCAGCCAGAATTGCTCAGAGGTTCAAGGATAGAGTACCAGTCA
TCTGTGAAAAGGTTGAGAATTCGATATCCCCGAAATTGATAAACGTAAATATTTAGTGCCAGTGG
ATTTGACTGTTGGTCAATTTGTTTACGTTATTAGAAAAAGAAATCAAGTTACCAAGCGAAAAAGCCA
TTTTCATCTTTGTCAATGACATATTACCCCAACCGCTGCATTAATCAGTACAATCTACGAAGAAC

FIG. 2 - 3

ACAAGGACGAAGATGGTTTCTTATACGTTTTTATACTCTGGAGAGAATACTTTTGGCGAGAACTAG
CAATTGACATTTTCATCATTAGATTTTCAGTGATATCCCTGATTATGTTTAA

YBL078C_homolog 135aa (SEQ ID NO 292)

MRSQFKDEHPFEKRQAEAARIAQRFKDRVPVICEKVENSIDIPEIDKRKYLVPVDLTVGQFVYVIRK
RIKLPSEKAIFIVNDILPPTAALISTIEEHKDEDGFLYVLVYSGENTFGEKLAIIDISSLDFSDIP
DYV

YBR073W_homolog 2891bp PathoSeq: 1..2891; CDS: 501..2888 (SEQ ID
NO 293)

GTGGCACATCCCAGGAAGTAGAGCATGGACAGTTCGTATGGTATTGCTGTGCATACGATACAAAAA
AACAGAAACGAGAAAAAAATCGATCGTCAACCTTTTATCAACTCATCTACAGCAGCAGCAAAGTT
CGTCCCATAATATGAGTCAAGTCCAACAGAAACCCAAATCGTTTGGTAGATTGTATACCATGTACT
ACTTTTCATTTTCCATTTGTTATGCTTACGACAACCTGAAACCATGCTACTTCATACGTTTGTATTGA
TGTTTGCCTTATTGGTTGCCATGGGATCTACGCTTATTTGCCTTCAAGTATCATGTTTGCAATCT
CCAGAGCATACTATTATGTTTTTGGCATGGATATTAGTACCATCAACGGTTATGCAAAGTAGCGCT
GTCTACTTAGTTTTATAGTTTAAAAATTTGTTAATATAAAACCCAAAGTTTCTAACAGGCTCTGTTT
GCTCGACTAAAAAGAATTTTGTCAAACGCGTATCAGAATGTTTACCCTTTTTTTTTTACCACAG
ATCAAATGAATGTTTCGACCTAATGCTCCGTTTCGGCCTCCTAGACCAATAAAGGGGGGTGTTGCGG
TGGTGCAGAAAGTAGTAAACGAAAATTGCCCACTACCACCAATCCTAAACCTGCAAAGATTTTGA
CTACCGATCCCGGCTCAACAAAATACGTGATCCAATGGAGAAAGAAAACCTCAAAGAAGAACAAAA
CATGGGACGGTGATGGGTATGCCGTGATTAAACAGCTTGAGAATGGGGCATGCGAGATATCTATCA
AGAACTCTGATGGCAAACCTATGGGGAAAAGAGTGTCTACTGCGACACCTAACCTTGACGACGTGA
TTAGTGTGGGACCCATGAATTAGAATTAGACGAAAAAGTAGGGTCTAACTCAACTCCCCAGACAG
TGACACGTGTTACCCACCAGTTCAAAAAGGTTGCTCCTCCACAGCTAGTAGTCGGAAAACCGCTTT
ATGACGACTGTGCCGATGCCATCGCGTTGCCTCCTCCTCCAAAAGCCAAAGATTATGTCAAAGTAA
ATATCGATCCACATTTGGCAAAGTGCTTCGTCCGCATCAGGTTGAAGGTGTGAAGTTTATGTATG
AGTGTTTAATGGGGTACCGTGGGTTTGGCGGGCACGGGTGTTTGTAGCAGATGAAATGGGGTTGG
GAAAACGTTGATGACAATCACTACAATCTGGACGTTGCTCAAACAAAACCCGTTTATGGAAAAAG
GTGCACTGGTAAATAAGGTATTGGTGGTGTGTCTGTACGCTTATTTCCAATTGGAGACAGGAGT
TTAGGAAATGGTTAGGTGCTAATAAGCTAAACGTGTTGACGCTCAACAACCCAATGTCAAACGAGA
AACAGGATATACTCAATTTTGGAAAGTTGAATGTGTACCAAGTGTAGTGGTGAATTATGAAAAAC
TTGTGGCACATTTTGTGAACTCTCAGCGGTCAAGTTTGAATTTGTAGTGTGTGACGAGGGCCATC
GTTTGAAGAATAGTGCAAATAAAGTATTGAATAATCTTATCAAGCTCAATATTCCGAAGAAAATTG
TTTTGACGGGTACGCCGATTCAAAACGAGTTGGTAGAGTTTACACGTTGATCTCGTTTCTCAACC
CGGGTGTGCTTCCCGAGCTAAAATTGTTTCAGCGAAACCTTTATAACACCTATATCTAGGGCCCGAG
ATATCAACTGTTTTTGACCCTGAAGTGAAGAAACGCGGTGAAGAGATATCGCAGCAGTTGATTGAAT
TGACTCAGAGTTTTATTCTTAGACGTACACAAGCGATTTTGGCTAATTACTTGACACAGAAAACCTG
ACATTTTGTGTTTGTTCACCTACATCGTTGCAGCTCAAGTTGTTTCGACTATATAACCAACTTGA
AGAAATTTAATCAGTTTGAGGCATTTACCATGATCAATTTGTTTAAAAAGATTTGCAATTTCCCTT
CGTTGTTGGCCGACGACGAGTTATTTAAAAAGATTGTTGAAGAAAAGTTAATTTGGGGATGGCAT
CCGTTAAAAATAAACATTTCTTGTGCCGTTGCTATTGGAAATTGCTTCGCTTGGGGAAAAGATTGTCT
TAATTTCCAACCTACACCAAGACTTTGGACTTGTGGAACAGGTTTTCGCAAGGTCAGCCTAACAT
TTTCGAGATTAGATGGGTGACCCCCAACAAATGTGCGTAGCAAGTTGGTTAATCAGTTTAACACGA
ACCCCGACATAAACGTATTTTTATTGTCGTCGAAATCTGGCGGGATGGGGATCAACTTGGTCGGGG
CTTCGAGGTTGATTTTGTGTTGACAATGACTGGAACCCAGCGACCGATTGCAATCGATGTCGCGAA
TTCACAGAGACGGACAATTGAAACCGTGTTCATTTATAGGCTATTACCACGGGGTGTATTGACG
AGAAAATCTTTTCAGCGACAGCTCGTGAAGAACAAATTGAGTTCCAAGTTTTTGGACAATGACGCCA
CGTCCAAATCTGATGTGTTTGAACAATGATGATTTGAAGAATATTTTTGAGATAGATACATCGACAA
TATCCAATACTCATGATTTATTAGAGTGTGTGTGTGAGGGCGACGGGTCGATGTTGAGTCAGCCAA
CCATAGAGGAAAGCGAACCACCCCCAAAACAAGCATGGGTTACTGCATTAGAGCTTAAGAAGAAGA
TTGACGATGGTGAGGCGCTAAAGAGGACGGCTGTTAAATTTGCCTTGAACGATTATCGACACTACA
ATCCAGAGGTGAACCGTAATTTGGATTTTGATTCTGCGCTACACCGAATTGCTAACAATTCAGCT
ATGAAAATAAGCAATTGCCAATTACATTTATAATGCTGAGAGTAACTAATTAA

FIG. 2 - 4

YBR073W_homolog 796aa (SEQ ID NO 294)

MFTLFFFTTDQMNVRPNAPFRPPRPIKGGVAVVQKVVRKRLPTTTNPKPAKILTTDPGSTKYVIQW
RKKTSSKKNKTWDGDGYAVIKQLENGACEISIKNSDGKPMGKRVFTATPNLDDVISVGPYELELDEK
VGSNSTPQTVTRVTHQFKKVAPPTASSRKPLYDDCADAIALPPPPKAKDYVKVNIDPHLAKVLRPH
QVEGVKFMYECLMGYRGFGGHHGCLLADEMGLGKTLMTITTTIWTLLKQNPFMKEGAVVNKVLVPCPV
TLISNWRQEFRKWL GANKLVLT LNNPMSNEKQDILNFGKLVNYQVLVVNYEKLVAHFDELSAVKF
DLLVCDEGHRLKNSANKVLNLIKLNI PKKIVLTGTPIQNELVEFHTLISFLNPGVLPELKLQFN
FITPISRARDINCFDPEVKKRGEESQQLIELTQSFILRRTOAILANYLTQKTDILLFVPPSTLQL
KLFDYITNLKKFNQFEAFTMINLFFKKICNSPSSLADDELFFKIVEEKFNLGMASGKINILVPLLE
IASLGEKIVLISNYTKTLDLLEQVLRKVS LTF SRLDGSTPNNVRSKLVNQFNTPDINVFLSSKS
GGMGINLVGASRLILFDNDWNPATDLQSMSRIHRDGQLKPCFIYRLFTTG CIDEKIFQRQLVKNKL
SSKFLDNDATSKSDVFDNDLKNIFEIDTSTISNTHDLECVCEGDGSMLSQPTIEESEPPPKQAW
VTALELKKKIDDGEALKRTAVKFALNDYRHYNPEVNRNLDFDSALHRIANNSSYENKQLPITFIMS
RVTN

YBR086C_homolog 2643bp PathoSeq: 1..2643; CDS: 501..>2643 (SEQ ID NO 295)

AAAGAATTTCAAATTTAGTTT TAGGTGATAATTATCGTTCGTCCTTTCTTAACCTACCAATTTTGA
CTTTGTGTACTCATACGATGGTTGTTATTAGTTAAAGTTGCTTTGCTTTTCAATTTCAATT
TCACAATTGAATTT CAGAATAGAAATTAGTTTACCTTTTCTTACAATCGGCTAAGATTTTTTTTCA
TTCTTCTAATTTAGTTTACAGAATAGAAAGAATAGTTTGCTTGTTTGCTCATATTTACAATCAATT
GGTTATTGGTGTTTATTATTTT TTTTGGTTCTCTTTTACCCCCCTTCCGCTCAATTGAGTTA
TTGTTTGGGAATAATTTATTACTTATTCAATATATTTTTTCTTCTCTTCCCTTCTTCAACTTCTTC
TTTATACATTTCAATCAACCTTCCAACAATCCTATAATTAATTACTTACTTACTTACTTCAATTGGATTA
ATTGGATTGGAATTGTTACAATTGAATACTTCAACGAGATGACTTTACCAATTCAGGATTTAGAAC
CTGATTATTATATTTCCGTCAATTATCCTACCACCGATAATGGATCACCAACCCACAAAGCTGAAA
AATCATTGAAAACATTAATTGATTTATTATACGATAAAGGGTTTGCCGCCCAAATTAGACCTGGTG
ATTTAGACCATTTGTAGTCTTTGTTAAATTGTCTTCATACAAGTTTCTGAAGAAGCTGAAAAAG
ATTTAATTA AAAATTAATGAATTTGGTGTCACGGGTAAAGATGACGTGTTAGCTTCTAAACTTAGAA
TTATTATCAATACTTA ACTTATCCACAATCAGTTGGTGATGTGGTATTACTCCTAATTTCTGGGG
ATTGGAATTTGTCAACAGTATTGTTCCAATTACTAATGCTTTAATGAAACCACTTTAGTTGAAG
ATTTAAAAATTAATGTTACTCAACCAAATTTATCAATTGCCACTATCAAAAAGACATATGGAGTTG
AAGTTGCTCTTTATTTTGAATATATAAAACATTACACTTTTGGTTATTATTGCTTTCTATTATTG
GTCTTGATCTCATTTTAGAAAAGATAAACGATTCTGTAACTTTTGCCTTTATCAATTTGCTTT
GGGGGGTTTATTCTTGCATCATGGCATAGAAGAGAACAACATTTGGTTAATGTATGGGGTGTTT
AAAATAGTCATTTAATTGAAGAACATAATCCGAATTGGCTAAAGTCAATGAAAGATATGAAGAAA
AATCAACTTATTTCCATGCAAATAATACCAATGGATTGAGTTT TTTTAAAACAATTTGGCATTATCC
CCATTGCCCTTGGTGTTTGTGGTGTTTGTGATTAGTTATCAATTGAGTTGTTTCTGTATTGAAATCT
TTTTAACC GATATTTATGATGGCCCCGGGAAATCTTTATTGACTTTATTACCAACGGTTTAAATCA
GTGTATTTGTGCCAATTTTGACCATTTGTTTATAATGCTGTCACGGATATTATTATTAAATGGGAAA
ATCATGATAACCAATATAGCAAAAATAATTCTATTCTTGTAAACCTTTGTGTTGAATTTCTTGA
CTGGTTATGTTCCATTAATCATCACTTCATTCATATATTACCATTGTGCTCATTTGGTGCAACCTC
ATTTAGGTGATATTA AAAACCACTATTGCCACATATGCTGGTGAAAATAGATTCTACACCAAATACT
TGTTGAAATTAAGAGTCAAGAAGAAATTTAAATCAATCAAGGTAGATTAGATGCTCAATTTCTTT
ATTTCAATTGTCACAAATCAAGTTATACAATTGGTATTGAAATATATTCTCCCATTTGGGTTTAAGAT
TTGTATTTAATTTTATTGAAACGAAAATTCAGAAGAAACCTCAATTACAAACTAAAGATGATAACC
CTGATGAATCTATTTGGTTACATAATGTCAGATTATCGTTGAAACTTCTGAAATATAATGTTGATG
ATGATTTTAGAGGATTAGTTTACAATTTGGATATTTGATAATGTTTGGTCCAGTTTGGCCATTGG
CACCATTGGTTTGTATTATTTCAATTTAATTTTTTCAAGTTGGATAATTTTAAATTATTGAATG
GTAAATATTTTCAAACCACCAAGTTCCAAGAAGAGTTGATTCTATTTCATCCATGGAATTTAGCCCTTT
TCTTGTTAGCATGGATTGGATCAATTATTTCCCCCGTGGTCACGGCATTTTACCGTCATGGTACTG
CTCCACCAAAATCTATGGGTCAATTTGCCCTTGATAAAGCTAGTGTTTCATGTTTCATCCTCAGTTT
TCTTGGTTTATTAATGTTTGTTCAGAACATGGATTTTGTATTTTGAGTTATCTTTTATTGAAAT
TCTCTTCTTTGTTCAAGAGTCAAGTTGAATGGGAAAATGATTTTGTGATAATGATATTAAATTGA

FIG. 2 - 5

GACATGATTATTATTCTGGGAAAGTAAAACCAACTTATAAAGTCCACTCGGATGAGTTGTGGGAGA
AGTTTACCCCAACAATCAACTTTGAATTTCACTGGTCTAAACCAACCGCAGAACTGATGATAAAG
TTGAAAAAATTGCTTCTACCGAAGATGCTTATCTGACTTCTGCAGAAAAATCTACTACTGCTA
CTT

YBR086C_homolog 714aa (SEQ ID NO 296)

MTLPIDLEPDYIISVNYPTTDNGSPTPQAEKSLKTLIDLLYDKGFAAQIRPGDLHLVFKLSS
YKFSEEAEDLIKNYEFGVTGKDDVLASKLRRIYQYLTPQSVGGCGITPNSGDWKFTSIVPITN
AFNETTLVEDLKINVTQPNLSIATIKKTYGVEVALYFEYIKHYTFWLLLLLSIIGLVSHFRKDKRFS
LTFAFINLLWGVFLASWHRREQHLVNVWGVQNSHLIEEHNSSELAKVNEREYEEKSTYFHANNTNGF
RFLKQLAFIPIALVFVGVLSYQLSCFCIEIFLTDIYDGPGLSLTLLPTVLISVFPILTIVYNA
VTDIIKWENHDNQYSKNSILVKTFLNFLTGYVPLIITSFIYLPFAHLVQPHLGDIKTTIATYA
GENRFYTKYLLKLKSQEEFKINQGRDLAQFFYFIVTNQVIQLVLKYILPLGLRFVFNFIETKIQKK
PQLQTKDDNPDESIWLNHVRSLKLPEYNVDDDFRGLVLQFGYLIMFGPVWPLAPLVCIIFNLIFF
KLDNFKLLNGKYFKPPVPRRVDSIHPWNALFLLAWIGSIIISPVVTAFYRHGTAPPKSMGQFALDK
ASVHVSSSVFLVLLMFVSEHGFLILSYLLFEFSSLFKSQVEWENDFVDNDIKLRHDYYSKVKPTY
KVHSDDELWEKFTPQSTLNTGPKPTAETDDKVEKIASTEDAYSTSAEKSTTTAT

YBR093C_homolog_1 1784bp public: 1..607, PathoSeq: 608..1784; CDS:
399..1781 (SEQ ID NO 297)

CGGTAATTATGTCACAAAAACAACAATCAACATATTAAATCGTTATCCCAACTTTGTGCTAGTTTAA
CTAACACCTTTTATTTTGTGTTATACAAATTGCACAATCAATTACTATAACTTTTTTTGAAACGT
GGGCTCTGTTTAGTTTAACCTCTTGTAGTTTATTATTCCGATTGGGTTAGCTCAATAACTGCATT
TCGTACAATAATGTTAATTCAATTCTAAATTCGATGAACCGAACACACAAAAACATCCAGTTCT
GGAGAGATTTTCAAACTTCTATTATAAATAGAACCCTATAAGTCCATAATAATTCAATTGAAGG
ATTATTTCTTTTCCCTTTTCTGATTACTTTACCAATTTTCTTCTCTCCAAAAAACACCTTCT
TCATGGTTTCTGTTTCTAAATTAATCAATAACGGGTTGTTATTAAGTCAAGTGTCTTCCAAAG
ATGTTGCTACTCCGCAACAAGCTTCTGTGCAACAATACAATATACTCAATTTTCTTGGCGGTAGTG
CCCCTTATATTCAAAGAAACGGATATGGGATTTCTACTGATATCCCTGCTGGTTGTGAAATTGCTC
AAATTCATTTGTATTCAAGACATGGTGAAAGATACCCAAGTAAAAGTAATGGTAAAAGTTTAGAAG
CAATTTATGCTAAATTTGAAACTACAAAGGTACTTTTAAAGGTGATTGTGCTATTCTTAAATGATT
ACACTTATTTTGTCAAAGACCAGAGTAAGTATGCTAAGGAACTAGCCCAAAAAATTCTGAAGGAA
CCTATGCCGGTACAACCAATGCCTTGCCTCATGGTGCTGCGTTTAGAGCCAAATATGGATCCTTAT
ACAAGGAAAACTCAACTTTACCAATCTTCACATCCAATTCTAACAGAGTACATGAAACTTCAAAGT
ATTTGCTAGAGGGTTTGTAGGTGATGATTATGAAGAAGGTAAAAGTGTCAAGTTTAAATCATCT
CTGAAGATGCTGATCTTGGTGCCAATAGTTTGACTCCTAGAAGTGCATGTTCCAAGAACAAAGAAC
TGAGCAGTAGTACTGCCAAAAAATATAACACAACATATTTAAATGCTATTGCTGAAAGATTAGTTA
AACCAAAACCAGGTTTGAATTTGACTACAAGTGATGTCAACAATTTATTCAGTTGGTGTGCTTATG
AAATCAACGTCAGAGGAAGTTCACCATCTGTGATTTATTCACCAATGAAGAATTCATTAAAGAACT
CTTATGGTAACGATCTTTCCAAATATTATTCTAATGGTGCTGGTAATAATTACACCAGAATCATTG
GTTCAAGTATTTGAATTCATCCTTGGAACTTTTGAAGGACACTAAGAACTCTAATCAAGTATGGT
TATCATTTGCTCATGATACCTGATTTGGAAATTTCCATTCTGCTTTAGGATTATTGGAACCAGCTG
AAGATTTACCAACATCTTACATCCCATTCCTTAACCCATACGTCATTTCTTCTATTGTTCCACAAG
GTGCCAGAAATATACACAGAAAACTTCAATGTGGAACGATGCTTATGTTAGATACATTATCAACG
ATGCTGTGCTGCCAATTCCAAATGTGCTACTGGTCCAGGGTTCTCTTGTAAACTTGATGATTTTG
AAAATTTGCTTAAAGAAAGAAATGGAGATGTTGACTTTGTTAAACAATGTGGTGTCAATAGTACCT
ACCATCTGAGCTTACTTTCTACTGGGATTATAAAAAATGTCACTTACAGTGCTCCTTTAGAATTGT
AA

YBR093C_homolog_1 461aa (SEQ ID NO 298)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHERYPSKSNGKSLEAIYAKFENYKGTFGKDLNFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAAPRAKYGSLEYKENSTLPIFTSNSNRVHETSKYFARGFLGDDYEEGKTVKFNIIS

FIG. 2 - 6

EDADLGANSLTPRSACSKNKESSTAKKYNTTYLNAIAERLVKPNPGLNLTTSVDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNSSLELLKDTKNSNQVWL
SFAHDTDL EIFHSALGLLEPAEDLPTSYPFPNPVYHSSIVPQGARIYTEKLQCGNDAYVRYI IND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFVKQCGVNSTYPSELTFYWDYKQNVYTSAPLEL

YBR093C_homolog_2 1871bp public: 1..1752, PathoSeq: 1753..1871;
CDS: 501..1868 (SEQ ID NO 299)

GAGTTTTATGGGATTGGGTTTTTCAATTAAAGACTCTTCGTGATAATGCAATACCAAAACCAAAT
TTATTTAACGATGCAATAATTATTTCAATGTGAGCTATCCATGAATCAGTGAGAATCTTTATTATG
GAAGAAATTGGTCAAAATTTGACAATGTTTAGTAACCTTTATATCTTGGTGTGGGATGGTGCCACA
AATGGAGATTGTTGAGTGACATGAAAAATACGTAGTTAAATTTTGTCTTGTCTTTATTATTATTA
GCCACTTTTTTATCCGATTCTTCATATTACCTTTGGTAAAGTGATAAGATTAATATCATATTAGTA
AAACACCCCCAATGATGAATGTTTGTATTTATAGCCAGACTATAAAAATTACGGGGATTTAATTCG
CGACTCACCCACGTTCTCACACAGTATGTGCTTTTTTTCATAAGTATGATTTGAACCCATAAATATC
AACTTTCATAATAAACATAATTCTTTCCAGACAACATAAATGGTTGGTTTATCACGAGTACTTAATG
CTGGGTTTTATTCTAAGTGGACAATCTGTTTTCCAGGATGTTGCTGCCCCACATCAAGCATCAATTG
AACAAATATAATATTGTCAAGTACCTTGGTGGCAGCGGTCCATATATTCAAAATTCAGGGTATGGGA
TTTCTACTGATATACCAGAAAAATGCACTATTGAACAAAGTCAAATGATTAGTAGACATGGTGAGC
GATTTCTTAGTAAAGGAGATGGGAAATACTTTAATTCAGTGATGGAAGTTTTCAAGAGATATGGTG
AATTTCTAGGAGATTTATCTTTTTTAAATGACTATGATATTTTCGTTACTAATCCAGATTATTATG
AAAAGGAGACTACTCTAAAAACTCAAAAGGTCCATATTTTGGAACTACAAATTTATTACGATATG
GAGCTTATTTTAGAAAAAGATATCAATCACTATTTGACCAAAAGGAGAAGCTTGTGTGTTTACTA
GTAATTCGGAAGGTGTTATCAAAGTGGTGTCTATTTGCTCGAGGATTTTAGGAGATGATTACT
CAGAAGATACAGTTGAATTTGTTGTTGTTGATGAAGACAAAAAATGGGTGGTAATTCATTGACAC
CAAGATACGCTTGTA AAACTTTGAATCAAGATTTACACAAAGATTTGGTGAATCAGTACGATAAGA
CTTATTTGGACGATATTTTATCTAGATGGCTAGTAGACAATCCTGGATTAGATTTAAGTGCAGATC
AGGTCTCGTCATTATTTCTTTGGTGTGCTTTTGAGATTAACGTTAGGGGGTATTCTCCATTCTGCA
ATCTATTTACAAAAGATGAATTTATCAGAAGTGGGTACCGAAACGATGTTGGTAATTACTATCAAA
CTGGTCCAGGTAATAATATGACAAAGGTAATTGGCTCACCTATGGTGAAGCGTCGTTGAAAATGC
TTCAAGAAGATTCAAAAATTTGGTTGACATTTACCCATGATACCTGATATTGAGATGTATTTGACAT
CTTTGGGATTGATTGTTCCACCAGGGGATTTGCCCCGTTGATCGAGTACCATTCCCAATCCATATA
ATGCAGCAGAATTTTCCCTCAAGGTGCTAGAACTTACACTGAAAAATTGAAATGTGGTGAAAAGC
AATATGTTAGATTTATTGTGAATGATGCAGTTTATCCATATCCGGATTGTAGTGGAGGCTCTGGGT
TTACTTGTGAATTGAATGATTTTATCAAATTAGTTAAAAAGTCGTTTACATGATGTTGACTATAAGC
TTCAATGTGAAGTGGACGGACGACGGAATTGACATTTTATTTGGGATTATAAAGACAGAAAGTATA
ATGCGCCGTTAATAGATCAGTAA

YBR093C_homolog_2 456aa (SEQ ID NO 300)

MVGLSRVLNAGFILSGQSVFQDVAAPHQASIEQYNIVKYLGGSGPYIQNSGYGISTDIPEKCTIEQ
VQMISRHGERFPSKGDGKYFNSVMEVFVKRYGEFHGDLNFLNDYEFVTNPDYEEKETPKNSKGPY
FGTTNLLRHGAYFRKRYQSLFDQKEKLVVFTSNSGRCYQSGVYFARGFLGDDYSEDVFEVVVDED
KKMGNSLTPRYACKTLNQDLHKDLVNQYDKTYLDDILSRWLVDNPGDLDSADQVSSLFLWCAFEI
NVRGYSPFCNLFTKDEFIRSGYRNDVGNYYQTGPGNNMTKVIGSPMVEASLKMLQEDSKIWLFTFH
DIDIEMYLTSGLIVPPGDLVDRVPFNPYNAAEFFPQGARTYTEKLKCGEKQYVRFIVNDAVYP
YPDCSGGPGFTCELNDFIKLVKSRSLHDVDYKLQCEVDGPAELTFYWDYKDRKYNAPLIDQ

YBR093C_homolog_3 1888bp PathoSeq: 1..1656, public: 1657..1888;
CDS: 500..1885 (SEQ ID NO 301)

TGTAGTATAAATAAGGGTATGAAATACCAACATCCAGAATATCAACGAGATAGAAGAGAGGAGTT
TCAATATATATCTTGTGAATAATAACTTCGTTCTAATTCACTATACACAACCTAGACGTGTACACGC
TCAATCTCAGGTAAAGAAAGTTTATATTCCATCACTATATAACAACAATCAGGCTTTGCAAAAAA
CATTTAAACCTAATACTGGTAATATGGAATATAACGCCTCGTAGTTCTACGCACGTGGCATCCTT
TATCTATTTTCAATTTACCCCTAATTTATGAATTAGCTTAATAAGAGCAGTCAAATTAACACGG
CTCAATTAATAGTACTTAATAATATGAAGCCGATCAATTAACCGATCCTTTGAATAATTTGAAAT

FIG. 2 - 7

AAAATAAGTAATATAAATAGGTATGCATTTTCCCTACATTTATTTCTCTTTCTATTTTAAATTTG
TTTCCTAAACAGCAACAACAACAAATTGAAATTCAAAAATGGTTTCTGTTTCTAAATTATTGAACAA
TGGATTGTTATTAGCTGGTCAAAGTGTCTTCCAAGATGTTGCTACTCCACAGCAAGCTTCTGTGCA
ACAATATAACATCGTCAATTCTCTTGGCGGTAGTGCCCCCTATATTCAAAGAAACGGATATGGGAT
TTCTACTGATATCCCTGCTGGTTGTGAAATTGCTCAAATTCATTTGTATTCAAGACATGGTGAAAG
ATACCCAAGTAAAAGTAATGGTAAAAGTTTAGAAGCAATTTATGCTAAATTTGAAAACTACAAAGG
TACTTTTAAAGGTGATTTGGCTTTCTTAAATGATTATATCTTATTTTGTACTGATAAAAAACAATTA
CGAAAAGGAACTAGCCCCAAAAAATTCTGAAGGAACCTATGCCGGTACAACCAATGCCCTTGCCTCA
CGGTGCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAAATTCAACATTACCAGTTTCTC
TTCCAATTCAGGTAGATGTTACCAAACTTCAAGATATTTTGTAGAGGATTTTGTAGGTGATGACTT
TAAAGAAGGTAAAACGTGTCAAGTTTAAACATCATTTCTGAAGATGCTGATGTTGGTGCCAATAGTTT
GACTCCAAGAAGTGCATGTTCCAAGAACAAGAACGGAGCAGTAGTACTGCCAAAAAATATAACAC
AACATATTTAAATGCTATCACTGAAAGATTAGTTAAACCAACCCAGGTTTGAATTTGACTACAAAG
TGATGTCAACAATTTTATTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCACCATTTCTG
TGATTTATTCACCAATGAAGAGTTTATCAAATATTCTTATGGTAATGACCTTTCCAACATATTATTC
TAATGGTGTGGTAAACAATTACACCAGAATCATTGGTTCAGTGATTTTAAATTTCTCTTTAGAACT
TTTAAAAGACACTAAAACTCTAATCAAGTATGGTTATCATTTGCTCATGATACTGATTTAGAAAT
TTTCCATTCGTCTTAGGATTATTGGAACCAGCTGAAGATTTACCAACATCTTACATCCCATTCCC
TAACCCATACGTCCATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAACTTCAATG
TGGAAACGATGCTTATGTTAGATACATTATCAACGATGCTGTCGTGCCAATTTCCAAAATGTGCTAC
TGGTCCAGGGTTCTTGTAACTTGATGATTTTGAATAATTCGTTAAAGAAAGAAATTGGAGATGT
TGACTTTGTTAAACAATGTGGTGTCAATAGTACCTACCCATCTGAGCTTACTTTCTACTGGGATTA
TAAAAATGTCACTTACAATGCTCCTTTAGGTGATTTTAA

YBR093C_homolog_3 462aa (SEQ ID NO 302)

MVSVSKLLNGLLLAGQSVFQDVATPQQASVQYQYNIIVNSLGGSAPIYQIRNGYGIISTDIPAGCEIAQ
IQLYSRHGERYPKSNKSLKLEIYAKFENYKGTGFKGDLAFLNDYTYFVTDKNNYEKETSPKNSEGT
YAGTTNALRHGAARAKYGSYLYKENSTLPVFSSNSGRCYQTSRYFARGFLGDDFKEGKTVKFNIIS
EDADVANSITPPRSACSKNKERSSTAKKYNTTYLNAITERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKYSYGNLDSNYYSNGAGNNYTRIIGSVILNSSLELLKDKTNSNQVWL
SFAHDTDLLEIFHSALGLLEPAEDLPTSYIPFPNPYVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVFVKQCGVNSTYPSLTFYWDYKNVYTNAPLGDF

YBR093C_homolog_4 1886bp PathoSeq: 1..102/1038..1062/1078..1886,
public: 103..1037/1063..1077; CDS: 501..1883 (SEQ ID NO 303)

ACTACTTAAATTGGCATATCCAAACAACTTGAAGTAGGAGTTTCTTATTTTATTTTGTATTTA
TATATTTGATTGCGATTAAATGTCATAAATTTTAGTTCGGTAATTATGTCACAAAAACAAACAATCA
ACATATTAAATCGTTATCCCAACTTTGTGCTAGTTTACTAACACCTTTTATTTTGTGTTATACAAAT
TGCACAATCAATTACTATAACTTTTTTTTGAACGTTGGCTCTGTTTAGTTTAACTTCTTGTAGTT
TTATTTATTCGGATTGGGTAGCTCAATAACTGCATTTTCGTACAATAATGTTAATTCATTTCTAAAT
TCCGATGAACCGAACACACAAAAACATCCAGTTCTGGAGAGATTTTCAAACCTTCTATTATAAA
TAGAACCTTATAAGTCCATAATAATTCAATTGAAGGATTATTTCTTTTCCCTTTTCTGATTACTT
TCACCAATTTTCTTCTCTCCAAAAAAACACCTTCTTCATGGTTTCTGTTTCTAAATTAATCAATA
ACGGGTGTTTATTAAGTAGTCAAAGTGTTTTTCCAAGATGTTGCTACTCCGCAACAAGCTTCTGTGC
AACATACAATATACTCAATTTTCTTGGCGGTAGTGCCCCCTATATTCAAAGAAACGGATATGGGA
TTTCTACTGATATCCCTGCTGGTTGTGAAATTGCTCAAATTCATTTGTACTCAAGACATGGTGAAA
GATTTCCCAACAGCAAGTAGTGGGAAAGATTATGAGAAAATTTATGCTAAATTTAAAACTACAATG
GTACATTCAAAGGTGATTTGTCAATTTCTTAAATGATTACACTTATTTTGTCAAAGACCAGAGTAACT
ATGCTAAGGAAACTAGCCCCAAAAAATTTCTGAAGGAACCTATGCCGGTACAACCAATGCCCTTGCCTC
ATGGTGTGCTGCTTTAGAGCCAAATATGGATCCTTATACAAGGAAAACCTCAACTTTACCAATCTTCA
CATCAATTTCTAACAGAGTACATGAACTTCAAAGTATTTTCGCTAGAGGGTTTTTAGGTGATGATT
ATGAAGAAGGTAAAACGTGTCAAGTTTAAACATCATCTCTGAAGATGCTGATCTTGGTGCCAATAGTT
TGACTCTTAGAAGTGCATGTTCCAAGAACAAGAACTGAGCAGTAGTACTGCCAAAAAATATAACA
CAACATATTTAAATGCTATTGCTGAAAGATTAGTTAAACCAACCCAGGTTTGAATTTGACTACAA

FIG. 2 - 8

GTGATGTCAACAATTTATTTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCACCATTCT
GTGATTTATTACCAATGAAGAATTCATTAAGAATCTTATGGTAATGATCTTTCCAAATATTATT
CTAATGGTGTGCTGGAATAATTACACCAGAATCATTTGGTTCAGTGATTTTGAATTCATCCTTGGAAC
TTTTAAAGACACCGAGAACTCTAATCAAGTATGGTTATCATTTGCTCATGATACTGATTTAGAAA
TTTTCCATTCTGCTTTAGGATTATTGGAACCAAGCTGAAGATTTACCAACATCTTACATCCCATTCC
CTAACCCATACGTCCATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAACTTCAAT
GTGGAACGATGCTTATGTTAGATACATTATCAACGATGCTGCTGCGTCCAATTCCAAAATGTGCTA
CTGGTCCAGGGTTCTCTTGTAACCTTGATGATTTTGAAAATTTCTGTTAAAGAAAGAATTGGAGATG
TTGACTTTATTAAACAATGTGGTGTCAATAGTACCTACCATCTGAGCTTACTTTCTACTGGGATT
ATAAAAATGTCACTTACAATGCTCCTTTAGAATTGTAA

YBR093C_homolog_4 461aa (SEQ ID NO 304)

MVSVSKLINNGLLLTSQSVFQDVATPQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERFPTASSGKDYEKIYAKFKNYNGTFKGDLSFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAARAKYGSLYKENSTLPIFTSNSNRVHETSKYFARGFLGDDYEEGKTVKFNIIS
EDADLGANSLTPRSACSKNKESSTAKKYNNTYLNAIAERLVKPNPGLNLTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNSSLELLKDTENSNNQVWL
SFAHDTDL EIFHSALGLLEPAEDLPTSYIPFPNPVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFIKQCGVNSTYPSSELTFFYWDYKNVTYNAPLEL

YBR181C_YPL090C_homolog 1635bp public: 1..938, PathoSeq:
939..1635; exon 1: 500..505, intron 1: 506..930, exon 2: 931..1632
(SEQ ID NO 305)

ATATATATATATTTATGTATTTTTTTTATTGTTGTTTCAGGAATTTTAAACATGTTTCATGAATAATGA
TAATCTATGAACAAATTAAAGAACTCTTTGGTTTCATTTGCAACCAATGTGCGTGACTTAGGGCTA
TAGCCCTACTTTTTACTTGTACGATAGTGCATATTTGTTGTTGTGCGAATAGTTAGCGTAATAATC
TTTTTTTTTGTGTGTGTGCGGTTTACTTACTCTTCTCTCTCGCACATATTTTATTAGAGCTTAC
AGTTGTTTGTATAGTGAGAGTTTCACTAACACAAAGCTTCAACAATACTAACAAATTTTCGCACGC
TGTGGAAGGAGAACTTACACTGTACACTACACTACACTGTACACTATACACCACCAACAGAAAAA
AAAAATTATCAAATTTTCAACCTTGAGAGAAAAAAGTGGAAAAAACTTCTTCTTACATTT
AGTTAATTTTCAGACAGGCACAAAGGAATTAATCACCATGAAGGTATGTGATTGAATATAACCTAT
ATCAGTGATTATAATTAGAGTCTTTATTGTTGATATTGCAATAATTGGATAATAAGAAAGAGCATA
AGAGTAGGAGTTTTTAAACAGGATAATTGGATTCAATAAGAGGAAAAATTTTATCGTCGTGATTA
TAACAAATACAAAGAAATTAAGCAATGAAGTGATATAAGCAAATGAAGGACTAGTTTATTAGGGGT
GACATTTTTTAGACTACGTAAAAGTACTTTTCGATTCAAGGAAAACCAATTTTAGTATCTATCAACA
AACTACAAATCAATTTAGTTAACTTCAATAATGACAATAATTTTAATCACTGAAAACAATAACAT
GCAACAAGCAAACTAGTCAAGCTTTACGAATCAGTCAATACTAACAATACTTTTTTTTTGTTTCA
TTTTAGTTAAACATCTCATATCCAGCCAACGGTACTCAAAAATCTATGGATATCGATGATGACACA
AAATTACGTGTTTCTACGGAAAAAAGAATGGGTCAAGAAAGTTGAAGGTGACTCAGTTGGAGATGAA
TTCAAAGGTTACATCTTCAAAATCACTGGTGGTAACGATAAACAAGGTGTCCCAATGAAACAAGGT
GTTATGCACCCAACCAGAGTTAGATTATTATTATCTAAAGGTCACCTTGTACAGACCAAGAAGA
ACTGGTGAAAGAAAAAGAAAAATCCGTTAGAGGTTGTATTGTTGCTCAAGATTTGTCAGTTTTGGCT
TTGTCATTGTTAAACAAGGTGACAATGAAATTGAAGGATTAAC TGACACCCTGTTCCAAAAGA
TTAGGTCCAAAGAGAGCTAACCACATTAGAAAATCTTTGGTTTAACTAAAGAAGATGATGTTAGA
GATTTTCGTTGTTAGAAGAGAAGTTACTAAAGGTGACAAAACCTTACACCAAGCTCCAAAGATTCAA
AGATTAGTTACTCCACAACTTTACAAAGAAAGAGAGCTTTGAAAGCTAAAAAAGTCAAGAATGCT
CAACAACAAAGAGATGCTGCTGCTGAATACGCTCAATTGTTGGCTAAGAGATTGCATGAAAGAAAA
GAAGAAAGAGCTGAAATTAAAAAGAAGAGAGCTGAATCTTTAAAGAACTAA

YBR181C_YPL090C_homolog 236aa (SEQ ID NO 306)

MKLNISYPANGTQKSMIDDDTKLRVSTEKRMGQEVEGDSVGDEFKGYIFKITGGNDKQGVPMKQG
VMHPTRVRLLLSKGHSCYRPRRTGERKRKSVRGCIQAQDLSVLALSIVKQGDNEIEGLTDTTVPKR
LGPKRANHIRKFFGLTKEDDVRDFVVRREVTKGDKTYTKAPKIQRLVTPQTLQKRKALKAKKVKNA
QQQRDAAEYAQLLAKRLHERKEERAIEIKKKRAESLKN

FIG. 2 - 9

YCL016C_homolog 1520bp public: 1..1079/1081..1520, PathoSeq: 1080;
CDS 501..1517 (SEQ ID NO 307)

GTGACGAGAACTTCTGTCATCTCGAGTCTGCCAACTGCCTCTAACAGCAACAACAATAAGAACAAT
GATAACGGAGGAGGATTATCCCATACAAACAGAATAGTTGTTGGTGTAGTTGTTGGGGTTGGTGGT
TCTATATTAATTTGGTTTGTGGCCGTTTTATTTTACTTGAGAAAGAGAAACAACCGTGATTATGAA
GGTGGATGGACTTTCTGGAGAAAGAATGAGAAATGGGAAGTGATGAGTTCTTCAATGGTGAATTG
GGTGTCTAGAGACAGAAATATTAATCAAGGATCAAATTTTAAACAAGGCTTATTTTGGATGAGGGT
GGTTTTTTTTATAAGTATTTTGTAGTTGAATTTAAATTTTGTACCTTAAAGTCTTTTAATTTAAT
TTTAATAAAAAAGTGGTGATTTGGCAAACCTCAAGAGTATATTTGGTGAAAAAAAAAAAAAAAAATTTG
GAACTGAACCGCTCTAACATCTTATACCTCTAAGCAAAATGTCAGAGTACTCTGTGTATCAACAGT
TGAATGAAGATACAAACGCAACTAAATATACCTTATAAATTACTACAGCTACCATCAAAGATACTAA
ATCAACTTGAATCCAAGTCAACTAACTTGTATATAAAATCTGATATCAATTCCCTAGCATTATGCA
CTGATTCAGAAACTTTCAAGTTACGACAAATGAACCATTCCAATACAGTCTTGCTATTGAACAAAG
AACCTGACAAACAAGTTAATTGGGTTTCAGAAAACCAGTTATGAATATGAGTTGACAGAAATCAAAG
GTTGATCGATACGTCGATATCCCTATTTTCAACGGACAAACAGCACAGCAACCTATTGATTTGA
TAGCATTGGAAGATAATTCGATTTGTTTACATCAAGAGTTTTTATCGAATTGGTATGAGTTGGGAG
GTTGTGAAATTGATAATGGAGCATATATAATGAGTGCAGATATTATTACTGAACTATTATATCTAT
TAATCACCAAATTGATGAGTTTACAAGTGCACGAGTTTTCTCCGAAGATGTTTCATCCATCATCA
CGCCCCCTTATAATGACTCAATGGTAAACATCAATACACAAATTTTGCACTATAGAAAAGTGA
AATATCAATTGAATGATTTTAAAAATTACACAGTGGTTTGGCATTTGTTGAGATGTCAAAAATCAATC
ATAAATGACCGATATTTTCAAGTCTTATTGAATTGGAAAACCTAGTTTGCCGTCATTCTATAACC
CTCCATTGGACATCAGTCAATTGGCAGGCTATTACTGCTCCCAATCGAAAACAAAATATTGTATG
TCGACCCAGAATCTTTATCAGAAAATTTGAGTCAACGATTCAAAGAATTGTTTGAATTGGATAAAA
GTTGGAATATGATGAGTTTATTCATTTCATTAATAAAGTTTGTTCCTGCCGGTAAAAAGGTGCACT
CAATTATTTTAAAGTATGGCAAGAAGAAGAAAGTTGGTAGAGATAGATTTATAGTCTGTCTTAGAT
AA

YCL016C_homolog 339aa (SEQ ID NO 308)

MSEYSVYQQLNEDTNATKYTYKLLQLPSKILNQLESKSTNLYIKSDINSLALCTDSETFKLRQMNH
SNTVLLLNKEPDNKLIGFQKTSYEYELTEIKGSIDTSDIPIFNGQTAQQPIDLIALEDNSICSHQE
FLSNWYELGGCEIDNGAYIMSADIITELLYLLITKLMSLQVHEFSPEDVSSIIITPPYNDMSVTSII
HKFCTIESEKYQLNDLKITQWFGIVEMSKINHMTDISEFLNWKTSLSFYNPPLDISQLAGYYC
SPIENKILYVDPESLSENLSQRFKELFELDKSWNYDEFIPFIKKFVPAGKKVDSIILKYGKKKKVG
RDRFIVCPR

YCR073WA_homolog 710bp PathoSeq: 1..710; CDS: 315..707 (SEQ ID NO
309)

GGTGGGGTTCCCATTTTAATTTAAAAAAATTTTTTACCATCCAAAGGATTTTATTTACCCAAAGAC
CAAAAAATTATTATTGAAATGGGGATTAAATGGGGATAATTTTATTTTGCCTGATGAAAAGATT
AGTACCCGTTTGAAAGTCCGTGATTCAAATTATGGTCAAGCTAAAAGAGAAATATTTGATTTAATTA
CTGGTGATAAAAAACCAAGATTTTCCATGTTGATGAATCATTAATTGATGATTCTCAAGAAGCTG
CTGATGAATAGGCAAAAAACAATTGATTAATAATTTTGCTAAAAAAGATTGGGTGAAATTACCTTTAT
TTGATTTATTTTATTAGGTTGTGCACCGGATGGTCATATTGCTTCATTATTTCTAATCATGGTG
AACAATTGAGAGAAAAATTAGCTTGGGTTTTACCAGTATCAAATGCTCCTCTGGGACCAGAAAAATA
GAATAACTTTATCTATCCCAGTTATATGTCAATCCGCAAGAGTGACATTTGTTGTTGAAGGGTTAA
CTAAGGCACCAATTATTAATAAACCATTATGGAAAGACCAGAAAAAGGTTTACCAAGTTCAATTGTTA
ATGAAGGTGCTGCTGGTAGAGTGAGTTGGTTTGTGATGATGATGCATTGAATGATTGTTTGATA
TAACTAAAAAGAAATACAAATATTTATCTATACCTGAACCAAGTCATTAA

YCR073WA_homolog 131aa (SEQ ID NO 310)

VKLPLFDLFLGCPDGHIALFPNHGEQLREKLAWLPVSNAPSGPENRITLSIPVICH SARVTF
VVEGLTKAPIIKTIMERPEKGLPSSIVNEGAAGRVSFWFVDDDALNDLFDITKKKYKYL SIPEPSH

FIG. 2 - 10

YDL010W_homolog 1190bp PathoSeq: 1..1190; CDS: 501..1187 (SEQ ID NO 311)

TGTTACAAAACATTCTGTTGGAGAGATAATTGAATTCAAAATTAACGTGTTGAATCCAACATTGAA
CAATGAATACACGTCCAAGAAAAATTTGACATGATTAGAATCGCGGTCAATTACATTTCCCGGAACG
TCTTGGACTACTTGGATACAACAATGGAAAATGAGGAAAATGAGGAAAATGAGGAAAACGAGGAAA
ACGAGGAAAATATTTACCGAAGAGTAATTATATTACAAGCATTGAAAGAGGAGAAGTGAACGCCCC
AAACAGAAAACAATACCGAACATCACAAAAAAGACAACAGCTAAAATTTTTTGGTCAGAA
CACAACTTTGGAAGAAAAGAAAAAACCGGAAAAAGAAATTCATCTAAAACACATACACAATATAT
ATATATATATATAAATATATCCATATACATATGCTTTAATTTAACCTTCCCGCCTTTCTTTTCTTC
TTTTTGAATTATATCGATTTTAAAACTACACTTCATCATGGCTGGAGTTAGACAATTAAGAATAA
TAGCATTAACGGCCTTTGTCTTGGTTTAAATTTTACTTTACATAAAGTTGGATCCAACGCTGCAT
CCTTGGTTTCATGCACAAGCATCAGACCAACAACCAACAAACATAACACCAAAAGTACTACATATA
CCGCCACTAATGACGAATCAGTTGCCAATCTCATTGATTCTAAAAATGATCCTCAAACCTGATGACA
AAATAAATCAAAAAATATCACAAAGATCAAGATGAAGCCATCAATGGTAATAAAGACACTAATAAAG
ACACCACCAAAAGTCAAAACAGATAATGGTGAATATGATCCAATATCTGATTTGATAAAAAATTAGAT
CATTATCACCAATGACAATTTTCAGTAAATCATATTGTCCATATTCAAAAAAGATTAAACAATTTGT
TATTAGAAAAATATGATATAACACCAGCAACAAATTTGTTGAATTAGATCGATATGAATATGGAG
CTGAATTACAAAGTTATTTGACAGAGAAGAGTGGGAGAAGAAGTGTGCCAAACGTATTGGTTGGTA
AATCATTTGAAAGTAGGGGTGGTTGTGATGAATTTGAAAACTTCATAAAGATAATGATTTGATTA
AATTGTTAGTTGAATGGGGTCTGGTCGTTTACAAGTTGCAAAGAAGAATACCCCATCAATGCCT
AA

YDL010W_homolog 229aa (SEQ ID NO 312)

MAGVRQLRIIALTAFLVGLIFTLHKVGSNAASLVHAQASDQQPNKHNTKSTTYTATNDESVANLID
SKNDPQTDDKINQKISQDQDEAINGNKDTNKDTTKVKPDNGEYDPISDLIKIRSLSPMTIFSKSYC
PYSKKIKQLLLEKYDITPAPNVVELDRYEYGAELQSYLTEKSGRRTVPNVLVGKSFESRGGCDEFE
KLHKDNDLIKLLVEWGSRLQVAKNTPSNA

YDL083C_YMR143W_homolog 1256bp PathoSeq: 1..1256; exon 1:

501..521, intron 1: 522..848, exon 2: 849..1253 (SEQ ID NO 313)

AGTGGTTGTTCAATAATGGTAAGTTCTTGGAAATAGCCATTGTTGCTTTCTGGTGGTTAGACTTGT
AGGAAGTAGAACTGTTTTCCAATGAAAAGTAGTTTTAATTAGAAAAATTTTCAAAGTGCGTGAAGC
CCAGTCTGAATGTGCGAGGAAGCCAGTCAGTTAGTAGTGCTTCCCTCCACTGTCTGTAATACA
AAATTTCCCTTAGTGAAAATGCGAAATATATCTGTACTGGGAACCCCCCGGAAAAAAAAAACCTA
TGCTCAAACTATATGTACTGTACACAATCTAGGGCTATAGCCCTAATATTGTACAGGAAGAAGCTT
TAACTATGGTGCGAAGAGCGTTTCCAATTTTTTTTTTTTTTTCAGGTGTAGTCTGTTCTATGGCAATAC
TGTGTTAGTAGAGAGTGTCTCGCACTAACAGAACATTTTTTTCAGAACAGGAAAAATTTTTGAAAT
CTAACATCTTTTACTGAAAGCCAAGCATCAACACAATAATGTCAACCCAATCTGTTCAAGTATGTA
AACGAATTGAAATAAAGAGATAGAGAGATGTTTTATTATCAAAATACGAAAGGAAAGGCAATTAAA
AAAGGAAATCAAAAAGTCCCAACCTTGCAGTAGAAGAATTGAGGTATATGAATTTGATAGATAGCC
AGAACGGTGTTACATAAATGGGATATAGAACAAAACCTATACGAGGAGTTTGTTCACCGATCATTC
AATAACCAGAAAACGATAATATTTTAGCGACCATTAAATGACACTTGAAGGCTCACTGGGCCAATA
GAATATCTCCATATACACTTTTGAAGTATTTACTAACAATTTACTTTTGTCTAGACTTTTGGTA
AAAAGAAGACTGCCACTGCCGTTGCTCATGTTAAAGCCGGTAAAGGTTTAAATAAAAATTAACGGTT
CCCCAATCACCTTGGTCCAACAGAAATCTTAAGATTCAAAGTTTACGAACCATTGACTTTGGTTG
GTTTAGATAAATTCCAAGGTATCGACATCAGAGTTAAAGTCACTGGTGGTGGTCACGTTTCTCAAG
TCTACGCCATCAGACAAGCTATTGCTAAAGGTTTGGTTGCTTACCACCAAAAATACGTTGACGAAG
CTTCTAAGAACGAATTAAAGAAAAATTTTCGCTTCTTACGATAAGACCTTGTAGTTGCCGACTCAA
GAAGAATGGAACCAAGAAATTCGGTGGTCTGGTGCCAGAGCAAGATTCCAAAAATCTTACCGTT
AA

FIG. 2 - 11

YDL083C_YMR143W_homolog 142aa (SEQ ID NO 314)

MSTQSVQTFGKKKTATAVAHVKAGKGLIKINGSPITLVQPEILRFKVEPLTLVGLDKFQGIDIRV
KVTGGGHVSQVYAIRQAIKGLVAYHQYVDEASKNELKKIFASYDKTLLVADSRMEPKKFGGRG
ARARFQKSYR

YDL125C_homolog 959bp public: 1..959; CDS: 501..956 (SEQ ID NO 315)

GTGGTAAGATATAGAAAGCTTACCACTTTGACAAGTTTGAAATAGGATGGGTGAAAATTTGGACAT
CTTGAATACTTAAAATTCTGAACCTTGATCACCAGATCCTTTTCTTTTACATAATTAGATATGATGG
ATAGGTTAGAATCGTCTTTAAAGAGAAGGTATAATATCTAACTGATTTGGCGAGGTGTTGGAAAAG
TCACTCCACTGTATATATTCTCGGAGTTTAACTGACTACAGTTCAGTGGGGTGAATACCTAAATAG
GGGGGTAGAATACGAACCTCTACAAATTTTAAAGGAGACTATGACCCGAAAAGAGAAGAAAAATTTA
TTACTCTAAGAACTTTATATACCTCCACAACCTCACTTTTTCTTTAGTTTCATTCTGCTTTTTTTTT
CTTACACATCTTAAGGTCAAACAATTTAACTTATTAGCTTGTGAAAATCTCACTTCAATTCAAGTT
CTCTTTCAATTGACATTATAGTATTTCCCAATTCAATTATGGCTTCTCATGCTTCTGTATATTCT
GTAAAAATTATCAAAGGTGAAATTCCTTCTTTCAAGTTAATTGAAACTGCAAAGACTTATTCCTTCT
TGGACATTCAACCAATTGCTGAAGCCACGTTTTAATTATCCCTAAACACCATGGGGCAAAGTTGC
ACAACATTTCCAGACGACTACCTTAGTGACATTTTACCAGTTGTCAAAAAATTGACAAAAGTCTTGA
AATTGGACGAAAATAATACTCCAGAAGGTGAAGGTTATAACGTTTACAGAACAACGGAAGAATTG
CTCATCAAGTTGTTGATCACGTTCACTTCCATTTGATTCTTAAAAAGGATGAGGCTACAGGTTTAG
GTGTTGGTTGGCCTGCTGAAGCCACTGATTTTGATAAATTAGGAAAATTGCATGAGAAATTAAAGG
AAGAATTGGCTAAGGTAGATAATGAAAAATTATAA

YDL125C_homolog 152aa (SEQ ID NO 316)

MASHASCIFCKIIKGEIPSFKLIETAKTYSFLDIQPIAEAHVLIIPKHGAKLHNIPDDYLSLILP
VVKKLTKVLKLDENNTPEGEGYNVLQNNGRIAHQVVDHVHFLIPKKDEATGLGVGWPAEATDFDK
LGKLHEKLKEELAKVDNEKL

YDL133CA_YDL184C_homolog 297bp PathoSeq: 1..297; CDS: 220..294
(SEQ ID NO 317)

CATAATTATTACATATAAACTCGCACTATAATTTTTTTTTTTCTATTCTGTGTGTGTGTGTGTGT
GAGAGCCAGAGAAACCAAACTGACTGAGTGATCGTCTCTCAACAATTTATTTCTCCTCGTCTTATT
TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTA
CCAAAACACTAGTATTTCAACATGAGAGATAAGTGGAGAAAAAAGAGAGTTAGAAGATTAAAGAGA
AAGAGACGGAAGGTTAGAGCTAGATCCAAGTAA

YDL133CA_YDL184C_homolog 25aa (SEQ ID NO 318)

MRDKWRKKRVRRLLKRKRRKVRARSK

YDL136W_YDL191W_homolog 1303bp PathoSeq: 1..1303; exon 1:

501..503, intron 1: 504..943, exon 2: 944..1300 (SEQ ID NO 319)

TATTGTCTGATGCTATACGGAATGGGCGTTACAAATATACAACTTATATTTGAAAGTAAATTCTA
TTATTTTCTTCTATCGTATGCATACCGATTATTATCACAAAGGACAATTGCCTATTGTTGTGTGGAA
TAAATTTAAATCCTTCTTATTGGTGTCTAGACTTTGCTTTTGTGGTGATTAGGGCTTTAGCCCT
ATCACGTGAAATACTGTATATAAAAAATCTTTATAGCGCGATAAAACATATTTTTTTTCCGTATT
AACAAATATGTGTGAAGTTTTGTCCTGGTGTTTTCTCACTGTTTTTCTTTTTTCTGGTAGTAT
CAATTAACGCTTAGATCCAATACAGTTTTGGTAACCTGTACACGAACAAAATCTCAAATTTGTTAC
TGTGTGAACCAACAAGGAAGAGAAAAAAAACCCATACAAAAATTTTTCAGTATCAAGGAATTAGA
AGAGACGTTTAAATCAACAAAGTTCAAATCTATCAACAATGGTATGTTTAAATATCGATATTATCCA
TAGATGTACATGTATCCTAATGGGTTTCATTATTTGGAAAGTTATGTTTATGGGAGTTCTATTTAT
TAAGATATGGGATAAGAATTAAAGTATTGGATGAGTAGTACAAGACCAACAAAGAGAAATAGCCCC
CTTTCCCTCCACTATTCAATATACTCAACAACATTATCAAGTTAAAAGTTCAGAAGATACACGTAA
ATGAAAAGTTAATACCAAGAAGAATACAAATTACCAGTCCATACCGTGTTTGGGTTTAGATTACTA
TATTTTACAAGAAACATATTATATGAAATGATACCCAATCCACAGCGACTTTTCAGATAGCCAAAT

FIG. 2 - 12

AACTAAGCAACTCAAGATAACATAGGATCATGCATCAATCACAAATGAAACATTAATACTAACTAA
CTTTTTTTTTTATTTATTAGGCCGGTGTTAAAACTTTTCGAATTAAGAACTAAATCTAAGGAACAATT
AGAATCTCAATTGGTTGAATTGAAACAAGAATTGGCCACTTTAAAAGTTCAAAAATTACAAAGACC
AAGTTTACCAAGAATTCACACTGTTTCGTAAAAACATTGCTAGAGTATTGACTGTTATTAACTTGAA
TCAAAGAGAAAATGTTTCGTGCCCTTTACGCTGGTAAAAAATACATTCCAAAAGATTTAAGAGCTAA
AAAGACTAGAGCTTTAAGAAGAAAATTGACTAAATTTGAAGCTTCTCAAGAACTGAAAAAGCTAG
AAAACAAAGAATTGCTTTTCCACAAAGAAAATTTGCTATTAAAGCTTAA

YDL136W_YDL191W_homolog 120aa (SEQ ID NO 320)

MAGVKTFELRTKSKEQLESQLELVKQELATLKVQKLQRPSPRIHTVRKNIARVLTVINLNQRENV
RAFYAGKKYIPKDLRAKKTRALRRKLTKEASQETEKARKQRIAFPQRKFAIKA

YDL167C_homolog 2690bp PathoSeq: 1..1640, public: 1641..2690; CDS:
501..2687 (SEQ ID NO 321)

CTCTGTGTAAATTGATGAAATCCACACAATAAAAAATTTCTTTCTTCTTTTAAAGAACCTAAAAACA
GAATCAACATTATTTGCCCCATACATATCCAAGAATTAAATACTTATTAGTTCTAAGTGGAATAGA
AGAGAATCAAACCTTAACATTACTGTTACGCAACGTCAAGAGGGCATTATTTTTTAGTTTAAATTTGT
TTCATTTCAATTGAATCTTTAAGAATCACCGAGTATACATACTTTCTTTTGTATTTTATCAGGGAA
GCCACATCCAACCACAGTTACATCCCAAAAATCCCTTAATCTTGTCTTAGTTGTATTATTAAT
CTATTGAATTTAAGTTTGATATGCGAGAGAATATTGTGGATTGTATAAGTTTGAACCTGGACTTGA
ATACTTTGAGGGGCTTAATCATATATTGCATTTTATACCCCTACTCGCGGTGTTGCTTACCACACTG
ACTAGTATGATCTTTCTGAGATTTCTAGCCAATAAATTATGAGTGATATTTATATTATTATTCATA
TTTCTACTACCTGTGATGACTCGCCGACATTTGTCACTAAGGATTCCTCCGAGTTAATTGAATTTG
CTTGGGAAACAGTCGATAGTGTCACCTTTGGAACTTTATACAAAGGATCAAACCTGGTTTCGTCCAA
CCAACACACCTATCACACCTTACTGCTCGAAGATTCATAGAATAACATGGGACAATGTCAAAAATG
CTGGTTCGTTCAAAGACGCCATCACAACTTTGATCAATAACGTACAAGAACACATAATTTCCAAG
AAAAGGAGTTTCAATTTGTGATGTTTGACATTTCCAAATTGAGAGTTTCAGTTGGTTTCGTGAAGCTA
GAGACAAATCCGTGGTTTTACCCTCGTATCTACAACATCCAAGGATTTTTGATTTACCAAGAGAAT
ATTTAAATTGGCAATCTAGCCACCCTGAAACATTATCATACCCCCCAACTTCTTTAACTAATATTA
TACTGCAATTAGAAGTTGAGGTTGAGAATATATCTGAATATGTCGACTTGCCAAACTTTTCTTCCA
CACCATCACCATCAAAGCTTCAGCAACAACGACGACGACAACCTGCAAATGTCACAGCCATTGACG
TCCTTTCCAGTGAACAGAACCAAAATGGTAAAGTCATTGCAAATTTGCACGCCAAAATTGCCAAAC
AATTGATCAAAAAATCCATCCCTGTTGAGAATCACCCTAATGTATTTACAAGACCTTTTGATTCCGG
CTCAAGATATCACTGCTTTTACATCAGAAAGATCAAAGTACTCTATCTTTCCAACCTTGCCAAACG
ACACCACACAATCAGAGTTGGAATCATGGTTCACCTCAGTATGGTGGGAAGACCAGGTGGGTTTTGGA
CTTTTAAGTCTGCAGATGATAACAATAATAACAACAACAATAGCAATGGCGGGAAAGGATATC
AGAATGCGAGAAAATATGGTATTTTCAAGGTTTGTGGCCTTTAATACTCATGAGGAAGCAGTTGATT
GTTTAGCTTTGAATGGGAGAGTGTTGAATGATCGTCTTATTGAAGTTCAAGCGTCTTCTAGTAAAG
TGTTTGATATGGCCATGGATAAAATTTGTTGACTCTGTTCCCACTCTCAAAGAACAGACCTAGAC
CCGGGGATTGGACTTGTTTATCTTGTGGGTTTTCCAATTTCCAGAGAAGAACACACTGTTTCAGGT
GCTCTTTTGGCGCAGTGGCGTTTCAGGATGTTTTTAACAGTAATACAGGCAATGCCAACGGTAATG
GCAATGTTAGCGGCAACCACAACCACAACCACAATAGTGGAGCTCGCCGTGGCATGAATTTACAGC
CTGCTCAAGCTAATGAGAAAAATTGGAACAGGCAATATTAGTATTCCTTCTTACAACGATCCAATCA
AGGGTCCAACAGGTAATGTCACCTAACCTCAACAATTCTGAGACCAATTTACTGAACAACACTA
ATCTTAACAACAACAATCATCATAGTAATAATTATCACAATAACTACCATCACCACAACAACAATA
ATAACAATCATGGGAATAGCAATGGTAACACCATACATGGTCGTTCCCATTAACAATAGTGTTT
CATTTAGAGCAGGTGACTGGAAATGTGAAATTTGCATGTATCACAATTTGCCAAAAAATTTGTGTT
GTTTAAAATGTGGTGTGCGCAAACCTGCTATTAACAATCAACAAAATAATACAATTCATTCCGTGA
ATTCAACGGCCGCTGCCATAGCTGCAGCAACAGCCAGTGGTCAACCTTTAAACTTGAATAATAATG
CATTTTGAACCTTCAGCAACAACAGTCTCAGTCACAACCCCAAGGTCAGCACCATTACAACCAAC
ATTCTCGTAACAACAATGCTTCTGGGGCATCAAAGTTCAACAATGGCTACAACCCAAAGAATCAGT
ATTACAATAATAATAGCAAGAATCTTAGCAACAATTTTGGTCTTAATGGTATGCATCAGCAAAACC

FIG. 2 - 13

AAAATCAAATTTTGTATGTTTACACAACAATTGCAACAACAACAGCAACAACAACAGCAACAACAGC
AACAAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACATGATTTAA
ATGGAAGTAGCTCTTCCCATCAACTGAACTTCAATTGAATAATACTTGA

YDL167C_homolog 729aa (SEQ ID NO 322)

MSDIYIIHISTTCDDSPFVTKDSSELIEFAWETVDSVTLETLYKGSNLVRPTNTPITPYCSKIH
RITWDNVKNAGSFKDAITNFDQYVQEHIIISKKEFSIVMFDISKLRVQLVREARDKSVLPSYLQH
PRIFDLPREYLNWQSSHPETLSYPPTSLTNIITALEVEVENISEYVDLPNFSSTPSPSKASATTTT
TTANVTAIDVLSSETEPNKGVIANLHAKIAKOLIKKSIPVENHPNVFTRPFDSDAQDITAFTSERSK
VLYLSNLPNDTQSELESWFTQYGGRPGGFWTFKSADDNNNNNNNNNSNGGKYQNARKYGISGFVA
FNTHEEAVDCLALNGRVLNDRPIEVQASSSKVDFMDAMDKLLLTSPFLSKNRPRPGDWTCLSCGFSN
FQRRTHCFRCSFAAFAVDVFNSTGNANGNGNVSGNHNHNHNSGARRGMNLQPAQANEKIGTGN
SIPSYNDPIKGPTGNVTNHLNNSNTNLSNNTNLSNNNNHHSNNYHNNYHHNNNNNNHGNNSNGNTIH
GRSHYNNVPPFRAGDWKCENCMYHNFKNLCCLKCGVAKPAINNQQNNTIHSVNSTAAALAAATAS
GQPLNLNNNAFLNLQQQQSQSQSQPQGHYNQHSRNNNASGASKFNNGYNPKNQYNNNSKNLSNNF
GLNGMHQQNQNLILMYSQQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQHDLNGSSSSHQSKLQL
NNT

YDR238C_homolog 3359bp public: 1..1467/1469..3040/3042..3359,

PathoSeq: 1468/3041; CDS: 501..3356 (SEQ ID NO 323)

AATAGCATTGAACAAGAAGAGAGGACAACGATAGACCAAGGTTGGTTTTAGCCAATCCTGATTAT
GATAGTGATGACAGTTTCATAGACAATTTACAGCCTTAAATGGATATATATGTATATTTAATAATAA
AGGACTTGTTTTTTTAGTAAGTAGTGATCTCTTTCTGGGTGTACATTTCCGATAGCCAACCA
GGTTATATTTTAGCAGTTTATAGACAGTGTTATCGATGGGTAATATAAATAAAAGCTCATTGAATA
CTATCTAGTGAAAAGTCGTGTGTAAATCGATTTGAAAAATATAAAACCATACACGTAAATGAAATG
TGTGTGAAAGTACAACCAACAACGAAAAAGAACAAAAAATGTTGTCCGCCAAAAAAGAG
AGAACAACAAATCAAAGTTTCAAGACTATCTCAAATCTTGTGTGTCACCATAACTATCAATTGTTCA
CCTCTTGAACCAACATCAAATGAATAAACATAGGATCATGAGTGACAGTGGTTATACATTAATCT
ATGAGCCTAATACGGCTACGAAAGTATCTGTCAATGAATTTAAAAATTTGTTGGAAAGGGTAAAG
ATGATGTGAAAAGTAGATACCATGAAGAAGATTTTGATTACCATATTAATGGAGACCCCTTACCTG
ACTTGTTGATGCATATAATCAGATTTGTCTATGCCTTCCAGAAATAAAGAAATGAAAAAGTTGTTGT
ATCATTATTGGGAGGTTTGTCCAAAAATGGATGAATCAGGTAAAATGAGACATGAAATGATTCTTG
TGTGTAATGCCATCCAACGTGATTTACAGCATCCAAATGAATATATTCGAGGCAATACTTTGAGAT
ATTTGACGAAATGAAAAGAGCCAGAATTATTGAAACTTTAGTTCCTAATGTCCGTCAATGTTTAG
AACACCGTCAATGCCTATGTCAGAAAAATGCTGTTTTTCGCATTATGGTCTATTCAATAAGTCAGTG
ATCATTTAGCTCCTGATGCTGACGAGTTAATTTACAGATTTTGTATGAGGAAACGATTCTGTTT
GTAAAAGAAATGCTTTTGTGTTGTCTTGGAGACTTGAATAGAGAAGCTGCTTTGCAATATATTCAGG
ATAATATTTAGTTATTGAGACTTTGGATCCATTGATACAATTGGCTTTTATTGAGTTTATCAAAA
AGGACTCTATTCAAAATCCAGCTTTAAAGCAACAATATGCCCAATTAATGACAGAAATATTGAAA
GCTCTTCAAATGTTGTTATGTATGAAGCTGCTAACACGTTGACTGTTTTGACTTCAAACCCACAAT
CAATTTTGTGTCAGGAAACAAGTTTGTGTAATTGGCTACTAGAGAGTCTGATAATAACGTTAAAA
TTATCACTTTAGAGAGAATAAATCAATTACACAAGCAACATCCTGGTGTGTTACAAGACTTGTCAT
TAGAAATTTTACGAGGTTTATCTTCCCAAGATTTGGATGTTAAAAAGAAAGCTCTTGATGTTACTT
TACAATTTATCACCACCAGAAATGTTGAAGATGTTGTTAAGTTATTGAAGAAAGAAATGTCAGTCTA
CAGCTTTATCCAATGATGACAAGAAATGCAGATTATAGACAGTTGTTAATTAATGCCATCCATCAAT
TGGCTATTAAATTTGTGGAGGTTGCTGCCAATGTCATTGATTTATTGTTGGATTCTATAGCCGATT
TGAATACCACTGCCGCTACGAGGTTATCACATTTGTTAAAGAAGTTGTTGAGAAATCCCAGATT
TAAGGGACGCTATTTTGAGAAAGATTGATTTTGGCTTTGCCACATGTGAAAAGTGGTAAAGTTTTCC
GTGGTGCATTATGGGTATTGGTGAGTATGCCTTAGAGGAATCATTAATACAAGAATCTTGAAAT
ATATTAGAGGAAGTATTGGTGAAGTACCAATTATTGCTAGTGAATTGAACTGAAAAAGCGTGATG
ATACTGAGGAATCACAAGAGGAAGAAACCGAGTATGATGGTAAACCTCGCAGAAAGGGTCCAGTTG
TATTGCCAGATGGTACCTACGCTACTGAGTCAGCATTGACAAGCGAAACAACCTGACTCTTTGAAA
GTGACAGCAAGACTCCTATCAGAAAGCAAATCTTGCTGGTGATTCTACTTAGGTGCTGTATTAG
CATCAACTTTGGTGAAATTGATTCCTCGATTGCAAAGTTTGAAACAACTCAAGAAAAAATTTTGA

FIG. 2 - 14

ACGGATTAAAAAGCAGAAGCATTGTTGATTATGGTTTCGATTTTAAGAGTTGGGGAATCTAGCTTGG
TTTCTAAGAAAATTGATGAGGATTCTGCTGACAGAATTTTGTCTTACATCAAGATTTTGAACGATG
AAGAAGACCTTCAGGAAATCAAGACAAGCTTCCTTGAAGATACTAAAGATGCATTTAAAGCACAAA
TTAATAATGCTGAATTGAAGAAAGCAGAAGCATTGGCTAAGGATTTGCATGATAACGCTGAACAAA
TTGACGATGCAATTGTTTTTAGACAGTTGGATAAAGATAACAAAAAGAGTAAAGCTTCTGTGGATG
ATGTTGCTGCTGCGTCAGGAAGCAATGAATTAAAGAAAGAAAATTTGTCGTCGAGATTGAACAAA
TTATACAATTGACTGGGTTTTCCGATCCTATTTACGCAGAGGCATTTGTCAAAGTTCATCAATACG
ATGTTGTGTTAGATGTCTTGCTAGTGAATCAAACCACAACACTACTTTAAGAACTTATCAGTTGAAT
TTGCTACATTGGGTGATTTGAAAGTGGTTGATAAACCAACTACCGCAAATATTGGACCTCATGGTT
TCTACAAAGTTCAAACAACATTTAAAGTTACTTCGGCTGATACTGGTGTCATCTTTGGTAACATAG
TGTATGACGGTCAACACTCGGACGATTACGTATAGTTATTTTGAATGACGTTACGTTGACATTA
TGGATTACATTAAGCCAGCCACTTGTTCAGAAAGTCAATTCGTAATAATGTGGAACGAATTTGAAT
GGGAGAATAAGATAACCATTAAATCACCTATTGAAACATTGAAAGAGTACTTGGATGAATTAATGA
AGGGTACAAATATGCAATGCTTGACACCGGGTGCAGTAATTGGAGAAGAATGTCAATTTTTATCAG
CAAACCTGTACTCAAGGTCAAGCTTTGGTGAAGATGCATTGGCTAATTTATGTATAGAGAAACAGA
GTGATGGACCAATAATTGGTCATGTGAGAAATAAGATCAAAGGTCAAGGTTTGGCTTTGTCAATTGG
GTGATAGAGTAGCTTCCATTTCAAGAAAAGGTAAGAAGGCAACTATTGCTCGTGTTTAA

YDR238C_homolog 952aa (SEQ ID NO 324)

MSDSGYTLIYEPNTATKVSVNEFKNLLEKGDVVDVTKMKILITILNGDPLPDLLMHIIIRFVMP
RNKELKKLLYHYWEVCPKMDSESGMRHEMILVCNAIQRDLOHPNEYIRGNTLRYLTKLKEPELLET
LVPNVRQCLEHRHAYVRKNAVVALWSIHKVSDDLAPDADELIYRFLYEENDSVCKRNAFVCLGDLN
REAAALQYIQDNISVIETLDPLIQLAFIEFIKKDSIQNPALKQQYAQLMTEIIESSNVVMYEAANT
LTVLTSNPQSILLAGNKFVELATRESNPNVKIITLERINQLHKQHPGVLQDLSLEILRGLSSQDLD
VKKKALDVTLQFITTRNVEDVVKLLKKELQSTLSDNDKNADYRQLLINAIHQLAIKFVEVAANVI
DLLLDSIADLNTTAAAYEVITFVKEVVEKFPDLRDAILRRLILALPHVKSQKVFGRGALWVIGEYALE
ESLIQESWKYIRGSIGEVPIIASSELKSKKRDDTEESQEEETEYDGKPRRKGPVVLDPDGTYATESAL
TSETTDSLESDSKTPIRKQILAGDFYLGAVLASTLVKLILRLQSLKQTQEKILNGLKAEALLIMVS
ILRVGESSLVSKKIDEDSADRILSYIKILNDEEDLQEIKTSFLEDTKDAFKAQINNAELKKAELA
KDLHDNAEQIDDAIVFRQLDKDNKKSASVDDVAAASGSNELKKENLSSRLNKIIQLTGFSDPIYA
EAFVHVQYDVVLDVLLVNQTTTTLRNLVSEFATLGDLDKVVDPKPTANIGPHGFYKVVQTTIKVTS
DTGVIFGNIVYDQHSDDSRIVILNDVHVDIMDYIKPATCSESQFRKMWNFEWENKITIKSPIET
LKEYLDELKMGTMQCLTPGAVIGECCQFLSANLYSRSSFGEALANLCIEKQSDGPIIGHVRIRS
KGQGLALSGLDRVASISRKGKKATIARV

YDR294C_homolog 2270bp public: 1..278/280..2270, PathoSeq: 279;
CDS: 501..2267 (SEQ ID NO 325)

GTTTGATCACATGTGTTGTGAACACTCGGGTAATACAAAATAGTGAGAGAGAAGAAGGGGAAAAA
AAAAGCAGAACACAAAACATGGAATTTGAAAACAATTTTGTAAATCAATCGATCCGAGACTTCCAT
AGCAAAGTTAACAAGCACAAATTGTCATTTTAACTTAATTGGTGGATTAATCGGGATCAATCTGAAT
TGTTTTCCCGTATTGTTTTAAACCAAAGAAAAAGGATAATCAAACTAAATCTTTCATATTAACACT
ACCATTTTGTAGTGGTCAGTTTATATAATTATCCACTGTTCTCTTCACAATTAACAAAAA
AAAGAAAAAAGAAAGCTCTCTCTCCCCAAAGAAAAAGCAAAGGTAATTCCTTCATACACACCTT
TGATATCTTTCTCTTAGACTTTTCTTTTAATACTTGCATCAATTGGAATATTACTTGTTCATACT
GGAGTTTTTCACTGAATAATATTATTAATAATTATTATGCTTGAATTGAATTCAATTACGATTC
CTCGGAATTTCACTGAATTCCAACCTCACAGCATTAAGATCTACTATCAACTTAAGATTTTATTTT
TTGCCACATACTGTGCTCAAGGATCATTTGGCTTGAACGGTTCAGTCTGTTTAGCAAGAGATATTT
TTGTTGGCTATGTGTATACACTCAATTATTAAGCTTTATCGAGTATTAAGAGGGTACGGTATTG
TAGATTCTATTCGAAGGTATACCTATATGTTAGTTCTACGGTGTCTCAATCTTTTCACTAC
CATTTATTAAATCCAAAATTGACAAGGAATTGCAAGCGACTATTGGCAAAGTAGAAGAAGAGATTA
TGAAAAACGATCCACAGTTATTACAGTTTCCCGAATTGCCAGAACAGGGTATTGACGCTGACAATG
TTTCTTGGAGTTGGATAAATTACAAAACCTGAAACATTCTGACTGGATCAATGGAAGAGTCAGTG
GAGCAGTTTATCATGGAGGTGAGAATCTATTGTCTATTACAAGTTGAAGCTTACAAGAAATACTCGG
TGGCAATCAATTGCATCCCGATGTTTTCCAGGTGTGCGTAAGATGGAGGCCGAAGTAGTTCATA

FIG. 2 - 15

TGGTTTTGGATATCTTTAATGCTCCGAGTGACGGGTGTGGATCGACAACCTTCGGGAGGTACTGAGT
CGTTATTGTTAGCCGGGTGTGAGCTAGAGAATATGGGAAGAAATATCGTGGAAATACTGAGCCTG
AAGTCATTGCCCCGTGACAATACATGCGGGAATTGAAAAAGCCTGTTTTTATTTTGGAAATGAAAT
TACATAAAGTTGACTTAGATCCGGTTACCTTTCAAGTTGACGTTAAGAAAGTAGAAAGATTGATCA
ATAGTAATACAGTTTTTAATCTGTGGATCAGCCCCAAATTATCCTCATGGAATAATTGATGATATAG
AGTCCTTATCCAAGTTGGCAGTCAAGTATAATATCCCGTTGCACGTTGATGCATGTTTGGGGTCAT
TTATTGTTTTCGTTTTTAGAAAAATCAAAAGTACATGGCGATAGGAAATTGCCCATATTTGATTTTC
GATTACCAGGTGTACGTCAATCTCATGTGATCTACAAATATGGGTTTGCTCCCAAGGGGTCAT
CAATAATTATGTACCGTTTCGCCAAAATTACGTGAGTGTCAATACTATATTGCAAGTGATTGGACGG
GTGGAATGTATGGTTCTCCAACCTTTGGCTGGTCTAGGCCAGGTGCTCTTGTAGTTGGATGCTGGG
CTACATTAATCAATATTGGGAAACAAGGATACACCAAGTTTTGTTACGATATTGTGCTGGCGTCAA
TGAAAGTTAAACGAGCAATTGAAACTGACCCGATCTATCCAAACATTTACAAATTATTGGTGATC
CAATTGGGTCCGTAATTTCTGTTTCAACTTGCACCTCAGCAATCGGGAAATTTAAGTATTTACGAGA
TTAGTGATTTGTTGACCAAAAAAGGTTGGCATTTTGCAACTTTACAAAACCCATCAGCATTTACATT
TTGCATTTTACAAGATTGACTGTCCCGGTGGTCGATGAATTGATTGCAGATTTGGTTGAAGCTACAA
AAGAAGCGGTGGCAATTGCCGAGGAACACAAAAAGAATGGAGTGACCAAAGCTCCAGGTGATACTG
CTGCGTTATATGGTATAGCTGGCAGTGATACATACAGCAGGGTTGGCTGATAGATTAATTGTTGCAT
TTTTAGATACCTTATACAAAATTTGA

YDR294C_homolog 589aa (SEQ ID NO 326)

MLELNSITIPRNFTEFQLTALKIYYQLKILFLATYCAQGSFGLNGSVCLARDIFVGYYVYTQLLKL
YRVLRGYGIVDSIRRLYLIVSVSTVSSQIFSLPFIKSKIDKELQATIGKVEEIMKNPQLLQFPEL
PEQGIDADNVSLDKLQNLKHSWDWINGRVSGAVYHGGENLLSLQVEAYKKYSVANQLHPDVFPVGV
RKMEAEEVHMLVDIFNAPSDGCGSTTSGGTESLLLGLSAREYGKKYRGITEPEVIAPVTIHAGIE
KACFYFGMKLHKVDLPVTFQVDVKKVERLINSNTVLICGSAPNYPHGIIDDIESLSKLAVKYNIP
LHVDACLGSFIVSFLEKSKVHGDRKLPIFDRLPGVTSISCDTHKYGFAPKGSSIIIMYRSPKLREC
QYYIASDWTGGMYGSPTLAGSRPGALVVGWATLINIGKQGYTKFCYDIVSASMVKVRAIETDPIL
SKHLQIIGDPIGSVISFQLAPQQSGNLSIYEISDLLTKKGWHFATLQNPALHFAFTRLTVFVVDE
LIADLVEATKEAVAIAEEHKKNGVTKAPGDTAALYGIAGSVHTAGLADRLIVAFLDLTLYKI

YDR430C_homolog 3605bp PathoSeq: 1..330/1927, public:

331..1926/1928..3605; CDS: 501..3602 (SEQ ID NO 327)

TTCAATTTTTTTAAAAAATAGCAAAAAGGTATTTCTTAGAAATTGAAAAAATCACA
AATTTTATAAACCGGATAGGGCCGTTATCGCAGGACGTGTCCCATGATCAATCTACAATGAAATGA
TTCACATGAAATATGTTACAATCCACACTTGCTGCTAAAAAGCAACAGTTTGCATAGAGAAAA
GCATGATATACTATCGATAATATCTTTTCGATAAGAACTTAAATGTAGCAACGTTGAATTTTAAAT
AAAACCTCCTTTTCTCGGTGATAAATTTGACTTTTGAAGCATAAAGAAGACAGAGCTAAAAA
CTACTCTCTAGACAAAATCAAAACCTCGAATATATTTTTGGTGTTTCTTTTTTTTTTTTGCCT
CTCGTTGAAATCATCTCCATTCTTTTCCACGCTTTTGTGAAAACCTTGCACCTAAAAAAT
AAGAATCACTCCAACAAGTTTAAACTACATTATCAATTATGTTGAAAACCTAGATTAAAAACAAAGCA
GGGCCATAAGTCGGGTGTAAGAAGATATGCATGCTCACACCCCATTTCTCCCAATCTTGATAAGT
ACCCAGTTGGTCTAAAATTGCATGGTTACGAAGTTACCCAAACATCACCTATCCCAGAATTTTCCC
TCACTGCTGTATCATTAACACACAGAGAGTGGTGCAACTCACTTACATTTGGATTCCCCTAATG
ACAGTAATAATGTATTTCTGATTGCCTTCAAAACAAATCCTCCAGATAATACTGGGGTTCCCATA
TTTTAGAACATACAACCTTTGTGTGGTAGTAAAAAGTTTCCGGTCCGTGATCCATTTTTTAAATGA
CCAACAGGTGCTTGAGTAACCTTTATGAATGCAATGACAGGCCATGATTACACATTTTATCCATTG
CTACCACCAATTCAAAGGATTTTGAACCTAATGGATGTGTATTTATCGTCAGTGTTTGAACCGC
AATTAAACCATACCGATTTCTTGCAAGAAGGATGGAGAATAGAAAATCAAAATGTTTCATGACATAT
CGTCCAAGCTTGAATTCAAGGGAGTTGTATATAATGAAATGAAGGGCCAGTATTCGAACCTGTCAT
ACTACTTTTATATCAAGTTCCTTGAGAGTATATATCCATCCTTGAATAATTCAGGGGGTGATCCCA
AGAAAATGTTGATTTGCTGTACGAGGGTTTACTAGAGTTTACCTGAAAAATATCATCCATCAA
ATGCAAAAACATTTACTTATGGAAAATTACCATTTGGAAGACAGTTTAAAGTAAAAAAGCAAATACT
ATGAATCATTCGAAAAAAGGTGTCTTCAGTTGACGTCAAACAACCTATATTTTCTACAGATAAAT
CAGAAATCTTTGATGTCACCATCCCGGGTCCAGTTGATACAATGAATGGTAAAGAGACTTCAGAAC

FIG. 2 - 16

AGTACTGCACATCTATCACCTGGAACCTGGGTAATCCATTGGATCCAAACATGCAGTATGATATTT
TTAAATGGAAAAATATTGAGCTCATTATTGTTTGATGGACACAACCTCTCCTTTCTATCAAGAGTTAA
TTGAAAGTGGATACGGTGACGATTTTTCTGCAAAATACTGGGTTGGACTCAACCACCGCGTTGCTTT
CGTTTACTGTTGGTCTCAACTACTTAACCAAGCAAAAAGTTGATAATTTTAAATGAAAAAGTTATGG
AAATCATTAATAATAAAATCATTCCCCGAATTAAGTAACGAAGAGTCCTCTTCATATCATGGTAGAA
TTGATGCTATATTGCATCAAATAGAAATAGGATTCAAAAAGACACAAGCCCCGATTTTGGATTTGGAT
TATTGAGCTCTATTGTTCCGTCATGGGTGAATGGAGTTGATCCAATTGACACCTTGCAAGTGGAAA
AGATATTGTTCGCATTTTAAAGAAGATTATAAACAAAATGGTTTAAAGGATCTTTAAAGAATTATTAG
AAAAGACATTGTGTAACCCCTCATTCGCAAAAATTTAAATTCACCATGGAGCCAAGAGAAGATTTTA
CCAAACAATTGGTAAAAGATGAGAATTTGATGATCGAGAAAAGAGTAAGTGAACACACAGAAGATA
ACAAGAAGGCAATCTATGAGCAAAACTTGGAAATTAGCTAAATTACAATTGGAGGATCAAAATACAG
AAGTTTTACCCACATTGACTATTGATGACATTCCAAAGAGAGGTGATTTTATGCCATTGATTTGG
GCCAAGTAAATAAGAAAGTTGTACATGAAAGGGTAGTTGATACCAATGGCTTGGTTTATGCCAACG
CTTTAAAGATATTTCTTATTTACCCACCAAACCTTTACAAGTACCTTCCATTGTTTAAACAACCTGTT
TGACGAACCTTGCTGGAACAGAAAACACACCCATTACGGAGTTGGAAACTAAAATACAAATGTTAA
CTGGCGGGATAACATTTAGTTCTAAAAATATCGACTGACCCCTATAATATTGAGCAACTAAAATTAC
AGTATGTGTTAAGTGGAATGGCTTTGAAAGAAAAGTCATCCTCAGTTTATGATTTATGGTTGGAGA
TTTTAACTACTACCAAATTCGACACCAGTGATGAGGTATTAGAAAAGTTGTCAGTTTTGATTAAAA
ACATGGGACAAAACCAAATCAATAATATTGCTGATCGCGGTCATTCTTATGCGGCTGCTGTGAGCT
CACTGAAATTGACACCGCTGAAATACATCAGTGACATCGTTTCAGGTTTGAGTCAAGTTCAATTTG
TAATGGAGTTGAACTCCAAATTAGAATCAGAAGGGAAAGAGTACTTGGCCAAAGAGATTATTCCGA
TATTGCAAGAAATACAAAAGTATGTATTGCAAGGTGAATTCAGGTATAGACTAGTTGGAAATCAAG
AGATTATTGTTGAAAACGAAAAGCTTATTGAGAAATTTGATAAGGATATTTCTTCCAACAGACCAA
CTTTATCGTTAACAGTAACAGATGGTPTACTGGCATTGTTGAACTCATTCAATTACAATCATACAA
GTGAAAATGCTCTTAGTTAACTTACCATTTCAAGTGGGATACTCTTCATTAGGTAAGATTGGCTCTT
CGTATTCATCAAAGGATGGTGCTTCTTTACAAATATTATCTCAGTTATATTTCTTTAAAAATATAC
ATTCCAAATAAGAGAAAGCAATGGTGCATATGGAGGTGGTTTGACATATGATGGGTTGAACGGGA
CATTAACCTTTTATTCGTATCGTGATCCTAATCCTGTAAAGTCGATTCAAACCTTTAGAGATTCTT
TACTGTATGGACTTGATGCTAATTGGAACGATAAGGATTTACAAGAGGCTAAGTTGCGGGTTTTCC
AAAGCGTCGATGCTCCAATTAATATCTCTTCTCAGGGTGCTAGTGCTTCTTTGAAAATATAGATG
ATTACTTGAGACAGGAAAGAAGAGAAAACCTTTTTGGGTACCACTTTAAAGGATCTCAGAGATGTGA
CTGAAAAGTATCTTGTGATAACCAAAACACCTTGTCACTGTTATTGGTGACAATGAAATTTTAA
ATGTCGATAATAAATGGCAAATTAGAAAATTTTCAAGTATAG

YDR430C_homolog 1034aa (SEQ ID NO 328)

MLKTRLKQSR AISRVVRRYACSHPI SPNL DKYPVGLKLHG YEVTQTSP IPEFSLTAVSLKH TESGA
THLHLDSPND SNNVFSIAFKTNPPDNTGVPHILEHTTLCGSKKFPVRDPFFKMTNRSLSNFMNAMT
GHDTFYFPFATTNSKDFENLMDVYLSSVFEPQLNHTDFLOEGWRIENQNVHDISSKLEFKGVVYNE
MKGQYSNSAYFYFIKFLES IYPSLNNSGDPKKIVDLSYEGLLFHSKNYHPSNAKTFTYGLPLE
DSL SKISKYYESFEKKVSSVDVKQPIFSTDKSEIFDVTIPGPVDTMNGKETSEQYCT SITWNLGNP
LDPNMQYDIFKWKILSSLLFDGHN SPFYQELIESGYGDDFSANTGLDSTTALLSFTVGLNLTQKQ
VDNFNEKVM EII NNKIIPELSNEESSSYHGRIDAILHQIEIGFKRHKPDFGFLLSSIVPSWVNGV
DPIDTLQVEKILSHFKEDYKQNGLRIFKELLEKTLCNPHSQKFKFTMEPREDFTKQLVKDENLMIE
KRVSELTEDNKKAIYEQNL ELAKLQLEDQNT EVLPTLTIDDI PKRGDFY AIDLQGVNKKVHERVV
DTNGLVYANALKDISYLP TKLYKYLPLFNNCLTNLAGTENTPITELETKIQMLTGGITFSSKISTD
PYNIEQLKLQYVLSGMALKEKSSSVYDLWLEILTTTKFDTSDEVLEKLSVLIKNMGQNNQINNIADR
GHSYAAAVSSSKLTPSKYISDIVSGLSQVQFVME LNSKLESEGKEYLAKEIIPILQEIQKYVLQGE
FRYRLVGNQEIIIVENEK LIEKFDKDISSNRPTLSLTVTDGLSALLNSFNYNHTSENVLVNLPFQVG
YSSLGKIGSSYSSKDGASLQILSQLYSFKNLH SKIRESNGAYGGGLTYDGLNGTLNLFYSYRDPNPV
KSIQTFRDSL SYGLDANWNDKDLQEAKLRVFSVDAPINISSQGASAFFENIDYLRQERRENFLG
TTLKDLRDVTEKYLVDNQNNLVTVIGDNEILNVDNKWQIRNFQV

FIG. 2 - 17

YDR450W_YML026C_homolog 1366bp public: 1..1366; exon 1: 501..548, intron 1: 549..976, exon 2: 977..1363 (SEQ ID NO 329)

TTAAGAACTAGCAGATGTAAATGTTTTATGTCATTATATAATTTGTTAATACATGTATATAGATT
TTTTAATGAATGTATTCCCTAAATAGAACAGAATTATGATGCTGTACAGCAAAAACCTGGTTTGAG
TATTGGAGAATGTTATAAACTGAAATTTGATTTACAACCAAAACCCGTGTCACGTGTAAGTAATTA
GGGCTTTTAGGGCTTTCTATATACAGGCCACCAGAAATTTTTTTTTATGGCGGATAGAAATAATGTAT
GCGCGCGATTCTTCTCTGCTAGAGGTTTTCTTTTTTGTTATGTCTGTAAACAGTGCAGCTCACATAGTT
AAGTAATTTTAAAGCCAGAGATTGTGTACAGTCGCACGCCCCCTAATCACATAGTTAATTTCTCAAA
CTTTCTCTCTTTCTCTCTTTGCTTTTCTCTCTAAGGAAAAAAAAAATTTATTTTCATTTGTTGAAAAT
TTTTGTATAGTTTCAGTTTAAACAACACCAGTAATCAAACATGCCATTAGTTGTCCAAGAACAAGGTT
CATTCCAACACATTTTACGGTATGTGAGTGTATTATAAGATTATTTGAATGAGATAGAAAAGGGTT
AAGGAAGGAAAGAAATTATCCAACCTACTGTTTTTGGGAAAGATTAAATCAGAAATTTGAATGCAATGA
AAAACTTTTTCAAGAGATGGATATGGAACAAGATTCGATTGTTATCAACAAATATAAAGAAAAGC
AATGATTTACTACTGTTTGGGAAAGATTTTGGATATGTGTATCAACAATACTACTATTTACTTTGG
AGTAATATGTTTTCAATATTATCAGAGACTTATCAAAATTTATGAGTTTATTATTATTGAAGTTCA
ATACCATCAAGCCTTTTTTTTAAACCATCACTCTATTCAACAATCATTTAAATATTAAAGTCTTTTT
TTTCCCTGTTTAAAGTATTCGATTTACTAACATTATGAATTATTATTATAGTTTGTAAACACCAA
CATTGATGGTAGAATCAAGATCATGTACGCCCTTGACCAAGATCAGAGGTGTGCGGTAGAAGATATGC
CAACTTGGTTTGTAAAAAGCCGATGTTGAATTAACCAAAAGAGCTGGTGAATTGACCCAAGAAGA
ATTGGAAGAATTGTCAACATTATGCAAAACCAACCACTATAAAATCCCAGCTTGGTCTCTTGAA
CAGACAAAAAGATCAAGTTGATGCTAAAGATTACCATGTTTTAGCTAACAACCTTGAATCTAAAT
GAGAGATGATTTGAAAAGATTGAAGAAAATCAGATCTCACAGAGGTATTAGACACTTCTGGGGATT
GAAAGTTAGAGGTCAACATACTAAACTACTTCTCGTGGTCGTAA

YDR450W_YML026C_homolog 145aa (SEQ ID NO 330)

MPLVVQEQGSFQHILRLNLTNIDGRIKIMYALTKIRGVGRRYANLVCKKADVELTKRAGELTQEEL
ERIVTIMQNPTNYKIPAWFLNRQKDQVDGKDYHVLANNLESKLRDDLERLKKIRSHRGIRHFWGLK
VRGQHTKTTSRGR

YDR471W_YHR010W_homolog 1327bp PathoSeq: 1..1327; exon 1: 501..530, intron 1: 531..946, exon 2: 947..1324 (SEQ ID NO 331)

ATAGTTATTACATATAATAAGCAAATAAAAGAAATGATAAAGAACCATTATTAACAAAGTT
TGAACGTGCTGAATGTAATCTTGTATACGAGAAATTCATCTTGGAAATATTTCTAAACGATACTG
GTAATACCTAATTCTATTTGGTGTGGTGCATCACGTGCTAGGGCTATAGCCCTAATAGTATATGCA
GTCGCATACATTAATTGGTCATCTCATAAGTAAATTATATAATGTATAGTGTGCGCGCACTGTAAT
TTTTCACACTAAGTTAAGGAGAGTGCAGAAAAATTTAGTACTAACAAAATTTGTATTGTGTGTGT
GGCTATTGGGCAGAGCGAAAAATTTACCCCTACTGAGAGGAACTGTGAGGGAGAGAGATACACAC
AAACTCTGTGCGCAAGAAGAAAGACAAAAATTTTTTTGAAAAAAAAAAAAAGAGACAACCAACCTT
TTATTGTATTAAACATTTTAAGATATCAAGAACTAAAAATGGCTAAGTTTCATCAAACTCGGTAAAG
TTGGTATGTAAAAATGAGTACCTATATGGGTAGACAATGATAGATTTATTGGCCAACCTATGAATGG
GATAGATATATATGATATGGGAGAGAATTTTGAAGGATTGAAATATTTTATATAAAAGAGAGAAGC
AAAGAGAAATAATGAACAATTGAAAAAGAGATACAAATCTGTTAATTAACTAGAATATGCCATT
GAAGATTTAAATGATTACCATCGTAATAAATTTATTGGAATTTGGGAGATTCTTTTGGAGTTAAGA
AAAAAGCAAGTGATTGATCAATCACTATGGAGCCGTCACAAGACATCAACGAATCCCAACACATTT
TTATTTATTTCATATCCATCATATGGCAGTAACAATCATGAATCTACAAATTACATTTAAAAAAGC
ATTATACTAACTAAATTTTTTAGCTATTGTTGTAAGAGGTCGTTACGCTGGTAAAAAAGTAGTCAT
TGTGAAACCACATGATGAAGGTACCAAATCTCACCATTCCCACATGCCATTGTTGCTGGTATTGA
AAGAGCTCCATTGAAGGTTACCAAGAAGATGGATGCTAAAAAAGTTACCAAAAGAACTAAAGTCAA
GCCATTTGTTAAATTAGTAACTACAACCATTTAATGCCAACTAGATACTCATTAGATGTTGAATC
ATTCAAATCTGCTGTCACTTCTGAAGCTTTAGAAGAACCATCTCAAAGAGAAGAAGCTAAAAAAGT
TGTCAAGAAGGCTTTTGAAGAAAAACATCAAGCTGGTAAAGACAAATGGTTCTTCCAAAAATTACA
CTTTTAA

FIG. 2 - 18

YDR471W_YHR010W_homolog 136aa (SEQ ID NO 332)

MAKFIKSGKVAIVVRGRYAGKKVVIVKPHDEGTSKSHPPPHAIVAGIERAPLKVTKKMDAKKVTKRT
KVKPFVFKLVNHNLMPTRYSLDVESFSAVTSEALEEPSQREEAKKVVKKAFAEEKHQAGKNKWFFQ
KLHF

YDR486C_homolog 1157bp PathoSeq: 1..1157; CDS: 501..1154 (SEQ ID NO 333)

TTCCAGTCATTCCGAAATGCATAAGCAAGACGTTAGTTGTATTGTGGTTGTTTAGTCTAATCCAAA
AATACTTGCCATGACGACCCACTGAAGTAACAACCTGCATTTGTTAAGGCTTTTCTCATCTTATTCA
ATTCTTTTTCAGCATCATTCTGTATCTTTAAGCACAGGGAATAGCAATGGATCATGTAACAAATCA
CTTTTCGTGATTTCGAAAGCCCAAAATGTTTCGTTTTTAACAACGCACACACATGTGAAACCTAAACCG
AGTTAGTCGTCAAGAAAATAATTCAAGTGTCTTAAAGTCTGTACCTTAAGCGTCAAACGTACTTCTGCA
ACCTCTGGCATTGAGTGTAATTTAAATATTCATGATAATCTGGAACCTACAAGCTACGAAAAAAAAA
GAAAAAGAAAAATAGTACGAGTTCTTGGTGAGATAAATAATGGAGAACACTTTTTTTTTTCTCTTT
GGAGGTTTTAGAAAGGCAAAACCAAATCTAGACAAGGAGATGAACAGATTATTCGGAACGAAAAGCA
CTGCGCCCAAACCATCTTTGAATGATGCAATCAAGGGAATCGATGAAAGAGTGGGGTCTTTGGATG
TTAAATTAAGCAAGATCAACTCGGAATTATCCACATAACCAACAAAAGATAAGCAGAATGAGAGACG
GACCCGGGAAGTCGGCACTAAAACAAAAGCAATCAAGTTACTAAGACAGAGGAAGCAGATAGAAG
CTCAAAAGGATCAGTTAGAGAATCAATCTTGGAAATATGACACAAGCTTCCATGACAACAGATAACT
TACAAAATACCATGGTCACAATAAATGCAATGAAAACAGCCAATAAACTGTTGAAACAAACTTATG
GAAAAATTAATATCGATGAATTGGAAGATCTTCAAGATGAAATGTTGGATTTGATTGATAAATCAA
ATGAACTACAGGAGGCACTTCTGACGAGCTATGATGTACCCGATGACATCAGTGAGCTGGAGTTGG
ATGCTGAATTAGAAGCTCTTGGCGAAGAAATGATTTTGAAAATGAAATGGCAGAGAGTGGGATAG
GTGCACCTAGTTACTTAAATGATACAGAACCTACAGCAGCAGATAAATTGCCTACATTTATTGACG
AACAACCAGAAGAAGCTCAAAAATCGCAAACCTAG

YDR486C_homolog 218aa (SEQ ID NO 334)

MNRLFGTKSTAPKPSLNDIAIKGIDERVGSLDVKLSKINSELSTYQQKISRMRDGP GKSA LKQKAIK
LLRQRKQIEAQKDQLENQSWNMTQASMTTDNLQNTMVTINAMKTANKSLKQTYGKINIDELEDLQD
EMLDLIDKSNELOEALSTSYDVPDDISESELD AELEALGEEIDFENEMAESGIGAPSYLNDTEPTA
ADKLPTFIDEQPEEAQKIAN

YDR507C_homolog 4550bp PathoSeq: 1..1424, public: 1524..4550; CDS: 501..4547 (SEQ ID NO 335)

GAATGAGATTTTTTTTTTTTACTAAGGGTGCACTACTACTAGTTATTTGTTTTGTTGTTGACGATCA
TTAAAGAAAAAATTTACAGTATACACAAAACACTTTACTTCTGCTGTTTTTTTTTTATTTTAGTTT
TTGGTTTCATAAATTATTTAAAGAAAGCAAATAATTATTGAAATAAATTTTATATTTTGGTTTTTT
TTTTCTTTGGTTTTCTTTGAATTTTGCAAACCAATCCAAATTTTTTTTGAAAATTTTTCTCTCTCT
TCATTTGTTGACTTTTTGAAAGTTTTATTCATCCATATTCTTCAAGTTAAAATAGTGTTCATATCT
GTCCAACCAAGAAGAAAACCAATAAACAACATCAATTCCAACCTTTGTTTACATCAAACAGAAACAA
AAAACAGATAATTTATAGACACCTTCATTCATTCGTTATTTTTTTTCCAAGTACTACACGCTTTTAT
TTTTAATACATTTATCATAAAACAAAATTTATATCAATAATGCCACATTCAGACAACCTTCGATAT
CGTCATCGATTATGTCCCAATCAAATCATAATCATCCACAGAAGATCGGACCTTGGAAATTAGGTA
AAACTTTAGGAAGAGGTGCCACCGGTAGAGTCTTATTAGCTACTCATCAAACCTACTGGTCAAAAAG
CTGCCGTTAAAGTAGTTTCCAAATCCGAATTACAAGACGAAGAAACCGAGAAAAATGGAGATGGAT
TACCATATGGTATAGAAAGAGAAATTTATTATAATGAAATTATTAACCTATCCTAATGTTTGGAGAT
TATATGATGTATGGGAAACATCTAAGGCTCTTTATCTTGTCTAGAAATACGTTGAAGGTGGAGAAT
TATTTGATTTATTGGTGGAAACGTGGTCCATTACCTGAAGTCGAGGCTATCAAGTATTTCCGTCAAA
TCATATTGGGTACGGCTTATTGTCTGCTCTTGGTATATGTACAGAGATTTAAACAGAGAATTT
TGTTACTAGATTTCTCAATTGAATGTAAAATTAGCCGATTTTGGAATGGCAGCTTTAGAAAAGTAACG
GCAAATTATTAGAGACTTCTTGTGGTTTCACCTCATTATGCTGCTCCAGAAATCGTTAGTGGATTGA
AATATCATGGAGCTGCTTCTGATGTTTGGTCTTGTGGGGTTATATTATTTGCCTTGTGACAGGTA
GATTACCCCTTTGATGATGAAAATATTAGAAATTTACTTCTTAAAGTCCAGGCTGGTAACCTTTGAAA
TGCCCCGTTGATGAAGTTAGCAGAGAAGCTAGAGATTTAATTGCTAGAAATGTTAGAGGTTGATCCTA

FIG. 2 - 19

TGAGAAGAATATCTACTGAAAAAATCTTAAGACACCCATTGTTAACCAAATACCCAATGTCAAACG
AAGATTTAATCAGTGAAAAATCATTACCACATCCACATACTGGTTACAAATCTTTAGGGTCAGTTA
GAAACATTGATAAACAGATTTTATCAAACTTGACAATTTTATGGAATGATAGACCCGAAGAGGAAA
TTGTTGATTGTCTTTTGAAAGATGGATCCAATCCAGAAAAAACATTCTATGCATTATTGATGAGAT
ACAAGCATAAATCAAGACGATAACACTAAATAACAATTCACCAAAGAAATCAACGAGTTTCAATAATA
AAGTGGTACGCAGTGGGTCCAAATACAGTCTTAATGGAACCCCTAGAAGAAAAAGAGCCAGTCACA
TAAGTGTGTCAAGACCAACATCTTTCCAATACAAGTCTAATCCTGGCGCTGGTGCAACAGCAAATA
GAACTCCGTTGCCAGACATTCTGTGGCTTCCTCGGCCAACAATTCTCCTCGTAAATCACCATACA
AGTCACCATACAGATCACCTTATAGATCACCATATAAATCGCCTTCTAAGAGATATTCATATAATC
AATCCCCAACTAAATCTCCTTACGGAAGAAGATCAAATTCACAAAGACAATTTGAAAATGAACCAT
TAAAGGCAAAGCCAAGAAATATTTACAATGAGATTGTTGATGCACAAAGCAACTTTTCTCTACCTC
CATCGTTCCACCTTCTTACCTTCAAAAGATTTCTCGTTATATGATCGATGAACCCAATCAACCCC
AGTTGCAACAACCTGCTTTAAGTCAAGTCCCTGAAAATCCTATTGTTGATGAATCCCTGATTTAA
TGCAGTCAGCAAAAATTTCTAGTGGAAAGAGAAATTCATAATAGGAAAGAACAACAACAGCA
ACAGCAACAAGAGAATGTCTAAGAGAAAATCAATTCGTGCATCTATGACCACGGGATTGAAAAGAA
ATTCCATAACCATGAAATTGTTATCTACTTATGCTAAATTATCAGGTGATGACGACTGGGAATACA
TGGATAAACAAACAAAAGAACATCGGCTACTTTTGCAGCATTGTGTGACAAAATATTTAATCAAG
AAGACTATGACGAAGAAGACGAACAATTAGTTGATCCTGAAGAAAAGGAAGCCAAGGAATATGAAA
GGTTAATGGAATTGGAAAGAAAAGAAACATGAAGCTGAGTTGAAAGCTAGAAGAGAAATGAAAAGA
AGAAAAGAAGACAAAAGAGACGTTCCATTTTGAGTTCTAAGAAATTAAGTATTATTGTCAAGAATG
ATGCTGATCCAAATAATAGTGAACAAGAGTTGGTCGATGAAGGTATAAAACAACCAAAACGTCAAT
CCAAAACCTTGACCGCTTTAAGAGCATTATCTGAAGGAAATCATGCATCTGAAGAATTGACATTGG
AAGACGTTGAGAATTTGAAGAGACGATCAGCATCACAGCCGGTTCCAAAAGAGACAAACTCCGG
TTTTGACAAGAAGACCTGTATCAAGATTAGATCCATTATGGCAAGCACACGAGAATGAACAGTTAG
ATAGAGCAAAAGATGCCTTGGAAACAAGAATGGAGGGATTACAAAAGAGAAAGTTCTACTGTTAGTC
GTAAAAAAGTCAACAGAGAGTCGATGATATCAGTTATGGATGATATTGTTGAAGAGGACCAAGGCC
GTGTCAACAGGAGATCAACACGAAACACTTACTATGAAAGGGAAAGAGACTATGAATTACCAGAAC
CAACTGTGGAAGATTCCAACCTGACTGATGACTACATGACAGAAATCAGAAAATCAAGACTTTTGA
ACAGTCAGTTAAATGTTAGGGATCCACTTAATGAAAAAAGAAATCTGAACCCAAGACTCTTATTA
GCAATGTTCAAATACCGAGTGTTACTAGAAAATCAAGAAATTTCACTACTTCCAACAAAAGGTTGT
CGGTATTGCTTATGTATTCAACAAAGGAATCATACCGTGATTTGAATTTCTATAATTAACCTACCAG
ATGAAAACCCCGAACAGCATCAAAACATGAACAAGCCAGCGTTACGAACCAGTATTGCTGATCGTT
TGGATAAAGCTGGATTGGCTGAACCAGAATATGAAACTGAGACTGATGGTGAAGATAAAGTGTCTG
TTATTGATTTGGATGATCATTTAGCTGATAGAAGGACTTCCTATTATGATGGATCTGGAAAGAGAG
CATCTAGAGCTTCAACAATAAACGTTACAATGTTCAATCCAGTTTCAGAAAAAGACCAAAATCCA
AAGTTCCTGATTTGCCAAAGAATGATTATGATGACACATTTGTCAGTAATAGTGATGAAGTTTATA
AGCGTCAGTATAAATCGATGGTTTCTGATGAGTCTAGTGCATCTGATGATGATTTTGATAAGATTA
AATTACCAGATGGTAAATCAACTAAATCTTCCATTGATGAATTGGCTAACGGCACGCTTACAAGTG
GTCATAGAAAACCAAGATAAGACATTCTCAACCGGGCCAGAAATGTTGATTCTCATTGTAATG
GAGGTATTGAGTCGTCTCAACCAATGTCTAAAGTTCGTGGTAACAATTCAAGTGGTCATGATGATA
GTGTTCCACCACCACCGCCAGCTCACAAGGTGAATAAAAAACCATTTGGATGATAAGACGAATTTCC
CTCCACCAGAAGTGGATCCAAAAGAAAAGGTTCAATTTTTAGAAAATTTCTTGGGGATCCAAAA
AAACCATTGAAAATAATACAAACGCCGCCACTAATACCACGACTCAACAACAATTACCAAGTCCCTG
CTGAATCAAAAGAGGAGAAACCAAAAGTTCAATTTTTCAGATGGTTTTCGTCTACTAATACTCCAT
CTGCTGCTGAAATTAGAAAATTCAACACCATTTTACCTAAACATGAAATGTCTACTGCTTTATTTG
CTTTATTGAATTCCTGGTCTAATTTTGGTTTGAAAGATTACGGAATGATCAAGTTGGATATTATA
TTACTGGTGCTATTTCTAAACATAATTCTTTTAATTTAAAGAGTTGTAAATTTAGAATTAAGATTA
ATCAAAGAGATTTTAATCAAAAATCAGAAATGTTTGTGTTAGAGTGAAAGGATCTAAAGTTACAA
CTGATACTTTATTTTGTGAAATTGAAAAGGTCTTACTCAAAGAAGGTGGTTTAGATAAATAA

YDR507C_homolog 1349aa (SEQ ID NO 336)

MPHSRQPSISSSIMSQSNHNHPQKIGPWKLGLKTLGRGATGRVLLATHQTTGQKAAVKVSKSELQD
EETEKNGDGLPYGIEREIIIMKLLTHPNVLRLYDVWETSKALYLVLEYVEGGELFDLLVERGPLPE
VEAIKYFRQIILGTAYCHALGICHRDLKPENLLDSQLNVKLADFGMAALESNGKLLTSCGSPHY

FIG. 2 - 20

AAPEIVSGLKYHGAASDVWSCGVILFALLTGRLPFDDENIRNLLKLVQAGNFEMPVDEVREARDL
IARMLEVDPMRRISTEKILRHPLLTYPMSNEDLISEKSLPHPHGTGYKSLGSRVNRIDKQILSNLTI
LWNRPEEEIVDCLLDKGSNPEKTFYALLMRYKHNDNTNNNSPKKSTSFNNKVVRSGSKYSLNG
TPRRKRASHISVSRPTSFQYKSNPGAGATANRNSVARHSVASSANNSPRKSPYKSPYRSPYRSPYK
SPSKRYSYNQSPTKSPYGRRSNSQRQFENEPLKAKPRNIYNEIVDAQSNFSLPPSLPPSLPSKDSR
YMIDEPNQPOLQOPALSQVPENPIVDESPDLMQSAKISSGKRNSIIGKNNNNNSNSNKRMSKRKSIR
ASMTTGLKRNSITMKLLSTYAKLSGDDWYMDKQTKRTSATFAALCDKIFNQEDYDEEDEQLVDP
EEKEAKEYERLMELERKKHEAELKARRELEKKRRQKRRLSSKKLSIIVKNDADPNNSEQELVD
EGIKQPKRQSKNLTALRALSEGNHASEELTLEDVENLKRRSASQVPVPRRQTPVLTRRPVSRDLPL
WQAHENEQLDRAKDALEQEWDRDSQKRSTSVSRKKVNRESMISVMDDIVEEDQGRVNRSTRNTYYE
RERDYELPEPTVEDSNLTDYMTETIRKSRLNLSQNLNVRDPLNEKRKSEPCTLISNVQIPSVTRKSR
NFTTSNKRSLSVLSMYSTKESYRDLNSIINSPDENPEQHONMKNPALRTSIADRLDKAGLAEPEYET
ETDGEDKVSVIDLDDHLADRRTSYDGSGRASRASTTKRYNVHSSSEKRPKSKVPDLPKNDYDDT
FVSNSEVHVRKQYKSMVSESSASDDVFDKIKLPDGKSTKSSIDELANGTSTSGHRKPKIRHSQPG
PEMLIPHLNGGIESSQPMKVRGNNSSGHDDSVPPPPPAHKVNKKPLDDKTNFPPEVDPKRKGSF
FRKLSWGSKKTIENTNTAATNTTTTQQQLPSPAESKEEKPSSFFRWFSSSNTPSAAEIRKFNTILP
KHEMSTALFALLNSWSNFGKDLRNDQVGYITGAISKHNSFNLKSKFKRIKINQDFNQKSEIVC
VRVKGSKVTTDTLFCIEKVLLEKGGDLK

YER102W_YBL072W_homolog 1121bp public: 1..1121; CDS: 501..1118
(SEQ ID NO 337)

ACAATACTAGGCACTGTTGAGTGAGTGAGCATTCTCTGTTCTCACTCAGTTAACAAAAATAAAA
AAAATTTTTCATAATTTAGAAAGTTTCATTATACAGTCTTTTTTCAATTAACAGTGATACAAGAGTGTA
TGTAAGACCAACATGTACTAGCAACTATAATGATTACCAATGATTGGGATCACAATAAATGTG
TTAATATGAATGAGAGAAGGATAGTGAATAAGAGATTACGAAAGAATAGATTCAACAAGTTCAGAA
TGGTATACAACATAAATGGAATTATTTTCAAATATGCAACTATCATTATGACTACTACGACAACAA
TTTTAATCGAGAGAAGATCATTAGATCAAGAGTTGGGAAACTAATACCAAGGAAATATCATTAAGA
ATTAATAGCTTTTGCAAAAATTTGTTTACTCATATTATTTGTTTTAGTTGGAAGCGATTACATCA
TGGAACAAAGCTTTACTAACAACATTTGTTATAGGTAAAAATGGGTATTTCTAGAGATTCACGTCACA
AAAGATCCGCCACTGGTGCCAAAAGAGCCCAATTACAGAAAGAAGAGAAAGTTTGAATTAGGTAGAC
AACCAGCCAAACCAAGATTGGTCCAAAAGAATTCACTCTGTGACAACAGAGGTGGTAAACCAAA
AATTCAGAGCTTTGAGAGTTGAAACCGGTAACCTCTCTTGGGGTTCCGAAGGTGTTTCCAGAAAAA
CCAGAATTGCTGGTGTCTGTTTACCATCCATCTAATAACGAATTGGTTAGAACCAACACCTTGACCA
AATCTGCTGTTGTTCAAATTGATGCTACTCCATTACAGACAATGGTACGAAAACCACTACGGTGCTA
CTTTAGGTAAAAAGAAGGGTGGTGCTCATGCTGCTCAGCTGCTGAAGTTGCCGATGCCAAGAGAT
CAAGAAAAGTCGAAAGAAAATTGGCTGCTAGATCTGGTGCTGCTGCCATTGAATCCGCTGTTGACT
CTCAATTCGGTTCTGGTAGATTATACGCTGTCAATTTCTTCAAGACCAGGTCAATCTGGTAGATGTG
ATGGTTACATCTTGGAAGGTGAAGAATTAGCCTTCTACTTGAGAAGATTAACCTGCTAAGAAATAA

YER102W_YBL072W_homolog 206aa (SEQ ID NO 338)

MGISRDSRHKRSATGAKRAQFRKKRFELGRQPANTKIGPKRIHSVRTRGGNQKFRALRVETGNFS
WGSEGVSRKTRIAGVVYHPSNNELVRTNTLTSAVVQIDATPFQWYENHYGATLGKKKGGGAHAH
AAEVADAKRSRVERKLAARSGAAIESAVDSQFGSGRLYAVISSRPGQSGRCDGYLEGEELAFY
LRRLTAKK

YFL014W_homolog_1 819bp PathoSeq: 1..819; CDS: 419..816 (SEQ ID NO 339)

TTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTGTG
TACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTTCGTCCA
AATTGAGACCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTTGCTATCGATAACGAAGG
TGAAGGCAGTTTAGCTTGGAGACATTTAGAGAACCTTAGTTACATCTCATCTTCCGTTTCGAGAAAT
CGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACGACCAACAGCAATATAGCAA
TCATAAATAAATTGCCCCGCGGTTGACAGTGATATCTTCGAGGAATGGCAACCTTTGCCCCCTC
TCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTTCTTTGAATCTTGTTTTTT

FIG. 2 - 21

TCGACATACACCATAAAATCCCATAGAAAACCTGCAAAATGTCTGACGCCGGAAGAAAAACATTTCT
ACTAAAATCAACGAAGCTATAACCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAACAA
GTCACCAGTACCCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTCAA
ACTGTTGCAGACAGCGTGCACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCGAA
CAAGCAGAGGGCGAACAAGACCCCTTGCTGAAACAGCTCAAGAATATGTCGAGGTTGCCAAAACCTG
AAATTGAAAAGGCTGCTGAATACGTGA

YFL014W_homolog_1 106aa (SEQ ID NO 340)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVTSTLDKAVGSNVDPDNQKSFTQTVADSVQQGSDN
AKADLKKQSEQAEGEQRLSKQLKNMSRLPKSKLERSNT

YFL014W_homolog_2 884bp public: 1..884; CDS: 501..881 (SEQ ID NO 341)

CCTTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTGT
TGTACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTTCGTC
CAAATTGAGACCCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTGCTATCGATAACGAA
GGTGAAGGCAGTTTAGCTTGGAGGCATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAA
ATCGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACGACCCACAGCAATATAGC
AATCATAAATAAATTGCCCGCGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCC
TCTCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTCTTTGAATCTTGTTTTT
TTTCGACAAACACCATAAAATCCCATAGAAAACCTGCAAAATGTCTGACGCCGGAAGAAAAACATTT
CTACTAAAATCAACGAAGCTATAACCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAAC
AAGTCACCAGTACCCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTC
AAACTGTTGCAGACAACGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCG
AACAAGCAGAGGGCGAAGCAAGACCCCTTGCTGAAACAGCTCAAGAATATGTCGAGGTTGCCAAAA
CTGAAATTGAAAAGGCTGCTGAATACGTGAGTGGAGTTGTCACCGGTGCTACCGAAGGTGCCAAAA
CCGGCGCTGATAGTACTAAAAAATAG

YFL014W_homolog_2 127aa (SEQ ID NO 342)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVTSTLDKAVGSNVDPDNQKSFTQTVADNVQQGSDN
AKADLKKQSEQAEGEAKTLAETAQEYVEVAKTEIGKAAEYVSGVVTGATEGAKTGADSTKK

YGL011C_homolog 1244bp PathoSeq: 1..1244; CDS: 501..1241 (SEQ ID NO 343)

GAAGGGCACCATAATGAAATCGACTCACTTCAGGATTATAATGGTATGAAACATTGTACTTGTATT
TAGTGCCAGGATGATTAGGATCATATATTGGGGTGTTTTCTCGAGTCTTGGTATCGGTTGTAAACG
TATCTGTTTTCACTTATCAGTATCGTCATTTATATTAATACTACTTTTCTCCTATGGTTATATATTGGT
AAACAAAGAAACAAAACAACAAAAAGAAGTAGTAGTTTGAATAATGTCAATAAAAGAAACAAAG
AATGAAAGAATGATTGAATGAAAGAAAAAATATGAAAGTGAGTGCACATAATGTAGAAAAA
TGTCGAATGTCTTGAACCTTACCCATTGAGTAGTTGTTGTAGTGTAGGAGGAAGAAACAACAGAA
AGAAAGAGAGAAAGAAAAATTTCCGCCACTACAAATATTCAACAAGTTTCATATAGTAATATAATCC
CAATTGATCATTACTTTATTCACACAATTATATAACAATGTCCAATTCAGCAGGTTTGTATAGAC
ATATCACTATTTTTTCTCCTGAAGGTAGATTATACCAAGTAGAATATGCTTTTAAAGCTATCAATT
CAGCAATATCACCAGTTTAGGAATCACAGGTCAAGATTCTGCCGTTATTATATCACAAAAGAAGA
TCCCAGATAAGTTATTAGATCCTAAAACCGTGTATATATTTTAAATCACTCCTAGTATAGGAA
TGGTTGCCACTGGATCAATTGCTGATGCTAGAGCTCAAGCCATGAGAGCAAGATCTGAAGCTACAG
AATTTAGATATAAATATGGTTACGAAATGCCGGTGGAAAGTTTATCAAGAAGATGGCGAATATAT
CTCAATTGTATACTCAAAGAGCTTATATGAGACCATTGGGTGTTGCTTTAACTTTTATTCAAGTTG
ATTTTGCTGATGAAGGTAGAGGTCCACAAATTTTTAAATGTGATCCTGCTGGATATTTCACTGGGG
TGAAAGCCGTGGCCACTGGTCCAAAACAACAAGAAGCAACGACTTATTTAGAGAAAAAATTCAAAA
AAACCGATGCTGTTAAAGGAGATTGGCAAAAACTGTTGAATTTGCAATAATTGCCTTGAGTTCTG
TGATTGGAACCTGAATTCAGAAAAAATGATATTGAAATTGGTGTGCTGCAAGGAGAAATTTAGAA
TTTGTACACCAGAAGAAATAGACGAAAGATTGATTTCAATAGCTGAACAAGATTAG

FIG. 2 - 22

YGL011C_homolog 247aa (SEQ ID NO 344)

MSNSAGFDRHITIFSPEGRLYQVEYAFKAINSANITSLGITGQDSAVIISQKKIPDKLLDPKTVSY
IFKITPSIGMVATGSIADARAQAMRARSEATEFRYKYGYEMPVESLSRRMANISQLYTQRAYMRPL
GVALTFIQVDFADEGRGPQIFKCDPAGYFTGVKAVATGPKQOEATTYLEKKFKKTDVKGDWQKT
V
EFAIALSSVIGTEFRKNDIEIGVATEGEFRILTPEEIDERLISIAEQD

YGL031C_YGR148C_homolog 968bp PathoSeq: 1..968; CDS: 501..965 (SEQ ID NO 345)

CATTGTAGGTACACCTGTTTTTGCTCAATGTACACACACACGCACCAGCAGTAGGAAAAAAACAA
AATTAAATGAAAAATCATTTCGTTCAATATTAAGCTTCTTAAGATAACCAACCAATTAATATGTA
TGTGACATACCATATAAAATAAAGCTACAAATGGGGATAACTATGTATTTAATGATAAATGAATGGA
AGACCAGAAATGTATAATGTTATAAGATAGTGATTATATTGAAAACACCCTTAAAAAAATCAACCA
CCCATCTAACCGTCGAATTGGAAATGTCAATTTAGTTAGCATCGAAAATCAACAAGACATGGGGA
ATCATTTACATATAAAATAATGAGAGAGAATTACAACTGCTACGTTATGTTTTGTTTCATTATGTC
TTGTTTCATTATGTCTTGTTCATTATGTCAAAAAATCTATAGTTACCTACCTCTACATCAATTTATG
GTCTGAAATACTAACATTTTTTTTATTTATAGTGAAAAATGAAGATTGAAGTTGACTCCTTTTCAG
GTTCTAAAATCTACCCAGGTAGAGGTACTTTATTTGTGAGAGGTGACTCTAAAATTTTTAGATTCC
AATCCTCAAAATCTGCTTCTTTATTTCAACAAAGAAAGAACCCAGAAGAATTTCTTGGACTGTTT
TGTACAGAAGACACCACAAAAAAGGTATTTCTGAAGAAGCTGCTAAAAGAGAACCAGAAAGACCG
TCAAGCACCACAAAGAGCTATTGTCTGGTGCTTCTTTGGAATTGATCAAGAAGAAAGAAGTCAAAAC
CATCTGACATATAAAAGCTGCTAGAGACTCTAAATTTAGTCTAAAAGACAAAGAAGCTAAAAAGCTGCTA
AAGCTGCCAGAAAGCTGAAAAGGCTAAGGCTGTTGCTTCTGGTGCTTCTGTTGTTTCTAAACAAC
AAGCTAAAGGTTCTTTCCAAAAAGTTAAAGCTACCTCCCGTTAA

YGL031C_YGR148C_homolog 155aa (SEQ ID NO 346)

MKIEVDSFSGSKIYPGRGTLFVRGDSKIFRFQSSKSASLFQQRKNPRRISWTVLYRRHHKKGISEE
AAKKRTRKTVKHQRAIVGASLELIKERRSQKPSDRKAARDSKLAKDKEAKKAARKAEKAKAVA
SGASVVSQQAKGSFQKVKATSR

YGL043W_homolog 1418bp public: 1..436, PathoSeq: 437..1418; CDS: 501..1415 (SEQ ID NO 347)

AATCTACCATTAGGCAATGTCATATAATTTAGATTACGAACAGCTGATGACGCAGTTTCATTATCT
CCATAATTTATAATGGCATACCCCTTTGGATTACCTGTTAATTCATCAAATAAATACTTCACATCT
AATACTGGTCCAAGTATCTTGCAATATCCCGCACCTGTTCTTCAGTGTAATCAAATGGAAATTTA
CCTATTGAAACACAAGTGCTTTTACTATCCATATTTAGTTTGAGCTGCCTAGTTTTCCTGATTCTT
GGTAACAAAAAACTATAATTATTTAACAATTTATCGATAGAATCTCTTCCAAAGTACAACCAATTT
CGATACATTTTTTTCTATGAGATGTTTTTTTCCCTTTGCTTTTAACTAATGTATTTGGGTACACT
ACCTGAACCTACCAGTTCAGTTCAGTCTAAAAAATTTTTTATTTATTGTGTTGTTTATACTACCC
TTTGTCATATATTACTAATATTTATCTTACCCTTTTCATCATGGATACAAAGGAAATAAGATCTACCG
TATCTAATCTTTGAAAAAGCAGTAGATGACACCACCATTTTAAAGTTGTTGAATATCTTGAATGATG
GGGTTAAACCATCCGAAAAACTCTTGAGAGAAACCAAAGTAGGTGTAGCTGTCAACAAATTCAGAA
GTCACGACAGTGCCGAAATCAACGGTTTATGTTAAAAAATGATCAGAAATTGGAGAGATGCCGTGC
AAGCCGAAAAGAACAACAAAAAGAAGTTAGCAATAGCAGCTGGAACAGGAACAGGAACACCTTCAA
GCTCAGCAATTTGCGCCATCATCATCGGGTTCTGGAAGTACAACACCAAAACCATCAGAGTCAACCA
CACCATCGGCTGCCCGTAAAGGTCCAAGAAATCCAAAACTGACGGTGTAATACTCAATTATACG
AAAATGATACCAGAAATGCATCGGTTAGTGCTTTATACACGTCGTTAGCAGTTGATCGTGACGATT
CACCAAAACACATTTTGAGAATAGCTATTGAAATCGAGGCTGAAGTATACAAGAGCGAATACCTGA
AAGTAAGTGACAGTTATAGAAATAGGTTAAGAAGCTTTACCATGAATCTTCGAAATAAGAAAAACC
CAGAATTAAGAGAAAGAATCTTATCGAAACAAATTTTACCTGCTGCGTTTCATTTAAATGACCCCTA
ATGAAATGGCTCCTGAGGCATTGAAAAAGGAAATTGAAAAATTGCACAAACAAAACCTGTTTGATG
CTCAAGGTGCTACTGAAAAGAGAGCAGTGACCGATAGATTCACTTGTGGCAAGTGTAAGCACAAGA
AGGTCAAGTTATTATCAAATGCAAACCAGATCAGCGGATGAGCCTTTAACTACATTTTGTACTTGTG
AAAATTGTGGCAATAGATGGAAGTTTTCATAA

FIG. 2 - 23

YGL043W_homolog 305aa (SEQ ID NO 348)
MDTKEIRSTVSNLEKAVDDTTILKLLNILNDGVKPSKLLRETKVGVAVNKFRSHDSAEINGLVKK
MIRNWRDAVQAEKNNKKLAIAAGTGTGTPSSSAISPSSSGSGSTTPKPSESTTPSAARKGPRNPK
TDGVNTQLYENDTRNASVSALYTS LAVDRDDSPKHILRIAIEIEAEVYKSEYSKVSDSYRNLRSF
TMNLRNKKNP ELRERILSKQILPAAFIKMTPNEMAPEALKKEIEKLHKQNLFD AQGATEKRAVTD R
FTCGKCKHKKVSYYQM QTRSADEPLTTFCTCENCNRWKFS

YGL103W_homolog 1301bp public: 1..688, PathoSeq: 689..1301; exon
1: 501..548, intron 1: 549..899, exon 2: 900..1298 (SEQ ID NO 349)
ACATTTATTGTTGGCTATAC TTTCCAGT TTTAAAGGAATGGTTAGGCGGGTCAGTCTACTTTATT
TTTACTGTAATGTGTTGTGCCAGTGTATGGTTTATCAAGACTAAAGTTCCCTGAGACAAAGGGTAAG
CATTCGTACCAGGAAGTCTGGAATTAACGGTAGTTACTTCCAGTATATATGGTGTTCATTGTGTT
TTGTGTCTAAAGTTGCGTTAGGGCTAAAGCCCTAATCAATAGTAGTGTACTTTGTTTGAAAAAAT
AATACATGCAAAATAC TGCATATTAGAATTATAAGGGAATGAAAATGAAAAAAGAAATAATTT
TG TAGATCGCATAGTGTGAGCGCGCACACACACAACTTTGTAGTGCTACAGTTTCTCTCTTC
CCATACACTCTCGCAGTCGCACGCTTGACAAAAGTTAATTAGAAATAGAAAAATTTCTCATTCTCTT
TTGAGTTTCCACCATAATCAACTAGTAATAACCAACAATGCCTACTAGATTAAC TAAACCAGAA
AACACAGAGTAATGTTTCTGGTATGTACAATTTCACTAAAGTTTAAACGGATGAAAGAGTATTGA
ATGTTCAAGGACATATGGAGATTTAGAGAAAACATGGAAAAC TAATCGAAAATGAATAATGAATGG
AAAATTTTAACTGAATATCAGAATAGACACAACACAGATCCAGAGTCATTATCACATTGA
TCATACAACCAAAGCAATGAATATGAGTAGTTTGGGAAACCACAACATACGAGTTATTTTTCAGAA
CAATCAAGTTTATCATTTACAGAAGACAGTTCCATCAATATGTCCAAAATACTCTTTGAAGTCAAT
TAAAGTCAAATGAACGAATTACTAACTTATTTTCTTTAGCCGGTAAGGGTAGAATTGGTAAAC
ACAGAAAGCACCCGGTGGTAGAGGTAAAGCTGGTGGTCAACATCATCACAGAACCAACTTGGATA
AATACCATCCAGGTTACTTCCGTAAAGTTGGTATGAGATACTCCACAAACAACAAACCCTTCT
GGAGACCAGAAATCAACTTGGACAAATTGTGGACTTTGGTTGATTCTGAAAAGAAAGACGAATACT
TGAGCAAATCATCTGCTTCTGCTGCTCCAGTCATCGACACCTTGGCTCACGGTTACGGTAAAGTTT
TGGGTAAAGGTAGATTACCAGAAGTTCCAGTCATTGTCAAAGCCAGATTGTGTTCTAAATTAGCTG
AAGAAAAATCAGAGCTGTTGGTGGTGTGTGCGAATTAGTTGCTTAA

YGL103W_homolog 149aa (SEQ ID NO 350)
MPTRLTKTRKHRGNVSAGKGRIGKHKRHPGGRGKAGGQHHHRTNLDKYHPGYFGKVGMRYPFHKQON
HFWRPEINLDKLWTLVDSEKKDEYLSKSSASAAPVIDTLAHGYGKVLGKGRLEPVPVIVKARFVSK
LAEEKIRAVGGVVELVA

YGL147C_homolog 423bp PathoSeq: 1..423; CDS: <1..420 (SEQ ID NO
351)
GCTATCAAAATCACTGTTCACAATGGTGACAGAAAACACGTTGCTGCTTTAAGAACTGTCAAATCT
TTGATTGCTAACTTGATCACTGGTGTCACTAAAGGTTACAAATACAAGATGAGATTGTTTATGCG
CATTTCCCAATTAACGTTAACATTATTA AAAAGATGGTCAAGATTACGTTGAAATTAGAAATTTCT
TTGGGTGAAAAAGAGTTAGAGAAGTTAAAATCCATGAAGGTGTCACCATGGAAATTTCTTCTACT
CAAAAGGATGAATTGATTGTTTCTGGTAACTCCTTGGAAGCTGTTTCTCAAATGCTGCTGATATT
CAACAAATCTGTCGTGTCAGAAACAAGGATATCCGTAAATTCTTGGATGGTATTTATGTTTCTGAA
AGAGGTACCATTGTTGAAGAAATCTAA

YGL147C_homolog 140aa (SEQ ID NO 352)
AIKITVHNGDRKHVAALRTVKSLIANLITGVTKGYKYMRFVYAHFPINVNIKKDGQDYVEIRNF
LGEKRVREVKIHEGVTMEISS TQKDELIVSGNSLEAVSQNAADIQQICRVNRNKDIRKFLDGIYVSE
RG TIVEEI

YGL213C_homolog 1655bp PathoSeq: 1..1655; CDS: 501..1652 (SEQ ID
NO 353)
GATGATCGCTAACAAGGTACCCGATTTATTCATCAACAAAGAAGCTACTTCATAGAATTGATTCTC
AACCTTAAATAGCTTGTAGTTT TATGATTGGGACTAATTGTGCAGCATCGAACAATATTGCCAGT

FIG. 2 - 24

TGCATAGAATAAATCGGTATTATTACGGCATACCAATCGATTGTAGGGGGTTGAAGCTGGTGCTAA
 TTCTGGGGTTGTTGCATTTCCAGTCCATAAACGTTGAAACACAAATTCGTGTGTAATTTGGTGAAT
 GAATTGATCAGATGATCCTATGGGTGGCATTGTTAAGGTTGTTTCGCTACGATGTATTTCTAGGATA
 ATGAAGGTAAAGTACGAACCTTATGAGTTTGTGATTTCCCTTCCTGATGTTTTTTTTCTTTGTTTCTT
 TTGTCTGTTGTAGCAAGAAGAAAAAAGTGTCTTCAAGTCTTGGACTCAATTTTCACCCCT
 CCACAACTCAATTTCAATTAATCAATAATCCAATATGGGTAAACAGTATATATCTACCGTCA
 GTGCATCTCAGGCTCATAAGCTGGATATTTCTTGGTGTAGCTATTACCAATAAGTTCACTGTATCCG
 TGTCTAGTGATGGATATGCGAAATTTTGGGACAACAAGCAAGACGAAGTTCATCTGCCTAAAGAAT
 TTGTCCAACCTGGTATTTATAGATAAAAAGCGGAATCCATGCGGTGGCTGC'TTACGAAAATGTTTTGC
 CAAGCTCTACATTGAAAGTGACATTATTAGCATTTGCATGTTTCAATGGATCTATCATCTTCAGAT
 ATTATATCAATGATGACTTTTCAACTATCGAAAGTTCAACTGATGATATAAAATCATTTGAAAGCA
 ATTGTTGGACCCCTGGCTTTTATCGCGATCCAGAATCCAAACAAGACTATTTTATTACAACCAAGA
 CCAATGGCACTACAGAGGTTCAATTTATGAAATATTGTTGATGAAAATGAGAAGGCTGTAATCACAT
 TTGAAAAGTTTGGGCAATTAAGGAACTCTTCTTCTTCCCAAATTCCTTTGGCTATATGTCCAA
 CAGAGAATAAAAAATGTGCTGTGGGTACATCAATGGTGATGTCTTGTATATGACTTTGTTAGCT
 TGAAATTGATATACACATTTTCGTTTCGAGTGATTTGGTGACCAGTAGAAATTCCTCAATCGACGCTA
 TACCTAGGGTGTGGCATTTCCTCCCTGGTGGAACCTTGTGGCTGTGGCAAGAGACAATCAAGCTG
 CTGGGTCAATTACATTATACGACGTTGAGCATGGTGAGAATGTGGGCTCTTTGGCCACCCCTCAC
 ACTCGGCCAAATCTGTTGTTGGTGGGTTTGCACATCAAGGCTGGATTTTGGGGTTGAGTTTGTATG
 AGGAAGGTAAGCACTTGGCTAGTTGTGGATTTGACAAATGCATAAGAGTCTGGAATTTAGAAACAA
 GCGAAAGGGAAGCAACAATTAGTATATCTATATCAGACTTAGATGATACTACACATAATGATCAAG
 ACGAGAGTGTCTGCTTCTGGTGTGCTTTTATTAAAAAGGGGGTTAGAGGTGGCTCTGGTGGTGACA
 GCAATGAAGGATTATGTGTCTGTGAGTTTCGATAGAGGAATAAGATGGTACCGAGAGGCAGGAGGAA
 TATAG

YGL213C_homolog 384aa (SEQ ID NO 354)

MGKQYISTVSASQAHKSDILGVAITNKFTVSVSSDGYAKFWDNKQDEVHSPKEFVQSVFIDKSGIH
 AVAAYENVLPSSLKVTLLAFACFNLSIIFRYYINDDFSTIESLTDDIKSFESNCWTFPGFYRDPES
 KDQYFITTKTNGTTEVHLLNIVDENEKAVITFEKFGQLKGNSSSPNSLAICPTENKKCAVGYING
 DVLLYDFVSLKLIYTFRRSSDLVTSRNSQSTSIPRVLAFFSPGGTLLAVARDNQAGSITLYDVEHGE
 NVGSLATPSHSAKSVVGGFAHQGWILGLSFDEEGKHLASCGFDKCIKRVWNLETSEREATISISISD
 LDDTTTHNDQDESVASGVAFIKKGVRRGSGGDSNEGLCVVSFDRGIRWYREAGGI

YGR085C_YPR102C_homolog 1418bp public: 1..1418; exon 1: 501..503,
 intron 1: 504..896, exon 2: 897..1415 (SEQ ID NO 355)

ATAGAGATGCTTATCTGGTGGTTCAGTTAATTTATATCATGTCACTGAACAAGGTTGGACTTATC
 ATGGTAATTTCAATGTTGGTGATCTCTTTTGGGAAGTTAAAGAAAAGGAACAATCATTTGTAAATG
 TAGATGGATAAAGTAAGTTGATTGTATAAAAAAGAAATGGATTTCATTAATATAAAATTTACAAATCT
 GATAATAAACTACAGTAACCTATTATGCAACAATTGAAAGTATCCTGTGTACGCTGATTAGGGCTCA
 AAAGCCCTAACAGGTTGCACGTGATGTTGATTTATTTATCCCTGCACACATTGAGTTTTTTTTCTA
 TGGTGAAAATTTATAGTGAGACGATGTTGTTTCGATTTTACCACACACTCTCACACTGAGTGTAGT
 CATACTAACAATCTTCTCACACTATACACAAAAAATCTTTTCGTTTGAAAAGTTTTGAAAGGTTT
 GTTTTCTCAATAGTATATCCATACAATAACTGCCAAAGATGGTATGTTCAAGTGTTTAAAGAGATC
 GAAATGTTTTGTTTTAATTGGAAGTGATATCATAATGAGAAAATATGGGAAATAGAGATAGGACCG
 AATTAATTGAAAGAGTTTTCTTTTGGGGAAATGGGTTCAATAAGATTTTTTCAAGATTGGAATCAAA
 TTATGTCAGATGTGAAGAAGAGTAAATATAACAAGAAGTTCAAATCATTAATAATTTTATGTAAAT
 ACAACGATTATCAATTACAGTCAACGAATAGAATAAAACAAAAGCCAGCATATAACAGATACCAGT
 GATTCATCCCAGTGATATAAATAATGATATTCAATTAAAAACAATATTAAGACATTTTTTATTTAT
 GTATCAACAAAATACTAATCTATCTTTCTTTAATTAGTCTGACAAATCCCAAATGTTATGCGTG
 AATTACGTATTGAAAATTAGTTTTAAACATTTGTGTTGGTGAAATCCGGTGATAGATTAACCAGAG
 CCGCCAAAGTTTTAGAACAAATTATCTGGTCAAACCCCAAGTTCAATCTAAAGCTAGATACACTGTCA
 GAACCTTCGGTATTAGAAGAAATGAAAAAATGCCGTCCACGTTACTGTGAGAGGTCCAAAAGCTG
 AAGAAATCTTGGAAGAGGTTTTGAAAGTTAAAGAATATCAATTAAGATCTAAAACTTCTCTGCTA
 CCGGTAACCTTTGGTTTCGGTATTGATGAACATATTGATTTAGGTATCAAATATGATCCATCTATTG

FIG. 2 - 25

GTATTTACGGTATGGATTTCTACGTTGTTATGGGTAGAGCCGGTGCTAGAGTCACCAGAAGAAAAGA
GAGCTAGATCCACTATTGGTAACCTCTCACAAAACCAACAAAGAAGATACCATCCAATGGTTCAAGA
CCAGATACGATGCTGAAGTTTGGATAAATAA

YGR085C_YPR102C_homolog 174aa (SEQ ID NO 356)

MSDKSQNMRELRIEKLVLNICVGESGDRLTAAKVLEQLSGQTPVQSKARYTVRTFGIRRNEKIA
VHVTVRGPKAEELERGLKVKEYQLRSKNFSATGNFGFGIDEHIDLGIKYDPSIGIYGMDFYVVMG
RAGARVTRRRKRARSTIGNSHKTNKEDTIQWFKTRYDAEVLDK

YGR118W_YPR132W_homolog 919bp PathoSeq: 1..919; CDS: 482..916 (SEQ ID NO 357)

TATTGCGTAATCGTTATCAATGTTTGGATTGTTGCAACGCTGGGTTGTGTGTATATGCGAGAAATG
AGTAATTGTTTAAAAATAATCGATGCAGCAGTCTGCCACTAAATAAAATGTCATATTGACAT
GATAAGGATTTATCAATACTGTTAGGTCTATAGCCCTAACTTTAATCATTACACGTGATACAAA
AAGTTGTTTGATCCCGCAGCTATGAGTACGCACTCACTAATTATAGCCTGAAAAAAAAAATTTTC
CACATAGTAAGGGGATTTTGTATGGTGGTGCCTCGCTAAGACGCTGCATACATTTTCTAAAGT
CACACTGATATAGGGATGTTGTGGTAGTGATTGTGTGTTCCACCAAATAACTTTGCGGACACTCT
CATATACTCAATTTTTCCTTACAAAAATTTTCTTCTACTTTTTCAGAAATTCTTCTTTTA
CAATTCAACAACATCAATCATGGGTAAAGGTAAACCAAGAGGGCTTAACCTCTGCTAGAAAATTAAG
AGTTCACAGAAGAAACAACAGATGGGCTGATCAAGCTTATAAAGCTAGATTATTAGGTACCGCTTT
CAAATCTTCTCCATTTGGTGGTTCATCTCAGCCAAAGGTATCGTTTGGAAAAAATTTGGTATTGA
ATCTAAACAACCAAACTCTGCTATCAGAAAATGTSTCAGACTCCAATTAATCAAAAACGGTAAGAA
AGTCAGTGCTTTTCGTTCCAAACGATGGTTGTTTGAAGTTTGTGACGAAAATGACGAAGTCTTGT
GGCTGGTTTCGGTAGAAGAGGTAAAGCTAAGGGGGATATTCCAGGGGTTAGATTCAAGGTTGTAA
AGTTTCCGGTGTCTCTTTATTAGCTTTATGGAAGAAAAGAAAAGAAAAGCCAAGATCATAG

YGR118W_YPR132W_homolog 145aa (SEQ ID NO 358)

MGKGKPRGLNSARKLRVHRRNNRWADQAYKARLLGTAFKSSPFGSSSHAKGIVLEKIGIESKQPN
AIRKCVRVQLIKNGKKVTAFPNDGCLNFVDENDEVLLAGFGRGKAKGDIPGVRFKVVKVSGVSL
LALWKEKKEKPRS

YGR277C_homolog 1164bp PathoSeq: 1..724, public: 724..1164; CDS: 196..1161 (SEQ ID NO 359)

AATTCATTTGATCTCTAAGAAGATGAACAGGCCTTGAATGGGAGGGGTTGGTTCGACTTCCACGAA
ATGTGGTTGGAAAAACTTGAGTCCCTCAAAAAGGTTCTCTCGTAAAAGGCCAGAGAAAAAACC
ACCAAACCCCCACCACCAACCTAACCTTTTCCTTCCATCCATTCCTCTTTCCTTACTTTGCAAATG
TTGAATCCAGTTATATTCAATTAAGATCCTATAAAATACGATTATTCACAATTTATTATATCTTTA
CTCCCGAAATTCATTAATTGTAATCGTATTGATTTAGTTATACTTTGTCAAATCACCGAATCAAT
CAATTGAATGAAATTTATGTTTTTATTATCAATTAATTCGTAATCATAAGAATAATGGAGATACT
GATGGAGATACCGACAGTTTGCCTATGTTTGATTATCGATTTGAAATTAATATATTATTTAATTTA
TCAACAAAAAATTTGAATCAATTATGTTTAAATAATTGGAATCATGGATATATTGCGGAAGGTGAT
AATGATAACAGTACTAATTTGTCATCTTTGCCATTGTCAATAACACAAATATCAACATTGAAATTT
CCAACAATCCAATCAAGAGCAAATAGTAGTAGTGCTTATAATGATGAGGATGATAAAATTAATCT
AGTCGGCAATATCAACAATTTAAAACCTACTGCTGTAGGTGGAACATTTGATCATTTACATGATGGT
CATAAAATTTTATTATCAATGGCAATTTTTTTAACTTCAAATAAATTAATTATTGGTATAACTGGT
TCTAATTTATTAATTAATAAAAAATTTAAATCTCAATTACAACTTTTAATCAAAGACAAAATTTA
GTTATTCAATTCATAAATTTATTATTATTGAGTGAAACAGTGTTATTTTTTTTGAATTTTATGAA
ATTAATGATGTTTGTGGTCCAACCTGGTTATATTAATGATATTGATAAATTTAATAATATCTCAAGAA
ACTAAATCTGGTGGTGAATTTGTTAACAAATTTTCGTAAAGATCATGGATTTAAATTATTAGATATT
ACAATAATTAAGTGATTGGTGGGAATATTGAAGAAAATTCATGGAAAGGTAAATTAAGTTCAA
CTGATATTAGAGAACAAGAATATAATCGATTATTAAATCAATAA

FIG. 2 - 26

YGR277C_homolog 322aa (SEQ ID NO 360)

MLNPVIFIKDPIKYDYSQFIISLLPKFINCNRIDLVILCQITESNQLNEILCFYYQLIRNHKNNGD
TDGDTDSLPMFDYRFEINILFNLSTKKLNQLCLNNWNHGYIAEGDNDNSTNLSSLPLSITQISNIE
IPTIQSRANSSSAYNDEDDKITTSRQYQQFKTTAVGGTFDHLHDGHKILLSMAIFLTSNKLIIGIT
GSNLLINKKFKSQLQTFNQRLVLIQFINLLLLSETSVIFFEIEINDVCGPTGYINDIDNLIISQ
ETKSGGEFVNKFRKDHGFKLLDITIIVIGGNIEENSWKGLSSTDIREQEYNRLNQ

YGR284C_homolog 1427bp public: 1..1427; CDS: 501..1424 (SEQ ID NO 361)

CAAGAGTAAAATCTAAATCGTTCCAATGATTTTTGGACAGCTCATAGGTTAAGAGGTCTACATGTGT
TGGTGGCAGTAGTATTGGTATTAAAGTGGGTGGGTGCTGATTGTACTGCTGTTCACTTTATTGTTT
GGTTGTGATTTTTTTTTTCCACTGGTGGTGGTGGTGTGATTGTACTGCTGTTCACTTTATTGTTT
CGTTTCGTTTTTCTTTTGTGTTGTTGACGTTGACATTTTTTTTGCTGTTGTTGTATGCGGAATT
TTTGTATTAGTTGTTCTTTTTTGTGTTTTTTTTTACTTGTTCAAAGTTTCATATAATAATAATTCT
TGTTTTTCATATTTTTTTTTTTCAGAACAAAGAACAAATACAACCTATATAATTTGATCTTACTCTTAT
CCCCAGGTTTTTCTATTTGTTTTTGGGTTTGCCATTCATATATATATATCTATTATTCAAATCAAT
TTGAGGAGTATCATTAATTTAAATTATATCAGTTAACAATGTCGTATCGTGGTCCTAATCAATTTG
GTAATCAACCTCCACATCATGGAATACCTTCTCAACCTCAACCACATATTGGTCCAATATCTTCCA
GCAAAAGTCCCTTTAGAACAATTTGAAGATGTTGCTAAAAAGTTGAAGATTGGATCGATGATTATT
TTAAAGTCTTGAAACCATACGTCCAGCAATTGGTAGAGCATTTTTTGGTGGCCACTTTCTATGAGG
ATACTTTAAGAATCTTCACTCAATGGAATGAACAAGTTTATTACTTGCACAACCTATAGACACTATT
GGCGTTGGTTGACCGTTTTATTCTTGATCAATAATATGGTGGTTATGACAGTTGCATCCACTTTAG
TAATTGCCAGAAAAAGAATAACATTTGCTACTATTGCATTGATCGTTGTTGTTATTATACAAGGTA
TTGGGTATGGTTTATTGTTTGATGCTCAATTTGTTTTGAGAACTTGTCCGTTGTTGGAGGGTTAG
TATTAGCATTTTCCGATAGTATTGTTAGAGATAAAAGATCCTTAAACATGCCAGGTTTACCGATGT
TGAACAATCAAGACAACAAAAAGTATTTCCCTTTTAGCTGGTAGAATTTTGTAGTATTATTATTTT
TGGGATTGCTCTTTTCTTCTGATTGGTCATTGGGTAGAGTTTTTCAATTATATAATCGGGTTAACTT
CTTGTGCTTCAATTGTTGTTGGTTACAAGACAAAGTTTTTCACTGCTATCATGCTTATTGTTTTAT
TCTTATACAATGTGTTCACTAACCAATTCTGGGCTTATGCATCTCAAGATGCTAGACGTGACTTTT
TGAGATATGAATCTTCCAAGTTTTGTCAATTGTGGGAGGATTATTGTTAGTGGTTAATGCAGGTG
CTGGTGAATTCTCCATCGATGAAAAGAAAAAGATTTATTA

YGR284C_homolog 308aa (SEQ ID NO 362)

MSYRGPNQFGNQPPHGHIPSQPPHIGPISSSKSPLEQFEDVAKKVEDWIDDYFKVLKPYVPAIGR
AFLVATFYEDTLRIFTQWNEQVYVYLNHYRHYRWLTVLFLINNMVMTVASTLVIARKKNNIATIA
LIVVVIIQIGIGYGLLFDAQFVLRNLSVVGGLVLAFSDSIVRDKRSLNMPGLPMLNNQDNKKYFLLA
GRILLVLLFLGFVFSSDWLGRVFIIIIIGLTSCASIVVGYKTKFSAAIMLIVLFLYNVFTNQFWAY
ASQDARRDFLRYEFFQVLSIVGGLLLVNAGAGEFSIDEKKKIY

YGR285C_homolog 1876bp PathoSeq: 1..1215, public: 1216..1876; CDS: 501..1781 (SEQ ID NO 363)

AATTATTAGTTGAAAAACAAATCATACCTATTGCCAGAGCTCAAATGAAAGTGAGAATTACGTTAT
CTAAAAAAGCATACTTAAAGACTTTTCAAGATGAAATAAAACCTGTTATTGATCAAATTGTGGAGG
AAGATAACAATGGGAAACAATATGAGATTGTTGGGATTATAGATCCTATAAATTATAGAGCTTTGG
TCACATTAATTGAAATACAGATGGAAGCAACAAAGTCGCTAAAGGAGAAGGGTCTATAGAAGTAT
TAGATATGTCTGCCATAAAAGAATAAAACTAAACTAGACAAGTGTATAGAATCTTTTTTATTAATA
GATGCTTATCTTAGTTATGTTCCAGAACAATTCATGTTAGGAGAGAGAGAAACGCAATCACTCAAT
TTTTGCACAAACAAAAACGAGAAGATGAAGAAGCAAAAAAGAAAATTTTTTTTTTCTCAACCATCT
TAAATCCTCCTACAATTAATTTCAATACCAATAAAGAACATGCTTATTGTATTACCATCAGGAACCTA
CTGACGGATTTAAAGCCGCTCTCCAAATACTCTGCCCCAGTGCCTCGTCCAATTGAACCAAGTTGGTC
GTTACTTCTTAGCCACGCCTCAAGAACCTTGGCTGGACACACTTGGTCTGAATTTGAAAAATTGG
AAGCTGAAAAGAATGTTAAACAAATCGAAGTCAACGAAGATGAGGATTTGGGAGATGAAGAACAAA
GTGAAGAGTTATTAGAACACGATCCAAGAGATGGAAGACTGCCAATTTATATGCTGTTTTAGGTT
TATCTCATTTGAGAAGTAAAGCCACTGAAGATCAAATCAGAAGAGCCACAGAAAACAAGTTTTGA

FIG. 2 - 27

AACATCATCCAGATAAAAAATCCGCTAGTGGTGGATTAGAAAACGATGGATTTTTCAAAAATTATTC
AAAAAGCCTTTTGAAGTTATGTTGGACCCAGTCAAGAGAAGACAATACGATTCTATTGATGTTGAAA
ATGATCCAAAACCACCAGCTCCAAAATCCAAATACGATTTCTTTGAAGCTTGGGGTCCAGTATTTG
AAAGTGAAGCAAGATTTTCTACTAAACAACCAAGTTCCATTGTTGGGAAATTTAGAAAGCACCAAAG
AAGAAGTTGATGCTTTCTACAGTTTCTGGGGAAGATTTGACTCTTGAAGACTTTTGAATTCAAAG
ATGAAGATGTTCCAGATGACACTGCCAACAGAGATCACAACGTTATATTGAACGTAAGAATATTG
CCCAACAGAAAGAAATTGAAGCAAGAAGATCACAAGAGATTATCGAATTGGTTCGAAAGAGCTCATG
CTGAAGATCCAAGAATTAAATTGTTCAAAGAAAAAGCCAAGAAAGAAAAAGGCTGCTAAGAAATGGG
AAAAAGAATCTGGATCAAGAAAAGCTGCTGAAGAGGCTGCTGCCAAAAAGGCTGCTGAAGAGGCCG
CTGCTAAGAAAGCCGCCGAAGAAGCCGCCGCTTTGAAAGCCAACCTCTAAAAAAGCTAAAGAAGCTG
CTAAGCTGCTAAAAAGAAAAACAAGAGAAACATCAGAGCTGCTGTTAAGACAAATAATTACTTTG
GTGACTCAGCTAAATCTGCCGACATTGATGCTGATGCTGATTTGTTAATCGAAAAATTCGACGATG
TCAAATTAGGTGAAGTTGCTGATAAAGTTAAAGATGCTGATGCTGCTTCAGTGAATCTACTTTTG
TTGAAGTTGCAAAGGAATTGGTTGGAGCTGGTTCTTTAGATGCTTCCTATTTGAAATATTTTAACT
AGATTTTTTTTTTTGTAGGAAAATAATATATATAGAATGTAACTATCAAAAACAATTATACAGAAG
CTGAACCTCAAACAAGACTAAACAGCAAG

YGR285C_homolog 427aa (SEQ ID NO 364)

MSIVLPSGTTDGFKAISKYSAPVRRPIEPVGRYFLAHASRTLGRHTWSEFEKLEAEKNVKQIEVNE
DEDLGDEEQSEELLEHPREWKTANLYAVLGLSHLRSKATEDQIRRAHRKQVLKHPDKKSASGGL
ENDGFFKIIQKAFEVMLDPVKRRQYDSIDVENDPKPPAPKSKYDFFEAWGPVFESEARFSTKQPV
LLGNLESTKEEVDAFYSFWGRFDSWKTFFEKDEDVDDTANPDHKRYIERKNIAOQKEIEARRSQE
IIEIVERAHAEDPRIKLFKEKAKKEKAARKWEKESGSRKAAEEAAKKAEEAAKKAEEAAALK
ANSKKAKEAAKAAKKKNRNIRAAVKDNNYFGDSAKSADIDADVDLLIEKFDVVKLGEVADKVKDA
DAASVKSTFVEVAKELVGAGSLDASYLYKYN

YHR021C_homolog 1178bp public: 1..537/917..1178, PathoSeq:

538..916; exon 1: 501..503, intron 1: 504..932, exon 2: 933..1175
(SEQ ID NO 365)

TTTCATTTGTAGGCATTGTGTAGAATGTGGACTGTAGGAAGGTGCAAAATATATATCCAATAAGTC
ACATCTCAAATTGGTAGTAGAAGAATTCAACCTTGGGACAGTATTCTCTGCTTAAATGAGTTTAC
TGATCAAATAAAATATTGGCTCAACCATTGAAAAGCTATTCTTGACACTTTTTCAGTTTTAGTTT
TGGTTGTTTCACAATTGAAAAAAAATGTTGAGCCCTAATAGCCCTAATGTTTGCACGTGATGT
ATTGCTTTGAGTGAAAAGTGACATTTGTACACACACAAACAAAAAACTAAGTTCTTCCCCCA
ATATGCTGCGTATAGTGAGAAATCTTCTTCTCTTGGCATACTATCGCATTTTTTTTTTTGGTAA
CTCAGGAAACCTAATTGGAAAGAAGAAAAGAGAAAAAAAATTTTCAGTTTCAATAGATTTTC
AGTTTTTTGAATTATACATATTAGAGAAACAAGTTAACAATGGTATGTTTATAGATTTACCATGAG
TTATGGAGGGATATTCCTGGATGATCAGAATATCATAATATAGGAGTATACTATTTTACTGGAATC
AAGATATAATTGAATTGAAATAAAATTTGAATAAGAGGAAGCATAGAATACGGAATGATGATTAAC
AAATCAGAAAACATTGTACTACCGAATAATGAATTAGGATCAACATATTAATATCAACTACTACTT
TAAAAGAACAGGAAAATGAGAAGAGAATCAGCATGAAAGTTACCACCTCAGAAAACGTCAAAGAAA
TATACTTTTGGTGTGGATCCATGTGTTATTACTGAAATCATCGAAACGAATATAACCCCTCCTTTTC
CCACATTGACATAACTCAGACACAATCTTTCAAATAAAACATGTAATACTAATACTATTATTTTTTTT
TCGTATAGGTTTGTAGTTCAAGATTTATTACATCCATCTCCAGCCACTGAAGCTAAACAACACAAAT
TGAAAACCTTTAGTTCAACAACCAAGATCTTTCTTTATGGACGTTAAATGTCAAGGATGCTTTAATA
TCACCACTGTTTTTCAGTCACGCTCAAAGTGTGCTGCTGACTGCTGTTCTACTGTTTTGTGTA
CCCCAACTGGTGGTAAAGCTAAATTGACTGAAGGTTGTTTATTTCAGAAAGAAAGTAA

YHR021C_homolog 82aa (SEQ ID NO 366)

MVLVQDLLHPSPAEAKQHKLKTLLVQQPRSFMDVKCQGLNITTVFSHAQTAVTCDSCSTVLCTP
TGGKAKLTEGCSFRK

YHR141C_YNL162W_homolog 1179bp PathoSeq: 1..1179; exon 1:
501..503, intron 1: 504..861, exon 2: 862..1176 (SEQ ID NO 367)
TTTATATTGTTTTTTGTTTCTATGTATAGTAATTATTTAATTTGATGTTCCATTATTCATGTAATT
GTGATGTATTTTTTTTGTGGTCCTTCTTTGTGTTTGGATATTTTGCAGCTGGTCGGATCATACAA
ATTTGGAAGGAGCTACCAAAGCAGAAATGATAGCAAAAAAAAAACAGGAGACTTTTGGAATTTCTTG
GTTTAGGGCTCTAGCCCTAATGCCTGTATATAATTGATTGATGCTTTAAAATTTGTGCGGTGAAAA
ACAGAAGCGAAAAAAAAAGAGCTGGAAGTGTGATTAACAACAACGAGGGAAGAAAAAAAAACTTAA
TTAGGTGAACAAAATTAATGTGTGAGCGTGTACATGCACAATTTTCAATTGGTTATTCTCACGCA
CTAACAACTCAACCTCCATTGTGAGAAAAGAGATTTTTCTTTGAAAAAAAAATTTACATACATATC
TTAGTTCACTAGTAACTTTCCAAGACAACATAGACAAGATGGGTATGTTCCAGTAGCAATATTC
AACAAAGAGATACAAGATATTTCTCCAATACAAAGAGATTAATGGTGTGTTTTGTATAGAGTGAAG
CCATGTGTTTTAATAAGAATGATTTGTCAAGGGATAAGATGAAAAGTGGAAATTGTCCAAACAACAT
TGAAACGAATTTTCTGGGATAGCGTTCAAACAATCAAACCTATCCAGGTTTCTTATGACAATTAAG
AAAACAAGTCAATATTATCAAAGATGGAGTTTTATAAGGAGAGATATTGAAACATCAAATTTGTGA
AAGAAATAGCCAACATTTGGCACCATTTCCTGTGATCATAGAAATACTAACAATCCTCTGTGTGT
ATAGTTAACGTTCCAAAACTAGAAAAGACCTACTGTAAAGGTAAAGAATGCCGTAAACATACCCAA
CACAAAGTTACCCAATACAAAGCTGGTAAAGCTTCTTTGTTGCTCAAGGTAAAGAAGATATGAC
AGAAAACAATCCGTTATGGTGGTCAAACCAACAATTTTCCACAAGAAAGCCAAGCATACCAA
AAAGTTGTTTTGAGATTGGAATGTGTCTGTGTAACCAAGGCTCAATTACCATTGAAAAGATGT
AAACATTTTCGAATTGGGTGGTGACAAAAACAAAAGGTCAAGCTTTACAATTTTAA

YHR141C_YNL162W_homolog 106aa (SEQ ID NO 368)
MVNVPKTRKTYCKGKECRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGYGGQTKQIFHKKAKTTK
KVVLRLCEVVCCKTKAQLPLKRCKHFELGGDKKQKGQALQF

YIL112W_homolog 3583bp PathoSeq: 1..3583; CDS: 365..3580 (SEQ ID
NO 369)
GTGCGAATAATACAAGCGATCGTTTGAATAATCCAATGATTAGCTCTGATCAACGAATTCAAAATT
TTCCCTCAAGGACGTAGTACAACAAGAGATGAGAAGGGGTTTGAACGTGTTTGATTTTCAGAGGAGA
TGACGGTGCAAAAGATCTACCACCAAGAAGCACATAATTTTTGAATGATTCACGAAAGAGTTT
CATTAGTGATATCTCAAGCCAAAAATTTTCAAGGGAAAGTTCCCGTAATGTTTCACGGGAAAGCAG
CAGGCGAAGTTCAATAATAAAAAATTGATCATCATACTAATGTGGACGTGTCAACGAAACCGGAAAA
TATAAATAGCAGAGATAACAAAACCTGAGAAGAATATGACTTTGAGTTCAGAGTCAACCAAAACCGAG
TGTCGAAGAAGTTAGTAAATCTTTGAAACCAACAATTACCAAGAAAACCTTCATTCACTGATTACTT
AAAATCTGCCAAAACCTAAGGCTAAAGAAGAAAAGGTAACAATCGAAAAAGTGACAAAACGATTAA
TTCAGAAGAACGAAAAACGGAACCAATTCACAAAGCGAGCAACTTTTAACGGACAAAAAGGATAA
TAAACTGGAACCCAATAGTGAAGTAAATTTGAAAGACAATAATGACGACCTGAAAGCTACAGCTGG
CTGTGCCCTAGGACCTGATAAGAATACTGGAAAAACGATTTCAGATAAATCAGAAACGACTCAACC
AAAACCTGCCCGCTCAGAATCATTTGCCGATACATCATTATTGTCTCCAGTTAATGAAAGTGATAC
TGATTTCAATTTCAATGAGTTAGCAGAGATACCGGAAGCAAAGGATGGTTTCAGTTGTGGCAGCAA
TGTGCTGGAGAACATTGATGAGAATGAAAAATTTTCAGAAGCTGAAACTGTTATAGCAGATGACCT
TCCACGTCTCGATGAAGGAAAGAACTTTTACGTGAACAAACAGCAGATGTAAAGAGACATAAATT
GAAGAAAACAAAATTGAATACTATTTTAGTTCCGATGAAGAGGAGGAGGAGATTCAAGAACCAGA
TTTCAAACCTCCAAGAACCAGAAAACTACCAGAAGATGACCAACATCCTGATTTTCAAATTCAAA
AGCAACAACAGAAATCAGTAACGATAAAAACAGAAGTAAATAAGCCAGAAGTGAAGAGGTTGGCGA
GAAAGAGAGAAATCACCAACTAGAAGATAGATTACCAATTAAGAAAGAGAAAATGCGGTCGGAGAA
TGCAAGAGACATCTGAAACGGTGTGAGTTCAAATCAGAATCTAAGATTTCAAAGTCGAAGAACT
ACCTTACAAAGTTAAACGTGATTCAAGTGGTCGATCATTATTACAACGAGCTTGCAAGAAGGGTAA
TTTTGCAGATGTCCAAGATTACATAGAGAGGGGTGCTAGTGCCAATGAAAAGGATTTCTGTGGATT
CACATGCTTGATGAGGCAGCATTGGAAGGTACATACAAAATTTGTGAAATATCTCATCGAAAATGG
TGCTAATGTAAATGCGAAAGCTGATGAAGCTGGTGATTCCGAGACACCATTGATCGATGACGCTGA
AAACAAACATCTTGATTGTGTTAAAGTGTACTAGAAAATGATGCTGATCCTACTATTTTCAATAT
TGATGGATTACCGCTTTAACTAAGATTTATAATGAACATGAAGGAGAAGAAGGATATGATGAAAT
TATTCAAGTTCTAGAAGAAGCAACTGCAAACTATAACAGTCGTTTACCAAGAGAAGTTCAGTTTGT

FIG. 2 - 29

ATCAGATGCTCCTATTGGTAGTGGACCAATCATGGAGGATCCAAATGACAACATATTTTGCAGAGCT
AATTAAGGTAAGGGAATATATAAATACGCTGCAGAGAATTCAAAAGAGAAAACAGCAGAATATTT
TGTTGCTGGTCATAATTTAGAAGGAAAACAGATATTTTAATTTTAGCTGCTAGAAACGGCCACAC
AGAACTTGTTGATATTATACTAGGGCTAAACCCTACACCTTTTAATATTGATACCGAGTCAAGTTG
TGGTGTTACTGCATTATTGGCCAGTATTGGACGCGGTCAATTTGAAGTTGTCGATTCTTGTGTGTC
CAAAGGTGCTGATCCATTCAAGACAAGAAAAAAGATGGGTGAATGCTTTAGAAATTGCACAACA
CTCGCCACATTTTGATTACGCGGAAGTTAGTGTAAATGAAATTCATGGAGAAGAAGAGTGGAAAC
CAAAATTTTGTCTGGTATTCGGTCAAGGGTAGTATCTCGTGCAACATCTCGTGACCTTCTGTTCC
CGTATCATCAGACGAAGATGACGTAGTGAAGAAAAAGAAATTACAGCACACACAGAAAATAAAAG
TGCTGAAAAGAAAGCTGGAGGATAAAATCACGAAAACAGTTAATGAGCATGTGAGCAATCGGAAACC
CCACGAGTCTACAGGTCGAAAACCTTGAAAAGACTCATAGCAATGAGGAAAGAAAGCGGAAACGTGA
ATGGTCAGACGATGAACCTAAAGAACCACATCTTTTGAAGAAGTCAAAGTCTGATTTGAAATTGAA
ATCACTACATAGAGAATTCACCTTCTGATGATCACCACACCAGTGAAAGCCATTGAGATTCTTTTGC
AGAAAAAGAAAACATTTATCGGCAACGCCACCTGCTCCTCCGCCACCACCACCACCACCTTC
TCAAGCAGTTATCAAGGCACAAGAAGAACAAAAATCAAAGATGCTGAAGAAGCTAGATTGTGGCA
AGAAAAGGTGGAAGCTAAAAAGAGGGCTCGAAGAGAAATGTTTTTAAAGTCCGAGAAAAGAGAAAAG
GCAGAAAACGGAAGAAAGAAAGAAATTGCGAGCACAAAGAAAGAAAACGAATTGCCAAAGCAAAACA
GGAAGAACAGGAGAGACTTGCTAGAGAAGCAGAAGAGAAATCGAAAGAACTAGAAGAAAAGAAAGT
GGGGTTGCGACAACAGTTGACATTAGATCATTATCCGGTTGGATTGCGTTATTGCAAGTTTGATGG
AAACCCAAATATCTCGGCTGTTGATAAATTTTGCCTTTCTATGTATTTGTAATCGACGATAAAAA
GTATGCTGTTGATTTGCAAGTCTCCTTGATCAGTCAACGGTTGTCAGCAAGGTTATCAATACTGT
ACAACCTCATCAGAAGAGAGAAATAAATGCAACTGAAAAAGCAAATTGTGGAAGCTCTTTTCAA
GTTTATTGGTATTGATCCTAGGAATCCAAATTGTGATCAAAGAAAGCTCAATAACAAATGGTCAAAA
ACAGTTTCAAATTTGTTGCTTCATTTTGTGGAGGTAGATTTAGCTGAAGAATTTTAAAGGAATT
TCCAGAAGTACACTCAAAGCAAAGATAACCAAATTGATGTTAGTTTAGAGTCTTTGAGTGGGTT
TTCTGATGCGTCAAGGATGATATAATAGTTGATGGAAATCTTGAAATTGATATTGATTCCAAGAA
AATCGAAAAGTTTATTCCTCCTCATTTGAATACTAGGAAAAGACATTATTAGGACTGTGAGTACTTT
AGCACACCCACTATGGTGA

YIL112W_homolog 1072aa (SEQ ID NO 370)

MTLSSESTKPSVEEVSKSLKPTITKKTSTFDYLSAKTKAKEEKVTIEKSDKTINSEERKTEPIQQ
SEQLLTDKKDNKSEPNSEVNLKDNNDSDKATAGCALGPDKNKGKNDSDKSETTQPKLARSESFADT
SLLSPVNESDITDFNFNELAEIPEAKDGSVVAANVSENIDENENISEAETVIADDLPRLEGGKLLR
EQTADVVRKHLKKTCLNTIFSSDEEEEEIEPDKLQEPKLPEDDQHPDFQNSKATTEISNDKTE
VNKPEVKEVGEKERNHQLEDRLPIKKEKMRSENAKTSSENGVSSKSESKI SKSKLPYKVKRDSGR
SLLQRAKCKGNFADVQDYIERGASANEKDFCGFTCLHEAALEGHTQIVKYLIENGANVNAKADEAG
DSETPLIDAAENKHLDCVKVLLENDADPTIFNIDGFTALTKIYNEHEGEEGYDEIIQVLEEATANY
NSRLPREVQFVSDAPIGSGPIMEDPNDNYFAELIKGKGIYKYAAENSKEKTAEYFVAGHNLEKPD
ILILAARNGHTELVDIILGLNPTPFNIDTESSCGVTALLASIGRGHFEVVDLSLSKGADPFKTRKK
DGLNALEIAQHSPhFDSREVSVMKFMKKSGTKILSGIPSRVVSRAVSVPVSSDEDDVVEE
KEITAHTENKSAEKKSEDKITKTVNEHVSNRKPHESTGRKLEKTHSNEERKRKREWSDDPEKPHL
LKKSksDLKLKSLHREFTSDDHHTSESHSDSFAEKRKHLSATPPAPPPPPPPPPPSQAVIKAQEEQK
IKDAEEARLWQEKVEAKKRARREMFLLKSEKEKEQKRKEEELRAQEEKRIAKAQEEQERLAREAE
EKSKELEEKKVGLRQQLTLDHYPVGLRYCKFDGNPNISAVDKFLPFYVVIDDKKYAVDLQVSLIT
STVVSKVINTVQPHQKREINATEKSKLWKLFFKFIGIDPRNPNCQDRSSITNGQKQFQNLHLHFE
VDLAEFLKEFPEVHSAKDNQIDVLSLSGFSDCVKDDIIVDGNLEIDIDSKKIEKFI PPHLNT
RKDIIRTVSTLAHPLW

YIL148W_YKR094C_homolog 659bp PathoSeq: 1..659; CDS: 501..656 (SEQ ID NO 371)

TAGTTTCTTTTGGCGGTATATCCTCACTCATGATTGATGTATTTGCCCACTAAAAAGAAAACCAAT
GAAACAATAAGATTGATTGATAGATTGGTTGTAATTAATCTGATGCTTTCAACATTGTTTTTGT
TCGTGTCTCGGTCAATTGAGGTTGGGTAAATGTTTTCTTTTGAAGAATTGTGAGCATGCAATGTGCG
CATGCAAAATATGATGTCGCTCAATTGCGACATACTACTTAGGGCTATAGACCTATTGCACGTGCGT

FIG. 2 - 30

TAGTTTTAAACCTAAAAAACAATTTTGTGCAGTCGTGCACCATTCGTTCTATTTTTCTACTGTGA
TTGACGTACAAACCTTCACAGTTCACGCACACTTTTGTGCGATTCTCAAACCTCTCTCACAGGCTTG
GTAGGAATGAAAAAATTTTGGTAAAGGCGAAAAAATAAAGTAACTTGAATATTTTGGGAATC
CCCTTTTTGATTACTACAATAGATTAAAGTAACTAAAGATGATTGAACCATCCTTGAAAGCTTTAG
CTTCAAATACAACGTGAAAAATCCATTTGTGCGTAAATGTTACGCTAGATTGCCACCAAGAGCCA
CCAACGTGTCGTAAGAGAAAGTGTGGTCACACCAATCAATTGAGACCAAAGAAGAAATTGAAGTAG

YIL148W_YKR094C_homolog 52aa (SEQ ID NO 372)

MIEPSLKALASKYNCEKSICRKCYARLPPRATNCRKRKCGHTNQLRPKKKLK

YIL150C_homolog 2297bp PathoSeq: 1..1162, public: 1163..2297; CDS:
501..2294 (SEQ ID NO 373)

ACTCAGCCTTTTGAATTCACTTTTGGTAAAAGGATATGTAATTGAATCCGCATAATGGACTTTCT
CTAACTCCATATTGTTGTTCCCTACCCTCTTGCGATAGAGACTTTGATCGTGACATTTTGTAAAGTGG
TAGAGGTATGGGTAAGATTATTTTACCACCGTTTTCTTTAGCAAATAGTCTAAAGCATTTTCTG
AATTGTTGAGTTTCCGTACATCATTAGCTATCTTTGTACAATTGATTTGCTTCTACCTCTAGTCA
TGGAATAACAAGTTAACAGCGTGTGTTGTTGTTGTTGTTGGAACAAATAAATTTGTGGTGTGTAAT
GTGTGTGTTTGTGTTTTTTTTTTTACCAGCATTTTGTCTTGTCTTAAAAATGAAACAGCGCAATGAT
TCTTTTCATAGTTTTTTTTTTTCCATACATAACTTCTGACGCGTGCACTATATCTGCTAACATACTC
GGCAACAACAAAGAAAGAGAATTTGAACTAATCCGAAGATGAACGACCCAGAGATGAACAAATTG
ACTCCGATGATGTATTAACAGAAGATTCATCTGATGAATTGAAGGACTTGGTGCAGGAGTTTGAAT
TGAAATATGCAGAATTAAGAAGAACAAGCCTTGAAAAACGTCGTTACAGTCAACCTGGAAG
ACATGTTGAATAAACAGAAACCCCATCAACCGGAGGTTCCCGAAGCCAGAAAAAGCTAAAGTCC
ATTTGGTAAGGTAGTAGAAGAACCAGCAAGAAAGATTTTACCAGAAAGGAGGATTCGGGATTCCA
AGATAAAGAATCAAACCTTCTTAAACAACTCTACGAGACAAGTAATAAGCATGATAAAGAAGATG
CCCATAAAATAGATTTTCACTAAAAGAAGGTTTGAGTTTCAATTGGATAAGTATACTTTTACGCCAA
AAGACGTTGTTGATGATTTAGAACCAGATATCCAAGCTTTACTTGCAGCAAGATACCTTGCCCAAC
TGCAAATTGCCGACATTATTTGCCGAAACTGATAGCAACATGAAATTCCTTAAAAATGACAAGTTTT
TAGCGAAAACCCATAAATCAAACAACATATGCTGAACCCAGTATTGTAATTGGTGTCTTGTGTCCT
TTGTGGTGCAGCAAGGACCCAGTGCAGGTTGCTGCCAACAACTCTAAATACATCAAGTTGAAGGTTG
GAAATTTTATGAATTCTGTAGACTTGATGCTTTTGTATAAGGCTTTTTCAGAAAAACGGGAAATCC
AACCAGGTTGATTTATTATTCATTTTGAATCCATTGATCAACAAGTATGAAATACAAGTTGGCAAGG
GCCAGTTTCAGTCTGGGTTCAATTTGAAAGTAGAAAACACCAATGTGTCAAGTATTTAGAGATAG
GATCGTTAAGAGATTTTGGGTTTTGCAAGTTTACTAGAAAGCTAGATAATAGCAGATGCAAAAGGG
CCATCAACACAAGGACGCAAGAATTCTGCGATATACATTTGGATATGAAGTTAAGTCTAGTACAA
GAATGGAATTAAGTGAAGTGTGTTTCGATTAGATCCCCGCAAAAAACAAGAAAAAGATGTACATGA
ATAAAAATGGGTCTGGCTTTATTAAAGCAATATAACGAGGAGAGTACTGTTATAGGAACAAGCTACG
GTTCTCCTCTTGATCCAAAAAGGTACCAAGACCCGAAAGTACTCCAGAACCAATCAAGCGGCGCA
AACTAATAGACGACAAGGCAAAGGAGATGCTTGAACAAAAGCTATCGAAACTAGGTTCCGGCTTCAT
TATTGAACAATTTACAATTATCTAAGAAAGAAGCAACAGATAAACTTGCGAGTGATCGTCTGAAGA
GCAAAGGATTCACCAACACAATGATTTTACATATTGGGTTTGATCCAAACAGGTACATCTTTGAACC
AAAATAGTACCCTGCTTGGCAGCAAGCTGATGGAATAATCTCGAGCACGGGAATTGCATGATTTGA
GTGTTGAAACATCTGGTCATAAGTCGTTGCTTCTGCTCTAAACAAGATCGCCAGTCGAAAGTTGCAA
AATGGAACACGAATATCAGAACTTTACAAAATTACGATCGACGAGTTGCCAGCCACTCCTTGAGTA
CCTCTCGTCTGGTTACAGAATCTTGTAGGAAAGCAACACACGCTACACTAGTAGATAAAAGGAAAA
GAGTGGTTGTCTCAGATGATGAACAACCGGGGATGGAAGAAGATGAAGAAGACATTGAAATCCAGT
TTGACGACGAAAAGTCTAAGATGTCTTACATGAAAATGACTGGAGCCAGGTAA

YIL150C_homolog 598aa (SEQ ID NO 374)

MNDPRDEQIDSDVLTEDSSDELKDLVQEFELKYAELKKNKALKKRRSQSPSEDMSNKQKPHQPEV
PRTPEKAKVHLDKVVVEEPKQRIFTKKEPRDSKIKESNFLNKLYETSNKHKDEDAHKIDFSKRRFEF
QLDKYTFTPKDVVDDLEPISKLYLRRRYLAQSQIADIIAETDSNMKFLKIDKFLAKTHKSNNYAEP
KYCNWCLVAFVVRKDPVQVAANNISKYIKLVGNFMNSVDLMLFDKAFQKNGKIQPGDLLFILNPLI
NKYEIQVGKGQFQSGFNLKVENTNVSSILEIGSLRDFGFCFKTRKLDNSRCKRAINTRTQEFCDIH

FIG. 2 - 31

LDMKFKSSSTRMELNGSVSIRSPQKNKKKMYMKNKNGSGFIKQYNEESTVIGTSYGSPLDPKRYQDPK
VLQNIQIKRRKLIDDKAKEMLEQKLSKLGSASLLNNLQLSKKEATDKLASDRSKSGFTNTMISHIG
FDPTGTSLNQNSTSLGSKSMEKSRARELHDLSEVETSGHKSLSSSSKQDRQSKVAKWNTNIRTLQNYD
RRVASHSLSTSRRLQNLVGKQTHATLVDKRKRVRVVSDEQPGMEEDEEDIEIQFDDEKSKMSYMKM
TGAR

YIL167W_YIL168W_homolog 1499bp public: 1..1499; CDS: 501..1496
(SEQ ID NO 375)

TTTCTTCATCAACTTGCTCAAATGTCTTTGAAAGTGAAAGCTTACTTTTTTGGTTTCGTTTAGGTG
GCATCAAGGTAAAGGAGGGAGTTTTGGTATAGTTAGGTTTTTGACTTATTTCCTTTTTTGAGTAGA
TATAACAGAATAACAAAAGTGAGCCACATCTGTTAATCTTGAAAAGCAAATTGAGAAAACCAT
TTATGCAAGTCGTGTACTGGTGATATTCTTTGGTCAATTGCTACACTTTTGTAAATGAATACTGTAAT
GTAGCCGACGTGGGTGAANAATATATATTTAAGTATATAGAATCAGGTCAATATAAAATGTTTGA
AATATAACAAAATGTTTCAATGTAACTGATGGTTAAGGGATTATAAATCAAATGAGTAGTGCTT
TTGTTCTTAAAAAACCCATCGTGGTGGTAACGTCAGGAGACCGGACATCAAATGGAATTCACACA
ATCAGTCTCCGAATTTATTACCCTTGAACTTAATTAAGAGAGCCTTCCATCACTACTACCT
TTGTTGAGGTTACAGACAACTTCTACAAAGCCTCCGTGCAGGGTGTTTTTCAAGAATGAGTATG
AGCAGCCCTCCGGCAGTGTCAAATTAAGAGGCTAGGACACTTGGTTGGCCAGTCTATAGATGTGG
CCAGAAAACCTTGGCAAATCGAACGTAGCACTTTTTTCGTCATCTGGTGGTAATGCAGGATTAGCAG
CTGCTTATGCCAGCCAGTTTTTTGGAGTATCGTGCACGTGTGGTGTGCCTGAAAGTTCGAAGCCAA
CTGTTATAGAAAAGTTGAAATCCTTGGGTGCAGATGTCATTATTCATGGGAAACATTGGGGAGAGG
CCGATAACTATTTAACTGATTTTTGTTATTAAAAATCTTGACAAAACAGTCTATCCGGTCTATTGTC
ACCCTTTTGATGACCCATTGTTGTGGGAGGGTCATAGTAAGATCATCACGGAATCATCGATCAAA
AGCAATTACCAACTTTGATAAAGTTAAGGGGGTCATTTGTTTCGGTAGGAGGGGTGGCTTATACA
ACGGAATAGTTGAAGGTTTGGAAAATCATAAGGAGATACCAAGTGTGGCAATTGAAACTAAACAG
CGGCCACGTTTCACGAGGCGGTCAAAGAAGGTAAAGTTGTTTCAATAAAAGTGCAAACTTTTGG
CCACTTCTTTGGCTTCGCCGTACCTTTCTTCCAAGGCATTAGCAAATATATTGAGCGTCTTACAG
TTCTTGCTGAAATTGATGACTTGGACGCTGTAAAGGTGTTGTTGATGTATACGACCATTTCCGGAT
ATATGGTTGAGCCTGCATGTGGTGCATCCGTTGCATCAGTGATGCACAGGCAAGATTTATTGAATA
AATTTGGTACATTAAAGTCCAGATGATATTATCATTTGTTGTCATATGTGGTGGATCGGCTATCAACA
AGTATATTATAGACGAATATAGAAGTTTATTAGAAAAAGACTCTTGA

YIL167W_YIL168W_homolog 332aa (SEQ ID NO 376)

MKEPSITTTTFVEVTDKLPKPPCRVFFKNEYEQPSGVKLRGMGHLVGQSIDVARKLGKSNVAVFS
SSGGNAGLAAAYASQFFGVSCTVVLPSSSKPTVIEKLKSLGADVIIHGKHWGEADNYLTDVFVKNL
DKTVYPVYCHPFDPLWEGHSKIITEIIDQKQLPNFDKVKGVICSVGGGGLYNGIVEGLENHKEI
PVLAIETKQAATFHEAVKEGKVHLQKVQTLATSLASPYLSSKALANYIERPTVLAIEDLDLDAVKG
VVDVYDHFHYMVEPACGASVASVMHRQDLLNKFGLTSPDDIIIVVICGGSAINKYIIDEYRSLLEK
DS

YJL034W_homolog 2564bp PathoSeq: 1..806/1401/2504, public:

807..1400/1402..2503/2505..2564; CDS: 501..2561 (SEQ ID NO 377)
TTTTTTGAAAACAGAGAATGAATGAACAATTGATGACCATAGAAATGAAGTGAGAACACATAAATCT
GCGACACTTCACGTGATAACAACAAAGTGACATGAACAACAAATGTCGTTTGTATAAATTGCGACA
TTTGTGTGTTCAAGCCAAAAAAGAAAGACAGAAACAGAAAAAAGAAAAATCTCAAAGTTGCCACGT
AAGCACAATTAATCTTTTTATGGTTGTAATATTCTAGTATATTCTACGTAATAGGTGAGGTCTT
ATATGCAGTACACACAGGTTTTTTTTCACAGATGTTGACACAGTGTGAAAATTATTCACGTTGATT
TATAAATATACAACCTTACCTTCCACGGTTTTTTTTTTGATTTTTTGATTTTTTGAATCTTCTTTCT
TTTTTTTGTGCATTTATTTATTTAAACATTCTCTTGTAACTTTATTTTGATAAATTTTACAAGATT
TAATTAGATCAATTAGATTATAGAATCATTTCAATATAATGAGATCATCACAATCTTCTTGGTTAC
CACGTATTGGTTTATTATATGTGGCGTTAGTTATACTTATACCATTTTTTGGTTTACCAGAACGACG
CATTTGCGGTTGCTGCAGTGAGCGATGATGAATCCTCGACAGATAATTATGGTACAGTCATTGGTA
TAGATTTGGGTACCACTTATTCCTGTGTTGGTGTATGAAAAACGGTAAGGTTGAAATTTTGGCCA
ACGATCAAGGTAATAGAATCACTCCATCATACGTGTCGTTCAATGGCGATGAAAGATTGGTTGGAG

FIG. 2 - 32

ACGCTGCCAAGAATCAAGCTTCCTCTAATGTCAACAACACTGTTTTTCGATATTAAAAGATTGATTG
GTTTTGAAATATAATGATGACACTGTGCAAAAGGAACCTAAACATTTGCCTTACAAAATTGAAAATA
AGGGTAACAAACCAGTTGTTAAAGTTGAATACCAAGGTGAAGAAAAAAGCTTTCTCCCTGAGAAA
TTTCATCTATGGTTTTGGGTAAAATGAAGAGTATTGCTGAAGATTACCTTGGCAAAAAAGTTACTC
ATGCCGTTGTCACTGTTCCAGCTTATTTCAACGATGCTCAAAGACAAGCTACTAAAGATGCCGGTA
CTATTGCTGGTTTTGAACGTTTTGAGAATTGTCAATGAACCTACTGCTGCCGCTATTGGCTATGGAT
TAGACAAAGGCGACCAAGAAAAACAAATTATTGTTTACGATTTGGGTGGTGGTACTTTTGATGTTTT
CTTTATTGTCCATTGAAGGTGGTGTTCGAAGTCTTGGCTACTGCTGGTGATACTCACTTGGGTG
GTGAAGATTTTGATTTCAAGATTGTTCAGATACTTGGCCAAACAATTCAAGAAGAAGCACAATATTG
ATATCACTGCCAATTCTAAAGCCATTTCCAAATTGAAGAGAGAAGCCGAAAAGGCCAAGAGAACTT
TATCTTCTCAAATGAGTACTAGAGTTGAAATCGACTCCTTTGTTGATGGTATTGACTTTTCTGAAA
CTCTTTCAAGAGCCAAGTTTGAAGAATTGAACATTGCTGCTTTCAGAAAGACTTTGAAACCAAGTTG
AACAAGTGTGGAAGGATGGTGGTGTCAAGAAATCCGATATTGATGATATTGTTTTGGTTGGTGGTT
CCACCAGAATTCCAAAAGTTCAAGAATTATTGGAAGGATTCTTTGATGGTAAAAAGGCTTCTAAAG
GTATTAACCCAGATGAAGCTGTTGCTTATGGTGCCGCTGTTCAAGCAGGTGTTTTGAGTGGTGAAG
AAGGTGTTGATGACATTGTTTTGTTGGATGTTAACCCATTGACTTTAGGTATTGAAACTTCTGGTG
GGGTATGACCACTTTGATCAAGAGAAACACTGCCATCCCAACCAAGAAATCTCAAATCTTCTCAA
CTGCTGCTGATAACCAACCAACTGTTTTGATCCAAGTCTATGAAGGTGAAGAACCATGGCTAAAG
ACAACAACAGATTGGGCAAATTCGAATTGACTGGTATTCCACCAGCTCCAAGAGGTGTCCACAAA
TTGAAGTCACTTTTCTCATGGAATGCCAATGGTATCTTTGAAAAGTTGAAGCTGCTGATAAGGGAAC
GTAAATCTGAATCCATTACTATCACCACGAAAAGGGTAGATTATCCAAGGATGAAATTGATAGAA
TGGTTGAAGAAGCTGAAAAATACGCTCAACAAGATCAAGAATTGAAGAAAAGATTGAAGCTAGAA
ACTCATTAGAAAATATGCTCATGCTTTGAGAGGTCAATTGAGTGATACTTCTGAAACCGGTTTTAG
GTTCTAAATTGGATGACGATGACAAGGAACTTTGGATGACGCTATCAAGGAACTTTAGAAATTTA
TTGAAGATAACTTTGATACTGCTACTGCTGAAGAATTGGAAGAACAAAAACAAAATTAATTGACG
TTGCTAACCCAATCACAGCAAAATTATACGGTGGAGCTGCTGGTGAAGGTGCTGGTGCGCTGGGG
ATGCCAATTCGGTGATGATGATTGATGATGAATTCGATCACGATGAATTGTAG

YJL034W_homolog 687aa (SEQ ID NO 378)

MRSSQSSWLPRIGLLYVALVILIPFLVSPKHAFAVAASVDDDESSTDNYGTVIGIDLGTTFYSCVGV
KNGKVEILANDQGNRITPSYVSFNGDERLVGDAAKNQASSNVNNTVFDIKRLIGLKYNDTQVQEL
KHLPYKIENKNKPVVKVEYQGEKTFSPKEISSMVLGKMKSLAEDYLGKKVTHAVVTPAYFND
QRQATKDAGTIAGLNLRLVNEPTAAAIAYGLDKGDOEKQIIVYDLGGGTFDVSLLSIEGGVFEVL
ATAGDTHLGGEDFDKIVRYLAKQFKKKHNIDITANSKAIKSLKREAERAKRTLSSQMSTRVEIDS
FVDGIDFSETLSRAKFEELNIAAFRKTLPVEQVLKDGGVKKSIDDIVLVGGSTRIKPVQELLEG
FFDGKKASKGINPDEAVAYGAAVQAGVLSGEEGVDDIVLLDVNPLTLGIETSGGVMTTLIKRNTAI
PTKKSQIFSTAADNQPTVLIQVYEGERTMAKDNRLGKFELTGIPAPRGVPQIEVTFSLDANGIL
KVEAADKGTGKSESITITNEKGRLSKDEIDRMVEEAKEYAQDQELKEKIEARNSLENYAHVLRGQ
LSDTSETGLGSKLDDDDKETLDDAIKETLEFIEDNFDATAEEFEQKQKLIDVANPITAKLYGGA
AGEGAGGAGDAKFGDDSDDEFDHDEL

YJL035C_homolog 1346bp PathoSeq: 1..125, public: 126..1346; CDS:
501..1343 (SEQ ID NO 379)

GCCCCATGGTGACAGAAAAGTATTGATCCAGGTTTCTTTGAAGGTTTGTAAATACGTTTAAACTTG
TGACCTAACTCATTTTTCATAAAATTCCTTGATAAAATTGGTTTCTTTGAATTGTTTGTAAATCTCTT
AAGATTGTCTCGTCTTCAGTGTTCAGTGGAGCTGCTATTGCCAGTCGGCGGCATAACAGCAGGT
TCTGGTATGTCATCTTCTACTAAGCCGACAATCCCAAAGCCGCTCTTGTCTTTTATTCTT
CTAAGGAATGCTTTATGTAGTTCTGACATTCTTGCCTAAAAGGAAGTACAGTATTAAAGCTCGAAA
CTCAATTGCAACAAAAGTCTTAATTTTTTCTTCTATAAGTAATTGATCTTGGTCCCCCAACAAAA
AGATACAGAGGAGAAAGGAGGGCCTTAGGCTGACAGAAAAAAAATTTAGTACCTGCCACACCAG
TAGCTCCAAACCATATATGATTTGATAGAGTTGAAGTATGCTGACAGATCTTACTTCACACTTTC
AGTACATGGCTATAAGCTTGTTTGTGCGTTACAAAGCCTTACTAAATAATGAGACACCAAGTGTCT
GTATAGTCGTGGATTCAAAATCAGATAAAATCATTAGCATAGGCTACAATTATACCAACCACTCTC
TAAATGGTACACAACACGCAGAATTTATTGCTTTACAACGATTTGGGGAACAAAACTGAGTATTG

FIG. 2 - 33

ACTATAATGATTTAATTTTGTATGTGACAGTGGAGCCTTGTATTATGTGTGCATCTTATTTACGTC
AGTTGGGCATCAAAAAAGTAATATTTGGTTGTGGGAATGATAGATTCGGAGGAAATGGTACCATTT
TATCAATACATAGTGACATCACCTTGCCTAACGCAGCTTATTCAGTATCGGGGGTATATGTAGGA
CAGAAGGAATCCAACATTACGAAATTTTATATTCAACAAAATGAGTCGGCACCAATCCA AAAA
TCAAAAAGAACACAGATATTGAGAGTAAGGAATACCCAGAGAATCAGTTTGTAGCATTTCAAAGG
ATGAATTTATAGAGTTTACGGAAATGAAAGAGTGCATATTTACGATGGGAAGATTTTGA AATCA
CTCCATTACAAAACAAGGGTTATGATATAAAAGAATTGATATCGTTGGATATGATGCAAAAAGTTC
CATTTCTAGAGGATGAGTTGGGACAAATTACAGATGAGCAAATAATTGAATTTCACAACTTATTTT
TCAACATAAATGATGATGGAACGGTTAATTATAAAAAACCAATAGGCAAATATAACAGTAAAAAGA
GACACTTTGCAACGATGAAGAATAG

YJL035C_homolog 281aa (SEQ ID NO 380)

MSTDLTSHFYQMAISLFVGYKALLNNETPVSCIVVDSKSDKIISIGYNYTNHSLNGTQHAEFIALQ
RFGEQKSSIDYNDLILYVTVPEPCIMCASYLRQLGIKKVIFGCGNDRFGNGTILSIHSDITLPNAA
YSSIGGICRTEGIQLLRNFYIQNESAPNPKIKKNTDIESKEYPENQFCSISKDEFIEFYGNERNVH
IYDGKIFEITPLQNKGYDIKELISLDMMQKVPFLEDELGQITDEQIIIEFHNLFNINDDGTVNYKK
PIGKYNSKKRHFANDEE

YJL180C_homolog 1504bp public: 1..938/940..1504, PathoSeq: 939;
CDS: 501..>1502 (SEQ ID NO 381)

CTTTATCTAATTGATTTAAATAATTATTAACATTAGTACCAATAAATGCTTTACCACAACCTTGCC
AAACTTTTTTCATTTGATTGGGTATTACATATTTTATTTAATTTAGCATTTGTAGTATCAATTATTG
TTAAATTTGTCATGGCTCGATCAAGTTGTAAATTACCCATGGATAATTCTGCTTGAGATTTATTTA
ATTGATTATCCATTTCAAGTAGGACTTTTTGTAAATGCTTCTTGATTCATGATTAAATGAGACGAGT
GTGTGTGTATGGGCGATGAAGCTGAAGGTTTTGCAGATGTGGTGTCTATAAGAGTAATTTGATGTG
AAAAATATACAATCTATAATCAGTATGTTCAGTTTTGGAATGGAAGCCCCAAGAAGAACAACAGGG
AAATTA AAAAATAAAAAGGTGTGAGAAAAA AAAAAAATTGAACAGAAAGATTCATCCTTTTAGA
TCAACGAAATATATCTTACCATCCCCCCCCCTCCAAATGCTTAGATTTACTAGGACTACTGCTT
GGAAATTAAGATCTATTCCAATTGCCACTATTC AATATAGACAATTTACTTATTTCCACTATATGTT
ATCAATTA AAAAACCCTTACTCCATCTTTAGGAATAAATAATACCATTGAATCCAATATACCTTCAG
AAACTAATAGATTAGCTAAAACTGGTACTAGATTTTTGGAAAAAAGGTGAAGTTAAATTC AATAATG
AAACTCAAAAATATGAAATTC AATTAGATGGGAAAACCTCTACGCACACCACCTTGATTCCCATTAG
AATTACCAATCAATAAAAAACAATTGGCATAATTTAATTGCTCATGAATGGACTCATTTACCTGATA
TTAAAGTGAAATCAAGTACTTTACCATTAAACAGCTTTAGCCACTAGAGCTATAGATTTGAGTCAAC
AACATTTGAGTGATATGAAGACAGAAAAAGCTGAAGAAATGTTAGCATTGGAAGATATTA AATTAC
AAATGTTAAGATATCTTGATACTGATACTTGTCTTATATTGCTACCAACAAAGAATGTGATGGTA
AATTAAGAAAAAGACAAGAAGAAATTTATCGTCCATTAATTAATGAATTTAATGAATTTTTCACAA
TTTATGCTCATAATAAAAAATTTAATCCCTCGACAAAAATCTATTGAATTGAAATATTTAGATTGTG
AAACTGATGGATTAAGAGGTAATAAACAAGATGAAACCACTCAATTAGTTGTATTGGATTGGTTAA
ATCAATTACCAATTTATGATTTAATTGCCTTGGAGAAAACAATCTTA ACTACTAAATCATTTTTAT
GTGGAATTACTTTATTAAGATCAAAATGTTAATGATATTGAAACTTTAAAAGAATTATATCAATTTA
ATAAAAATTCCATTGATGAAGATTATTATCATAAAACTTTAGAAGAATTAGTTGAATTAGGAAATT
TAGAACTATTTATCAAACTGAAGAATGGGGTGAAGTAGAAGATACTCATGA

YJL180C_homolog 334aa (SEQ ID NO 382)

MLRFTRTTAWKLRSIPIATIYRQFTYSTICYQLKTLTPSLGINNTIESNIPSETNRLAKTGTRFW
KKGEVKFNNETQKYEIQLDGKTLRTPLGFPLELPINKKQLAYLIAHEWTHLPDIKVKSSTLPLTAL
ATRAIDLQQHLSDMKTEKAEEMLALEDIKLQMLRYLDTDTCLIFATNKECDGKLKRQEEIYRPL
INEFNEFFTIIYAHNKNLIPRQKSIELKYLDCE TDGLRGNKQDETTQLVVLDWLNQLPIYDLIALEK
TILTTKSFLCGITLLRSNVNDIETLKELYQFNKNSIDEDYYHKTLEELVELGNLETIYQTEEWGEV
EDTH

FIG. 2 - 34

YJL187C_homolog 3689bp public: 1..452/3414..3689, PathoS q:
453..3413; CDS: 501..3686 (SEQ ID NO 383)
TATTTATATATAATCTAACAACAAGTACTATCCCTTAACTATTAGCTCAATGTCATTCTTCATTA
AACAAAGAGATATGGTAATTGTTGATTAGACAACAGTTGGGTATCCATTGTTATTGGAACGCTTTTT
TTAAACTGCTGTTTTATTGTAAAAATTTATGTCGCTCTTTCTTCATAACATTATTTGTAACAGTCTC
TAACTGTATTGTTGGGCTGACAGTAGAGTATTGCGGTCAATTTTAGGAGTGATTATAATTCTCTGT
GAGAAACGCAAGCAACAAAAAAGAACAAGGAAACACAATCATGATTAAATTATATTAATAGTAGA
AACTCAAGGGTGAGCTAGATGACTGAGCGTGCGAGAAAAAACAATCATCCAAAGTTTAAA
CAAAGTATTCTTTTTTTTTTCAATTTTACAACCAAGATAAATAACTACACAACACCCAAACATTA
CAGCCAAAACCATATCTGTGCAATATTTACGCTCCAATGGATTCAAACCCGTGTCAAGACGTAT
CGGGTGATACCGTAGCACACCAATGGCCAAACAATAATCCCACTAATGACAGCACAATCTCTCTC
AGAACCATTCTAAAACCTGGCTTGAGAAAACACCAACAACACTACCACCAACACCTGCACCTGC
AAATGCATTCTCATTACAGCAGTCACCTTATATTAATCAATTGGAATACTTTACCAATAACCAGT
TTTCACGCTCTTTCAATAGTTTAATTTTGGAGGATGCCAATGATGCCAACACCAACAATAGTTCAA
CAACAACCTTAAATAAGAAAACCATTAACAAAGTCACCACCATTCAATATCAAGCAGGACTTATTAA
ACGATAGTATCGACACGTTTCTTGATAACTCCAACACGGAAACGATAGAAGATGGAGACGTCACAA
CAACAGACGACGATCAGGATTTTGATGATGAAGATATTGAAGATCCTGAAGCAGTGCAGTACACCC
CAACTTTGAATATCTTGAAATCCAAAAAGTCGATAGCTTCAATATTATATAGCAAGCATAGAA
AGAGCAATAGTCAGATTACCTACAATCTGCACGTACGGAAGCCATCCGAAGAAGATACGTCATCAT
CGATGGCTACAATAAGGTTATCTAACAACCTCACAAAGTTCAATTAAGAGATCGTCAAAGTATTTGA
ATTTATCTATTGATTCCAATTTGAAAACGGTTGATGGAGGTAAAATTCCCGATGAAATAGATGACA
TTAGTTTGAACGAAATAGATGTTGCACTGGCACCTAACGATTTTTCATCACCCTATCAGCAAGAA
AGCCGGACATATTTGCTGCTATAACTGCAGCAAACGGGAATTCCAATAATCAATTTAAAGGCCAC
ACAAGTTGGTTAGTCAATCGCCTTCCCGTCGTCAAAGAATAAGTTTCGCATATCATCATCAACCA
CATCTTCGCCACAGTCTAACTTGCATTCACCTTCCAAGTTGGGACTGAAAGGATTCAAATGTTTA
AAAATGCAATAGAGACGCGATAATGTCGTCAAGCAGAGTTATGACTCCAGAAAACCGAAAATGG
TATCTAAAATATTTGGCAAGTCAGCAAAAATAAGGCGAGCTTATACCCCAACCCATACATCTACCC
CAATGGCTGTCTCATCACTCAACCTCCCTTCATCATCTACACTGAATTCACAACGGCAGCAATAA
CATCTACAAGTCCAGCAGCTGATGAGCATTATGATATTGACAATGACTGTGACAGTCCGTCAAAAA
ATAGAAAACGTGCTAATATTTCTGCATCTTCAATTATTATTATCAAGATGAAAATCATATCAAGT
CAAAATCATGCTAGAAAATCTAGTAATCCAAATACCATAACCTCCGACCGAACCACTACCGACAAATA
TTTCTGCTTCTGTGGCTGAAACAGGGAAAGGGTCAACTACAACCTAAAAGCAACCTATCTAAGGGTT
GTCCCTTATTTGATGATAAAGAGAATAAAGCTTCTTATCAGTTTGTAAACCATTGCAACAGCTT
TCAATTCCTCGGGGTTGGTCAAAAAGAAATAGCATAAGTGGTCTGCTGGACAGGAAACTACCTCCAG
AAACACCAATCAAAGAAATCCATTAATGATTTTAAATACCAACAAAGTTGTACCTCCATATAGCA
GTGGATTTGCTGAAGGAAAAGATGTAATGGGTGATCAACATGATATATATTTCCCATATTCCATGTC
AAAATCAACGTTTTCTGGCAGCGTGAATCCCAACACTACTACGAACAACAACAACACTCAACAGC
ATCATGATAGTGATCTTTCTATTGAAGTTGGAAGGAATAATTCTTATGATGCCAGTAGTAGCACTA
TCAATAACACAAGTTATATCAAAAATTTCCCTTCTTCGGAATTGAAAAAGGAGCAGGTGCTTCAGC
GACCACAAGAAGATTTAGAATTAGTTTCAATTCTGACATTGAACTAGATGATAACATAATACCAG
AAACACCAACAAGAAACTGCTACTACCGAATCAGCACCATCAACATCACTTACCCCTTTACACGC
AATCCAAGAGTCCATTGTTGAAGTTTGACACTGAGAAAGATGGAAGAAGGAATTTGTCAATAGTCT
TAGATAAATCAAATGCAACTAAACGAGAAATTAGCGAACCACTTCAACACCAATCAATATGTCAT
TTGCAAGAATAGTTTTAAGAAACCTATGAATAATGCTGAAAGAGGTGATGACCCTGATAGTATAA
TTGCTCAACGCATAGATATTATGCCATCGTTAGATGAAGTTGACTCAGTGTCTGTTTATCCTTCAA
AGATAGATGAACATTTAATTGAAAAGTTTGAATGAAGAATATCAAGTATATTGGATCGGGAGCAT
TTTCCATGCTTTTGAATGTTTATTTAATAACGAAAAGTTTGTCTATCAAAGAATAAAAAACCAC
TTATTGGAATAATTGGAGAAACAACTATAAAACGAGAAATTGAAGCATTGAGAGTGTGACAAGCA
TTAAAGAAGATGAAGCAACTAATATGCAAGAACAAGAAGAGGAAAGAGTATCTAGTTTATTTCAT
TTGAGGCTGGGATTTTAATAATTACTACTATATAATGACAGAATTCTGTGAAGGTGGTACATTAT
TTGATTTCTTAGAGGAAAATAAACATTACAAAATTGATGAATTTAGAATTTGGAAGATCCTAATTG
AAATTTCTAAATGGGTTAAAATTTATTCATCTGAAAAATTATTTACATTTGGATTTAAAACCAGCAA
ACATTTTATCACTTTTGAAGGGTCATTGAAAATTGGTGATTTCCGATTGGCTACTAAATTGCCCTA
TACTAGAAAAGGACTTTGATCTTGAAGGAGATCGTAATTATATTGCCCGGAATTGATTAATGACA

FIG. 2 - 35

AAATTTATACTCCGTTTGCAGATATTTTCAGTCTTGGATTGATTATATTGGAGATCGCTGCTAATA
TAATTTTACCAGATAATGGAACGCCATGGCGTAAATTGAGAAGTGGAGACTTGAGTGATGCTGGCC
GATTATCAAGTGATAATATTTCAATGTTTTTACAACACAATCCAAATACCAATAGCAATATCAGTG
GCAGTGGAAGTAGAAGTGGTAGTGGCAGTACAGGAGGCAATGGTAGTGCTGGTGATTGA

YJL187C_homolog 1062aa (SEQ ID NO 384)

MDSNPCQDVSGDTSSTPMANNPTNDSTISSQNHSTGLRKHQQQHYHQHSHSQMHSHSQSPYIN
QLEYFTNNQFSRSFNSLILEDANDANTNNSSTTLNKKTKINKSPFNIKQDLLNDSIDTFLDNSNT
ETIEDGDVTTTDDHDFDDEDIEDPEAVQYPTPLNLKSKKVDSEFNISSKHRSNSQITYNSHVR
KPSEEDTSSSMATIRLSNNSQSSIKRSSKYLNLSDSNLKTVDGGKIPDEIDDISLNEIDVAVAPN
DFSSPLSARKPDIFAAITAANGNSNNQFKRPHKLVQSPSPSSKNKFRISSTTSSPQSNLHSPSK
LGSKGFKMFKNANRDAIMSSSRVMTPEKPKMVSkipGKSakIRRAYTPHTSTPMAVSSSLNPPSSS
TSNSTTAAITSTSPAADDEHYDIDNDCDPSKNRKSSNISASSIIYQDENHIKSNHARKSSNPPIPY
PPTPLPTNISASVAETGKGSTTKSNLSKGCPLFDDKENKASYQFVKPLQTAfnSSGLVKNSIS
GSSDRKLPPETPIKRNPMLILNTNKVVPYSSGFAEGKDVMDQHDYSHIPCONQRFPGSVNPNT
TTNNNTQQHSDLSIEVGRNNSYDASSSTINNTSYIKIFPSELKKEQVLQRPQEDLELVFNSD
IELDDNIIPETPTKSLLPNQHHQHHLPLYTQSKSPLKFDTEKDGRNLSIVLDKSNATKREISE
PPSTPINMSFAKNSFKKPMNAERGDDPDSIIAQRIDIMPSLDEVDSVSVYPSKIDEHLIEKFGMK
NIKYIGSGAFSIAFECLFNNEKFAIKRTKKPLIGKLEKQTIKREIEALRVLTSEKEDATNMQEQE
EGKEYLVYFIEAWDFNNYYYIMTEFCEGGLTDFLEENKHYKIDEFRIWKILIEILNGLKFIHSKN
YLHLDLKPANIPITFEGLKIGDFGLATKLPLEKDFDLEGDRNYIAPELINDKIYTPFADIFSLG
LIILEIAANIILPDNGTPWRKLRSGDLSdagRLSSDNISMFLQHNPNNTNSNISGSGSRSGSGSTGG
NGSAGD

YJL189W_homolog 887bp public: 1..666, PathoSeq: 667..887; exon 1:

501..506, intron 1: 507..737, exon 2: 738..884 (SEQ ID NO 385)
AGTCAAGAATTTTATGATGACTTTGGAGGATGGTCTGATTAAAGACTTGTCTTTTACCAGTTTTTTC
AGCATTGTTGATGGCGTTTAAAGCATCAGCTAAGACGGAGGTTCTAGTCATGGTTGAATTGTCTGT
TGATAAAAAGAAACCGTGAAAAGGAAGTATTGTGAAAAATCGATTGATATTTTTTTTTTCTCCT
TCCTCACTGTAAACAGTAGTAAACACACTAGTTACAACCTGATGACCTGCATATTATAAATCTTCTG
AAAAAATTTTTTCCCTGTATTTTTGTAATCTTTTCGCTCTTTCTCACTCACTCACACTTATTAAT
GAATGAAAGGTTTGGTGTCTACAACTCCACTAACAAAATCTCACTCCTGTGCCTAAACACACACA
GACCCACACGCAAACTTTCTCTCAGAAACAGAAAAAAAATTTCAAGCAAAAATTTTTTCCATC
TAGATTTTCTTTCTTCAGAATATCAAGTAACTTTAAAGATGCCTGTATGTACAATAACAGTGTTAT
AATGATGTCTTTCACTCTTTTATTGGGTGATTATTATAATAATGGCAGATGAGAAATATATTGGA
TAATAAACCTTGCAAATGAAATCAGTTGACCATTTGAAATAATGGACCATTAGCAATACCCAGAT
TGCTGGAACAAAGACGAGAGAACTAGACAATCAGATATAATAGAACATCCATACTAACTTCACTC
ATTTCTTATAGTCTCAAAAATCATTGAGAACTAAACAAAAGTTAGCTAAGGCTCAAAAGCAAAACA
GACCATTGCCACAATGGATCAGATTGAGAACTGACAACAAAATCAGATACAATGCTAAAAGAAGAC
ACTGGAGAAGAACTAAGTTGGGTATCTAA

YJL189W_homolog 51aa (SEQ ID NO 386)

MPSQKSFRTKQKLAKAQKQNRPLPQWIRLRTDNKIRYNakRRHWRRTKLGI

YJL190C_YLR367W_homolog 893bp public: 1..893; CDS: 501..890 (SEQ ID NO 387)

GATTTTCATTTGCAAGGTTTATTATCCAATATATTTCTCATCTGCCATTTATTATAATAATCACCCA
ATAAAAGACTGAAAGACATCATTATAACACTGTTATTGTACATACAGGCATCTTTAAAGTTACTTG
ATATTCTGAAGAAAGAAAATCTAGATGGAAGAAAATTTTGGCTTGAAATTTTTTTTTTCTGTTTCTG
AGAGAAAGGTTTGGTGTGGGTCTGTGTGTGTTAGGCACAGGAGTGAGATTTTGTAGTGAGGTT
TGTAGACACCAAACCTTTCATTCAATTAATAAGTGTGAGTGAGTGAGAAAGAGCGAAAGAATTACAA
AAATACAGGGAAAAAATTTTTTCAGAAAGATTTATAATATGCAGGTCATCAGTTGTAAC TAGTGT
GTTTACTACTGTTACAGTGAGGAAGGAGGAAAAAATATCAATCGATTTTTTCAATACTTC
CTTTTCACGGTTTCTTTTATCAACAGACAATTCACCATGACTAGAACCTCCGTCTTAGCTGATG

FIG. 2 - 36

CTTTAAACGCCATCAACAATGCTGAAAAAACTGGTAAAAGACAAGTCTTAATCAGACCATCCTCCA
AAGTCATCATAAAAATCTTGACTGTCATGCAAAAACACGGTTACATTGGTGAATTCGAATACATTG
ATGATCACAGATCCGGTAAAATTGTTGTTCAATTAAATGGTAGATTAAACAAATGTGGTGTCAATTC
AACCAAGATTCAACGTCAAAATCAACGACATGAAAGATGGACTGACAACCTGTTGCCAGCTAGAC
AATTCGGTTACGTTATCTTAACCACTTCTGCTGGTATCATGGACCACGAAGAAGCTAGAAGAAAGC
ACGTTTCTGGTAAAATCTTAGGTTTCGTTTACTAG

YJL190C_YLR367W_homolog 130aa (SEQ ID NO 388)

MTRTSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLTVMQKHGYIGFEFYIDHRSGKIVVQLN
GRLNKCQVQPRFNVKINDIERWTDNLLPARQFGYVILTTSAGIMDHEEARRKHVSGKILGFVY

YJL197W_homolog 4619bp PathoSeq: 1..3041/3260..4619, public:
3042..3259; CDS: 501..4616 (SEQ ID NO 389)

CAACGACAACAACAATAAGAAGAATCTTTTCCAGATATTGTAAAATCCTTATATTAAATGTTAATA
GAAGCCTAAAAATTGCTTGAATTGATAGATTTGCTGATTCTTTTGCTAGAAACACGCGTTATATTA
CTTATCCTTTCTGTAAATTTCTTGATCTCTGTTTGAATCAACAACGCTTTGTTTCTCTTTCTGCC
TCCCTCTGCCACCCCCAGTTTATTTGTTTGCTTGTCGACGTGCTGCCAAAAAAAATTTAGATTTC
TCTCTCTCTTTTACACAGAGAAGAGACAAAGAAAAAAAACATCAAAATTAAGATTCAAGC
TTTTTTTTTTAGTTTTTTTAAACAACAAAAATGAAATTACAATCCTTGAATTTACAACCTTCATATTC
AGCTCTAAATACTAATAATTATAACAATAATTAATTGAATTATTCTATAAACCACTGATATTTGAT
TTTATCTTTTTATTTTTGTTTGTCCATAATTGTGTCATGCCTGACAATATAGAAGATCGATCCG
AGATACCTTCTGATGCAAAGGAAATTTGTGACTACAAATGAAATTGAAGCAACAGATTCAGAACATA
CAACAAATGTCGATAATGAACCTCCCTCAAGGTGAATCCAATGAACAAACAGGAGATGACTCAAATG
ACAACCTTGCAATCCAAACGTCAATTAATCAATGATTATTACACAATGATCATTTTGAAGAAGGAA
CAGAACGTTACATCATCCCTCAAAATTTCTTACATGAATTTTTTGAATTTACCAATCGATAATTTTA
GTGATTTGAAAGATCAACTTGGTCCTATTGATTTCCACTCATTACTTAATGAACAAGGTAATTTAT
ATCCCGAGAATGAAGAACCAGTCACTTTTGTGTCATGTATCGCCAGAAGTATTTCAACATTTGGGTG
AATGGTTTGGAAATATTGGGCCAACCAATTATTAGAGCTATCATTATTAATCCAGACACCAAAGAAA
AACAGATTGAAAGATTTCCCGCCATTATTTTGGGTTTCATCAATTAGGTAAAAAGACGCAACCAACAT
ACTTGCGACACCGTCATAATGGAAGCAACCACAATCATCATCACCATGGTCATCAGATTACCAA
TACCAGTATTGCTTTTCCAAAACAAGCACTTTTCATAGATTAAATGGATGTTATACGTTATAATGTTT
TTAAAGCACCACGAAAATCGACGAAAAGATTTTAGGATTTGGTTTATTGTCCCAAGATAAAGGCT
TACAGTATTTGATTTCAATACAACTTTTATGTTTGATATCTCCAAAAAACTTTGGTTTCCACAA
ATATGCTTGAGGATGCTTTGAAAGATCACGGTATTGTGGCCAGTTCTTATAATATAATGGTAGAAG
CAAAAGAAAAACATCAACAGAATTTCTTATTGATCAATTTATTTTATCTCATTCTAACGCATATG
AAGAAGTATCACAGGGTGGTGGACACCTTGGAATTATCAACATGGGGAACACATGTTATATGAAC
CGGCTTTACAATGTTTATTACAGTTTCTGAAATCAACTATTATTTTTTTTACAACATTTATAAAA
AAGAATTGAATTTTGACAACCCCTTGGGATATCATGGAGATGTTGCCAATGCATTTGGTTCACTTT
TAAACAAGCATTTGATCACGTGAAAAATAGTTCTAGTATATCTCCTCGAGAATTCAAATCAACTA
TTGGGAGATATTCTTCGATGTTTCTGGGTATCTTCAACAAGATTCTCAAGAGTTGTTGAGTTGGC
TATTAGATGCTCTTCATGAGGATTTGAATAGAATTCACCAAAAACCATATTGTGAAAAGCCCGAAT
TGAAAGATGACGAAATTGATGACCCCCAAGCCATCACCAACTTGCCAATACCTTGCTGGAATCAAC
ATAAGGCAAGAAACGACTCGGTGATAATTGATTTATTTACTGGGTGTATCAATCTACATTAATCT
GTCTTGATTTGTGGTAAGAAATCCATAACTTTTGATCCCTTTAATGATTTAACTTTACCTTTACCCA
TCAGTAAGAAATGGTATCACACATTTACAATTTGTTGATTTGTCCAATCAAGGCGTTATACCGGAAA
GGATAATGAAGTTGGAAGTTGAGTTGAATAAAACATCCAATTTGATGATTTACTTAGCTATTTGA
GTAATTTCTTGAATGTTCCATCTACTGAGTTGTTTGTCTATGAGATTTTTCAAATGCAATCTATA
GTGACTTCCAATTAGATTACACCAAGAACAAGTTTTTACCCTATCAGTGATATTATCAGAGATAACAG
ATGATGTTATAGTTGATGTTCCACATAACCTTGCCGTTGACATCATTTGTGCCAGTGTTCGAATG
CCGTTGAAGATGCTGATAGTTTATATCAATGGTTAATTTTTTTTGAATCCCATTTATTTGTGGTGA
TGAATAAAGAAGTCGATGTCAATAGTTTTGGTTTTATTAGAAAGAAATTATTAGAAACAGTTTCTT
TATTGAGTAAAAATTGATTTGGTTGATGAATATGAAAAAATAAAAAGGAGTAATGAAGATTACGTTG
AAAAAGTATTTTACAAAAAAGTGGATTTCCCTGCATTGTCAAGCCATTAGAAACCTCCGATTGTG
AAAAAACACAATAATACTAGCGACAACGACGACGATGAGGATGCTGACAACGATGAAGGCTATG

FIG. 2 - 37

YJL198W_homolog 2693bp PathoSeq: 1..899/1285..2693, public:
900..1284; CDS: <3..2690 (SEQ ID NO 391)
TTCATTTCCCTAAATTCAAATGAATTATCATCACCAATGCCACCATCATTTTCTATTAACCTATGGTA
GTGAATGGGATTTAGAAATCATTCAAACCTAGTTTAGATAATGAAAAAGAATCAGAACTAAATCAT
TTACTGGTGAATTAGAATATACTTCAACTTCTTCCAATGGTGAACATGACACCACCACCATGCCA
CTAAACATGAATTGATATTACAACAAATTTGAATTCATATGATGAATCATATTAATCCTAAAT
CATTAACATTTGATCCATTAAAAATTTCACTAAACAATTAATTGGTGAATTAATTAATAATTAATC
AATTTTACAATTCAAAAGAATCGGAAATTTTCAAATTTATAATAATTTAATTCATGATTTACAAA
ATCAAAATATTAATATTGATGATGTATTTAAATTCACCTCAAGCTTATAATTATTCCGATCCAAATA
TAATAAATACTGATGATCATCATCAATATCATTTTAAATCAACTTTATCAAGAACAGTTACTAATG
CTAGTGTATTTGATACCATTAAATCATATTGATAATGATTATGATAATAATAACAACCAAAAAGA
ATAATTATGATTTGGAGAAACAAAATAATACTACAGTTGCAATTCATGATGATGATGATTGAGAAG
ACGATGAAGAAGGAAGGAAGAACTCATAGTCATGATTGAGTATTACTTAATCATACACATT
TTAATGTTAAACAACAATTAATAATCACATTAAACGTAAGCCATTACATTATTATAAATCTTT
CTGAATTAAATCATTTATTGAATTGAATAGAATTGGATTACGAAAAATTTGTAATAAATTTGATA
AACTTGTGGTTATTCAATTAAACAAGATTTTATTAATGAATTTTACCTCAATATTCTCGAGTAT
TTGAAAAATGATACCATTGAAGAATTAGATTATAAATTGAATCAAAATTTATAAATTTATGCCCTTT
TATCAATAAATTAACCTCAATCAACAATAAGAAGATTTGGATAATATAAATTTGAATTAA
GATCTTATTTACGTGATCATATTGTATTTGAAAGAAATACCGTTTGGAAAGATTTATTATCATTAG
AAAAGAAATCTTATAATATTGATTTAGATAAATCTGTGGTTCAAATAATAAATGGGTGATGAAG
GTCATATAATTAATTCAATGATGAATTTATCCATGAAAAGAATTAATTTACCACAATGCCCTTTAAA
AATTGATTAAATATGATCATATTGATTTCCACAATTTTATTAACTACTCAATGCTTAAATTA
TTATTATTGTCATTGTTTTTATTATATTATTAGCAGTGAAAACCTTTAATGATCCAGTTCAAGGTC
GTTGTTTAGCAGTATTAGTTGCTGCTGCCATGCTTTGGGCTTCAGAAAGCATTACCTTTATACACTA
CAGCTTTATTAATCCCACTTTTGGTTGTTACTTGTAAAGTTTGTAAACTCCGGGAACCGATGATC
CAATGGATGCCACCAAGGCATCACAATATATTTTGGGACAATGTGGAATTCACAATTATGATAT
TAATTGGTGGGTTTACATTAGCTGCTGCATTATCAAAATATAATCTTGCCAAAATATTATCATCAT
ATATTTTAGCATTAGCAGGTACAAATCCAAGAAATGTATTATTGGCAATCATGTGTGTATCATTTAT
TTCTTTCCATGTGGATTTCTAATGTTGCTGCCCGCTTTTATGTTTTTCATTAATTCAACAGTTT
TAAGAAGTATCCCCACAGATTCCCCCGTTGCTAAAGCATTAGTGTAGGGATCGCTTTGGCGTCTG
ATGTTGCTGGTATGGCTTCACCAATTGCATCTCCACAAAATGTTATTGCTCTTGAATCAATGAATC
CTAATCCAGTTGGGGGAAATGGTTTGTGTGGCATTACCTGTGGCAATCATTAGTTTAATTTTAA
TTTGGGTGGAATTATTCATGACGTTTAAATCAATAATGTTAAATCAACAATTCAAACCAATTA
AAGAAAAATTAACCATGAAACAATGGTTTGTATTGCGCTCACTATAACTACTATTCTTTTATGGT
GTGTTATGCAAAAATGATGGAACATTTGGTGAATCAGGTATAATCACTTGTATCCCAATTGTAT
TATTTTTCGGTACCGGTTTATTAAGAGTTGATGATTTAAATAATTATCCTTGGTCAATTGTTATGT
TAGCCATGGGTGGTATTGCATTAGGGAAAGCCGTTACTTCTTCAGGTTTATTGAAAACCTATTGCTT
TAGCATACAAAACGAATTATGCATTATGATGCCATTGTTGTATTAAATCATTTTGGAGCATTA
TTTTGGTGGTAGCTACATTTGTAAGTCATATGATGACCACTTATTATTATCCCTTGGTTAAAG
AAGTTGGAGATTCATTACCTAAACCTCATCCATTAAATGCTTATTATGGGTGTAGCTTTAATTGCTT
CAGGGGCAATGGGATTACCAACTTCAGGATTCCTAATGTGACGGCAATTGGTATGAGAGATGAAG
TTGGTAAACCTTATTGACGGTTAATTTATTTATTACTAGAGGGGTTCCGGCAAGTATAATTGTTT
ATGTTTGTATTATCACCATTGGTTATGGTATTATGTCATCATTTGAACCTTTTAA

YJL198W_homolog 896aa (SEQ ID NO 392)
HFLNSNELSSPMPPSFSINYGSEWDLIIQTSLDNEKESETKSFTGELEYTSTSSNGEHDTTTTAT
KHELILQQLNSNDESYINPKSLTFDPLKIFTKQLIGELIKINQFYNSKESEIFKIYNNLIHDLQN
QNINIDDVFKFTQAYNYSNPNIINTDDHHQYHLKSTLSRTVTNASVFDITINHIDNDYDNNNNQKN
NYDLEKQNNNTVAIHDDDDSEDDEEEEEETHSHDSVLLNHTFNVKQQLKITLKRKAITLFINLS
ELKSFIELNRIGFTKICKKFKDKTCGYSIKQDFINEFLPQYSRVFENDTIEELDYKLNQIIKIYAFL
SNKLTQSTTKEDLDNIKFELRSYLRDHIVFERNTVWKDLSLEKKSYNIDLDNSVQNNKMGDEG
HIINSMMNLSMKRINLPQCLKKLIKDYHIDI PQFLTQMLKIIIVIVFIIILLAVKTFNDPVQGR
CLAVLVAAAMLWASEALPLYTTALLIPLLVVTCVKCTPGTDDPMDATKASQYIFGTMWNSTIMIL
IGGFTLAAALSKYNLAKILSSYILALAGTNPRNVLLAIMCVSLFLSMWISNVAAPVLCFSLIQPV

FIG. 2 - 39

RSIPTDSPVAKALVLGIALASDVAGMASPIASPNVIALESMPNPNPGWGKWAVALPVAIIISLILI
WVELFMTFKINNVKIKQFKPIKEKLTMKQWVFVAVTITITILLWCVMQKIDGTFGESGIITCIPIVL
FFGTGLLKVDLNNYPWSIVMLAMGGIALGKAVTSSGLLKTIALALQKRIMHYDAIVVLIIFGALI
LVVATFVSHTVSALIIIPLVKEVGDSLPHPLMLIMGVALIASGAMGLPTSGFPNVTAIGMRDEV
GKPYLTVNLFITRGPASIIIVYVCIITIGYGIMSSLNF

YJR049C_homolog 2279bp PathoSeq: 1..839, public: 840..2279; CDS:
501..2276 (SEQ ID NO 393)

TATAAAGTTTCAAGTATAAAAAGGCGTTTAAATTAATTCCTTGTGATTTAAATAAGTTAAATTCCTT
TTTTTTTTTCTTTGTTAGTTTTTCGCTTTATCCGTTTACCCAAGAAAGGAGCAATACTGTTTCAC
CCCCTCCCCCTTCCCAGTTCCATGGCCCGCCCCCCCCCTCTCAACAGTTGCTGTCTGTTCCCTGCCTC
ATTTTCCACGCCCATTAATTATATGACTAATATCCGTTGCCTTATTATTAAAGTCACAATACATT
GAAAGATAGAAATAGCAAGCAAGGTGGAATAAATTTTTTTTTTTATCACATTCATACTTATATCC
TAAATTGATAAACAATAGAGTAATTGATACTTTCGAAGGACAATAAAACGATATATATTTATATAT
TAGAGTGAACAATAGCGATTGCCAATCACAGACAACAGATAATTTATCTTTCTCCTATTTCATTTGC
ACAATTAAATCAAAAAAAAAAAGAATCGAATTCATATGTCGCATAAGACTCAGAGCCAATTAT
CTTCACAAATGAAAACTTGAATACTCCACCAATAGACTTCAACTCAACTCAAGTAACAATACCA
TGCCTTCTGAACCAATCTGCAACCGCAACAACAACAATCACAACCAGAAGCAAAAACGGAGCCAC
AAACCATACGCCCTGCTACTTTTACAACCTAGTGGCAATTCATCATCTTCGTCGATATCTACCTTAT
CAGCAGATATCATTCAACCACTTCATCAACTACTGATAAATAACAACAATTCAACTGTGACGCAAC
CAGCGCCACAAAGCTCATCGTTTCAACGCCGAAACAATCCACAACGTTTCAATCGGAATCAACTCA
ATGTATACACTGACTTCAATAGTACTACTTCATCTGCTTCAAGCATTTAGTAGTTCACCAAAAAGATT
TCTTCACCAGAGAGCCACCACGGATCCATAGTAAATTGATATGTGAAGAGATTGCCTCTGCCAATA
ATCGAGCTGCTAAAGAGGTTTTATCACGTTTATCTACTGATGAATTGCGTTTCAGTTAAATCACATA
CTGAATTAGCTGAAACTGCTAATGGAGTGAGAAATTTAGCCAAAATTTATCCCGAGCAACCATTTC
AATTAGACGTTAGAGCTATTATGATTATCACTAAAGCTAGAGATAATGGACTTATTTATTTAACAA
AAGAAGTTGTTGAATGGATTTTGGATCAACATCCTCATATAACAATTTATGCTGATGAGAAATTAG
CAAAGTCGAAAAGATTCAATCCGGAAAGTATTTATGCCAAATTATCCAAATGGTTGTAAGAAATTAA
AATATTGGAATAAAAAATTAACACGAAAAATCCAGAAATTTTCGATTTAGTACTTACATTAGGTG
GTGATGGTACTGTATTATTTGCTTCAAACTTATTTCAAAAAATTTGTTCCACCTATACTTTTCATTTT
CATTGGGCTCATTAGGTTTTTTAACCAATTTTGAATTCAGTGCATTTAGAACAGTATTGAGCAAAAT
GTTTTGATTCTGGAGTTAAAGCAAATTTGCGTATGCGATTCACTTGTGAGTACACACTGATGAAG
GGAAGTTGATTTGTGAACAACAAGTGTGAATGAATTTGGTAGTTGATAGAGGACCTAGCCCATATG
TTACTCATTTTGAATTTATACGGCGATGGATCATTTGTTAACGGTTGCCCAAGCTGATGGGTTGATTA
TTGCAACTCCAATGGTTTCGACTGCTTATTCATTATCTGCTGGTGGGTCTTTAGTTACACCTGGTG
TGAGTGCCATTAGTGTACTCCAATTTGTCTCACACCTTATCGTTTCAGACCTATACTATTACCTG
ATGGGATGTTTTTGAAGGTTAAAGTCCCACTGAGCAGTAGAGCCACTGCGTGGTGTTCATTCGATG
GTAAAGTGCGTACTGAATTGAAGAAAGGTTATTATGTCATTTCAAGCTTCACCATTCCTTAC
CTACAGTAATGTCTTCCAAAACAGAATATATTGATTCGTGTCAGTAGAAATTTACATTGGAACATCA
GAGAGCAACAAAACCATTTAGTTTCATATTTGAAACCAGAAACGCGACAAAGTATTGCTGAAAGTG
AAAGATTGGATAATTTACATATTTCAAGTGAACAAGATGAATCGAATCATGAGGAACCTGAAATAA
CTGAAGATTTTGTATTAATTATACTGACAATGAACGTGATTCTTCTAGTTCCACTCCTAGTGAAG
AAAGCAACGAAGAATGTGCTAATACCACGACATAA

YJR049C_homolog 592aa (SEQ ID NO 394)

MSHKTQSQLSSQMKNLNTPPIDFNSTSSNNTMPSEPNSQPQQQQSQPEAKTEPQTIRPATFTTSGN
SSSSSISTLSADIIQPLHQLSINNNTSTVTPAPQSSSFQRRNNPQRFNRNQLNVYTFNNTSSA
SSISSPKDFFTREPPRIHKLICEEIASANNRAAKEVLSRLSTDELRSVKSHTELAETANGVRML
AKNLSRATIQLDVRAIMIITKARDNGLIYLTKVEVWILDQHPHITIYADEKLAKSKRFNPESIIA
NYPNGCKKLKYWNKKLTTKNPEIFDLVLTGGDGTVLFSNLFQKIVPPILSFLSLGLFLTNFEF
SAFRTVLSKCFDSGVKANLRMRFTCRVHTDEGLICEQQVLNELVVDRGPSPVVTHLELYGDGSL
TVAQADGLIIATPTGSTAYSLSAGGSLVHPGVSAISVTPICPHTLSFRPILLPDGMFLKVVPSS
RATAWCSFDGKVRTELKKGYVYTIQASFFPLPTVMSSKTEYIDSVSRNLHWNIREQQKPFSSYLKP
ETRQSIASERLDNLHISSEQDESNHEEPEITDFDINYTDNERDSSSSTPSEESNEECANTTT

FIG. 2 - 40

YLR048W_homolog EMBL_entry 1042bp public: 1..1042; CDS: 28..786
(SEQ ID NO 395)

ATAGCGGCCGCGCATATAATAGAGAATATGTCATTACCAGCTTCATTTGACTTAACTCCAGAAGAT
GCTAAATTGTTATTAGCTGCCAACGTCATTTGGGTGCTAAGAACGTTCAAGTTCACAACAAACCA
TATGTTTACAAAACCAGACCAGATGGTATGAACATCATCAACATTGGTAAAACCTGGGAAAAAATT
GTTTTGGCTGCCAGAATTATTGCTGCTGTTCCAAACGCTTCTGATGTTGCTGTTTGTCTTCAAGA
ACTTTTCGGTCAAAGAGCTGTTTTGAAATTTGCTGCTCACACTGGTGCTACTGCCATTGCTGGTAGA
TTCACTCCAGGTAACTTTACCAATTATATCACTCGTTCATTCAAAGAACCAAGATTAGTTGTTGTT
ACTGACCCAAGAACCGATGCTCAAGCCATCAAAGAATCATCTTATGTTAACATTCCAGTTATTGCC
TTGACTGACATGCAGTCTCCATCTGAATACGTTGATGTTGCCATTCCATGTAACAACAAAGGTAAA
CACTGTATTGGTTTAATCTGGTGGTTGCTTAGAGAAGTCTTGAGATTAAAGAGGTATTATCCCA
GACAGAACTACCGAATGGTCAGTTATGCCAGATTTGTACTTCTACAGAGACCCAGAAGAAATTGAA
CAAATGCCGTCGAAGAAGCTAAACTGAAGGAGTTGAAGGAGCTCCAGTTGCTGAAGCTGAAACC
GAATGGACTGGTGAAGCTGAAGATGTTGATTGGGCTGATTCTGGTGCTACCCCGAGCTGCTGAAGA
TGCTGCTGCTTCTATCTGGTAAACACTGAAATCTACCAATAAGAAGTAGAAGTAGAAGTAGAAGAA
GAAACAATAACAACAATAACAACCAAAATAAAAAAAGGTTAATGATGTATATTATCGATAAGGA
GAAAGAAGAGATTTTCTTTTAAATAATGAGGATGCCATTTTATACAAATCCAAATTTGTAATTAA
GAAAGATTAATAAATATAAAATATATATATAAAGTAAAAAAAAAAAAAAAAA

YLR048W_homolog SWISS-PROT_entry 253aa (SEQ ID NO 396)

MSLPASFDLTPEDAKLLLAANVHLGAKNVQVHNKPYVYKTRPDGMNIINIGKTWEKIVLAARIIAA
VPNASDVAVCSSRTFGQRAVLKFAAHTGATAIAGRFTPGNFTNYITRSFKEPRLVVVTDPRDTDAQA
IKESSYVNIPVIALTDMQSPSEYVDVAIPCNNKGKHCIGLIWWLLAREVLRLRGIIPDRTEWSVM
PDLYFYRDPPEIEQNAVEEAKTEGVEGAPVAEAEETEWGTGETEDVDWADSGATPSC

YLR088W_homolog 1335bp public: 1..80/494..776/821..1335, PathoSeq:
81..493/777..820; CDS: <1..1332 (SEQ ID NO 397)

TCGGGGCTACAAATTTTCGTCCATGAAAATTTGGGTTGCCACCAATACTTTGTATGCGATTATGCAT
GCTCCACGAGGTGAAAATACCGAGGCAATGGCGTTGGTTGTGCCATGGACTAATTCTGACAACGAG
TACAATGAAGGTGCTATGAGTTTGGCGGTGGCTTTGGCACGGTACTTTACAAAGATGTCGATCTGG
TCGAAAAACATTATTTTGTATTTTCCTGAGACGGGCCACAGACCGTTGAGGTCGTGGGTTGAGGCA
TACCATACGGTGTGGACGATACTGCGGGTTCGATTGAGGCGGCGATTATTATGGAGTACGGCAAG
AACGGTGATTATTTTGAGTATTACGATATGTTCTACGAAGGGTTGAATGGGCAGTTGCCGAATTTG
GACTTGTGTAATACGGCCAATGTAATGACGTATCATGAACAGATCCCCTGTGCCATGCAAGGGATG
TCGGATAGGGTTATCAATTATAGCACCCGGTTGCAGACTTTGTTTAGGGGTATCCTCAAAATGACG
CTTGTGCGGTTGACTGATGAAGTTCATGGGTGTGAAGCATTTTCGGGGTGGCAGATCCAGGCATTT
ACGATCAAGGTAAAGGGGACTGAAGGGAAAGATGTTACGCAGTTTGGCCGGATTGTTCGATTCTACG
TTTAGGTCCGTTAACAATTTGCTTGAAAAGTTTACCAATCGTTTTTCTTTTACTTGATGTTGTCTG
CCAAAACACTTTTGTGTCTATTGGGACGTACTTGCCGTCGGCGATTTTGTTGGCAGTATCGTATGCG
TTGAGCTCTGTCAGTGCGGTGGTGGTTGCCGGGTTTGATTTTCGAAAGCTATATTTGTGGTGGTG
GTTGAAATTGCGTGTGCTATTTGGCGTTTGTGCCGGTGAACCAGGTGATGCTTGTAGCGATTCTG
GCGGTGGTGTGTTGCCGCGCCAAGCCATCTTTTCCAAGCAGGCGCGCTTTTCGCTAATTTCTATT
GCGTTGTTGGCAGTGGCATTACTTATTACCGCCCTCTTGATTGTACATTTTGCATTGGCGTTTAGT
ATTGGGATTTTAGCCCTTCCATTGACATTTGTCCCGACATTAATGAAGAACAAGTCTAGGCTAACA
GCTTTTTGTTTGGCGGTGTGCAATCCGTTTTTTGTGATTTTCGTTGCTGGGAAAGTGCTTGGCCAC
CCCGAGCTATTTGACCGGTTGGTCACTGCCTGGTCGGACATACAGTGTGGACATGGTTTATCGTT
GTTTTGGGGTGGTTCCAGCGTGGGTGATTATCACACTAAGCTACTGTGGCTACAAGCCAGTTAAG
GAAAAAGTGAATAG

YLR088W_homolog 444aa (SEQ ID NO 398)

SGLQISSMKIGFATNTLYAIMHAPRGENTEAMALVVPWTNSDNEYNEGAMSLAVALARYFTKMSIW
SKNIIFVFPETGHRPLRSWVEAYHTVLDDTAGSIEAAIIMEYGKNGDYFEYYDMFYEGLNGQLPNL
DLLNTANVMTYHEQIPCAMQMSDRVINYSTRLQTLFRGILKLTLVGLTDEVHGCEAFSGWQIQAF

FIG. 2 - 41

TIKVRGTEGKDVTFQGRIVDSTFRSVNNLLEKFHQSFYYLMLSPKHVFSIGTYLPSAILLAVSYA
LSSVSAVVVAGFDPRKLYFVVVEIACAILAFVPVQVMLVAISAVVLLPRQAIFFSKQAAFSLISI
ALLAVALLITALLIVHFALAFSIGILALPLTFVPTLMKNKSRLTAFCLAVSNPFFVIFVAGKVLGH
PELFDRLVTAWSDIQCWTWFIIVLWGFPAWVIITLSYCGYKPVKEKSE

YLR167W_homolog 1190bp public: 1..1190; CDS: 501..1187 (SEQ ID NO 399)

TAGGTCATTTCATAACAATTGATAGATGCAAGCTAATTGGAATGAAAAATCCATCTTGTATCAAAAC
CCTTTGTTCTCATAGTTAATCCGACTAAAGAAGTGTTTTTTTTTCTTTTCTTTTGTCTATATC
CTAGTTGCCCTTAACGACAGTAATAGTTAAAGCGTTGGGAAGTAATGGTGAACCTGAACCATTTGGT
TGACGCTGACGATTAATAATGTGAATTTCTTTTTTCTTTTTTGGTTGTAGTAATTGCTTTGTTTGT
TGTCTAAATTAGGAAAATGTCGTGACCTTACGTACAGCACACACATACCACTGTCGTGCACTGACC
AACAACAATGCGGTGTTAATCGATAACCAAAAGATTATAAATAGGGGGTGAAGGTCGCCACTGTT
TGAAATGAATCAACACAGTTTTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG
CAATCGTCAACTAACATATATATACAAATCTACAAGCAATGCAAATTTTCGTTAAAACTTTGACTG
GTAAAACCAATTACCTTAGAAGTCGAATCTTCTGACACCATCGATAACGTCAAATCCAAGATCCAAG
ACAAAGAAGGTATTCCACCAGACCAACAAAGATTGATTTTCGCCGGTAAACAATTAGAAGATGGCA
GAACCTTGTCTGACTACAACATCCAAAAAGAATCTACTTTACATTTGGTTTAAAGATTGAGAGGTG
GTATGCAAATCTTTGTTAAAACTTTAACTGGTAAGACTATCACTTTGGAAGTCGAATCTTCTGACA
CCATCGATAACGTCAAATCCAAGATCCAAGACAAAGAAGGTATTCCACCAGACCAACAAAGATTGA
TTTTCGCCGGTAAACAATTGGAAGACGGTAGAACCTTGTCTGACTACAACATCCAAAAAGAATCTA
CTTTACATTTGGTTTAAAGATTGAGAGGTGGTATGCAATCTTTGTTAAAACTTTAACTGGTAAGA
CTATCACTTTGGAAGTCGAATCTTCTGACACCATCGATAACGTCAAATCCAAGATCCAAGACAAAG
AAGGTATTCCACCAGATCAACAAAGATTGATTTTGTCTGGTAAACAATTAGAAGATGGCAGAACCT
TGTCTGACTACAACATCCAAAAAGAATCTACCTTGCCTTGGTCTTGAGATTGAGAGGTGGTTTCT
AA

YLR167W_homolog 229aa (SEQ ID NO 400)

MQIFVKTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQQLIFAGKQLEDGRTLSDYNIQKEST
LHLVLRRLRGGMQIFVKTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQQLIFAGKQLEDGRTL
SDYNIQKESTLHLVLRRLRGGMQIFVKTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQQLIFA
GKQLEDGRTLSDYNIQKESTLHLVLRRLRGGF

YLR234W_homolog 2390bp public: 1..2390; CDS: 501..2387 (SEQ ID NO 401)

TCCAGAATAGTAATTAGGGACTTTAATTTTATTAGGAGTGGATTGCATAGAATATGCTATCTAATA
GATACATCTTATTATATTCTTATTTCATGGGAAAGCACCAGTATATGGAAATGCTGCCCAAGGTAGT
GCACACAACAACTAGTTTACAAAGTAAATTCGAAGTTACGTCAAAGCTTAGAATGGTTCTTATA
GTAGTTGTCTACTCTATCAAAAAACCCATAATTTGTCTATATAACGTAAGGATCACTATATGCTGT
TGAGTAAGAAATATGTTGCGAGCCGTACCGACAATGGATTGGCTGAAACTTGTCTCATCAAACCTT
GCAAAACACTTGGAGACGCGCGCGCTTTCAACACACAATAAACAACACGAAAAATAAGGTAGAAA
ACAAAAAATAAAGGAACCTTTAAACAAGAAGTAATCCCCATTAAACTTGATCAACACTTTT
AGGGTTTCCGATTTCCCATTTTCTTGACTAAAATAATATGAGAATACTATGTGTTGCCGAAAAAC
CATCGATTTCAAAGAGGTGGCAACATTTTGGGAGGAGGGCGAAAAAAGTAAGAAACTCACGAG
AAAAATTCATCAAAACTACGATTTCACTTCACTTTCACTCTGAAGATGGGCCATGTCAAGTAA
CCATGACTTCGGTGGCTGGACATATCACAGGACTTGATTTTGGGTCTGCCTTTTCGTGGGGAAATT
GTGTTCCCGGGCGACTATTTGAAGCAGACATCAAGACCATTATCACCAGAAATCTATTTATGAAA
ATATTGCAGAAGAGGCAAGAAACGCTGATAAGTTGATGATCTGGACAGATTGTGATAGAGAAGGAG
AATACATTGGATTTGAAATTATGAATGCTGCAAGAAATACAATAGGAACCTTGGGTAAACAATA
TTTGGCGAGCTAGGTTTTACATCTTGAACGAAATCACATTATTCGAGCAGCAAAAAATCCCGTGA
ATTTGGATATGAGTGCAGTTTCTGCAGTTTCTTGTCTGATGGAATCGATCTTCGAGTGGGTACCA
GTTTTACACGTTTGTGACTGATCAATTGAGACAAAAGGGGATAATTGAAAAGAAATGAAGTACGTT
CTTATGGTACATGTCAATTCCCGACATTTGGGTTTGTGTTGATCGATACAAACGAGTCAAGAGTT
TTACACCGGAACCATTTCTGGTATATTGAGATTGAACTAGGAAAGAGAATAAAAAAGACAATTTTCA

FIG. 2 - 42

ATTGGGGTTCGAGGTCATTTTTTCGACAAGATGTATGTGGTTATGCTTTATGATCGATGCTGCAAAA
GTGGAGAATTTGGAACCATATCAAAAATAGAATCAAAACGGAACCAAATTTCCGTCCATTCCCAT
TGACAACCGTGGAGTTACAAAAAGATTGTGCTAGATTTTTTAAGATGTCTGCTAAGACGGCGTTGG
CAGCTGCTGAAAAGACTTTATAACCTAGGGTATTTGTCGTATCCTAGAACTGAAACTGACAGGTTTG
CCAAAGAAACCGATTTCAGAGCTTACTAGAGGTGCACAAACAAGATCCGCGATGGGGAAGCTATA
CAACAAAGCTTTTGAACGAAGGTTTCGAAACTCCTCGAAGCGGTTCTCATGATGATAAGGCGCATC
CTCCAATCCATCCTATCAAATATGTTTCTTTGGACACCCTAAACACCCCTCGATGAAAAGAAAGTGT
ATGAATACGTTGTGCGACGCTTTATTGCCTGTTGCTCCAAAGATGCTGTTGGTACGCAAACCGTGG
TGACTTTAAATGGGGAGATGAATTCTTCACCGCAAGTGGATTAATGGTGCATGAAAAAATTATT
TGGAAGTGATATACTTACAAAAAATGGGAAAGCTCTAAACAACCTACCGAAATTTACAGAGGGAGAAC
AGGTCAAGTTGTGCGAGTGGGAATATTGAAAGACGGTAAACAAGTCCACCCAATCATATGACCGAGC
CCGAGCTAATTGCATTGATGGATGCCAACGGTATTGGAACCGATGCTACTATCGCTGAACATATTA
ACAAAATAGAGACTAGGCACTATATTAATAAATTGAAAAAGGGGAAAAATGAATATATTCTTCTTA
CTCCTTTAGGAATGGGGCTTATAGAAGGCCTTGAAAAAATGGAATTTGAAGATGTATCACTATCGA
AACCATTTTTGCGGAAGTCGTTGGAACGATCACTTGAGGACATAGCAACCGGGTCCCGGCCAAAAAG
TGGATGTTTTGAATACAACAATAGGCGTATATGTTGACGCTTATAGTGTGTTCTCATCAGATAC
TTGTTTTGTGCAATGAATGTAGGAGAATTATACTTGGAATAGCAGTAACAACAACAACAATA
ATAATAATACGTAA

YLR234W_homolog 629aa (SEQ ID NO 402)

MRILCVAEKPSISKEVANILGGGRKKVRNSREKFIKNYDFTFTFNSDGPQVMTMTSVAGHITGLD
FGSALFSWGNVCVPGRLFEADIKTIITKKSİYENIAEEARNADKLMIWTD CDREGEYIGFEIMNAARK
YNRNGLNLNWRARFSLERNHIIIRAKNPNVLDMSAVSAVSCRMEIDL RVGTSFTRLLTDQLRQK
GIIIEKNELASYGTCQFP TGLFVVDTRYKRVKSF TPEFFWYIEIETRKENKKTIFNWVRGHFFDKMYV
VMLYDRCKSGEFGTISKIESKRKPNFRPFPLTTVELQKDCARFFKMSAKTALAAAERLYNLGYLS
YPRTETDRFAKETDFKSLLEVHKQDPRWGSYTTKLLNEGFETPRSGSHDDKAHPPIHPIKYVSLDT
LNTLDEKKVYEVVRRFIACCSKDAVGTQT VVTLKWGDEFF TASGLMVHEKNYLEVYTYKKWESSK
QLPKFTEGEQVKLSSGILKDGKTSPPNHMTEPELIALMDANGIGTDATIAEHINKIETRHYINKLK
KGKNEYILPTPLGMGLIEGLEKMEFEDVSLSKPFLRKSLERSLEDIATGSRPKVDVLTNTTIGVYVD
AYSVCSSHQILVLCNECRRIILGNSSNNNNNNNNNT

YLR241W_homolog 3098bp public: 1..827/2190..3098, PathoSeq:
828..2189; CDS: 501..3095 (SEQ ID NO 403)

ATATATAGAATTATGGCTTAGTGCCCTTTATTAACTAAATTAGAGGTTACATTAATACAACCTTAAC
AAACAAGGAATAACATCCACGTATAGGGCTTCTTATATTAATATACCTAATTCAACCTGATTAT
ATTGCCTTATATACAGCTTGTAAAAAAACAATAGAAAGTTTACATCTCAAGATGATATATCCCT
CTATTGTAAAAAGTACATCGCCTAATGATAGACATCATAGAGTACTGGCGACTCCTTACATGATGG
TAACGACAACAAC TACAACAAAAAACAATTATCTTGACGGTATAATTAGTAGTGTGCGAGAGG
CACACGATAAGATTTATCAGTTTCCTTTCTCGGTTGACCTTAATCTGTTTTTGTATAGACTTTAT
TTTTTTTTGTTTTTGACCACACCCACTTTTAAATATCACAAGATATTTAACTGATTATAGAAAACAA
CAACAATAACCCAAATACGTTAACCCTTTTATTACATATGATAGACAATATAATCAATAATTGTC
AAATCATACTACAGCAAAATGATGATAATTTACATCCCCTCACGACGATGTGATATATCGACCAC
ATTCTGCTCGTGTAGCACGATATCAAGTAATAATTGCATCTACATTGGGACTCACTGCCCTATTAC
TATTTTCTATCTTACGATTAAAATATCCCAAAATATATGTGGCAAACCTTAAATCATTTGAATTTCA
GTCTACATTTCGACCTCAAGAAGGAATTTACCTGAATTGCCTTCAAATTCATTATTTGGTTGGATTTC
CTACAGTTTACAAAATTACTGAGCAAGAAATTTTGGAACATGCTGGATTAGATGCAGTTGTGTTTT
TGGAATTTTTTAAATGTGCATTGCAATAATAAGCATATGTTTAGTATTTGCCATTATTATCATAT
CTCCTATCAGATACAAGTTTACAGGGAGAGTAGATGAAGATTATCCCGACGATGATAGTGACAACG
ATGACGATGATGGAAGTAATAATAATGGTACCACAATAATTAAGCATATAGTGTGAGCTGGAATTC
TGGTGGCAAGTAAAAATAACGATGGGAGAACAGTATCAACAATTTCTTTGGTTATACACTATTTTCA
CCTATGTATTTACATTTGTTACTGTTTACTTTCTATTCAAACAAACCAATAGGATTATTTCTATGC
GTCAGAAGTATCTTGGATCGCAAAATTCAGTCACCGATAGAACGGTAAAAATATCTGGGATACCAG
GATCATTACGAGATGAAGTGGCACTCGCACGGCACATTGACCGTTTGAATATTGGTGAAGTGGATT
CTGTGTTGATTGTCAAGGAGTGGCAAAATCTAAACAACCTATTCAAAGAAGGAGAAGAATAGTTC

FIG. 2 - 43

GAAAATTAGAGGAAAGTTGGGTTGAATATTTTGAAGGATAACCAATAAGAGCGATTGGA
TATCGTTGCATCCCCAAGTTGGCGAACTGTATCGTTTTCCTAATAGGTATACTGATGATGCAGAAG
AATCACCAGACTGGGGATCTCAAAATTCGAACTCTGCACAAGCTTCAATAATAGATCAAGACTCAG
AATCTGTTGAAGGAGATTCTTCTGACACTTTGAATCGCTTGTGAATGATGAAGTGAACAAGAC
CAAGTCTTCGGAAAGGTTGGTTCCGATTGTTTGGACCTAAAGTGGATTCAATAAACTACTACCCG
ATAAATTGGAGGTCATAGATAAAGAGATTACCAAGGCCAGAACTAGAGAATATCCCGCCACTTCGA
CTGCATTTCTCACTATGAAAACCGTGGCTGAAGCACAAATGTTGGCACAGGCAGTCTTGGATCCAA
AAGTCAATCATCTTATCACCACCTTGGCCCTGCTCCTCATGATATCCGATGGGATAATTTGTCAT
TAACTAGACAAGACAGAAATACAAAGATCCTTGCTGTCACGATATTTATTGGTATAATGAGTTTGT
TGTTGGTTTATCCAGTCAGATTTATGGCTAGTTTAAAAACACTAAAAGCATTCTAAAAATATGGC
CATCATTTGGGAAAGCTATTGAATCGCATAAATGGGCCGAACTTTGATTACTGGATTATTGCCAA
CTTATTTATTTACAATTTTAAATATTGTGATCCGTTTATTTTATGTATGGATTCTGAAAAGCAAG
GTTATTTATCTCATAGTGATGAAGAGTTGTCTATCGGTATCCAAGAAGCTTTTCTATATTGTGA
ACTTATTTTGGTTTTTCAACTTTTGGTACCGCTCTTTTGTGATACGACCAAAATTCATTTG
ATTTAGCAAGATCACTCAGAGATTGTCAATGTTCTATGTTGACTTAATAATTCTACAAGGATTGG
GTATATTTCCATTCAAATTATTATTGGTGGGGAACCTTACTTCGCTTTTGTAGTGAATTCATTATTA
GGTGCAAGACCCCAAGAGATTACTTGAATTTGTACAAACCGCCAGTTTTCAATTTTGGTCTACAAT
TACCACAACCAATATTGATATTTATTATTACGTTGGTATACTCGGTAATGTCTTCGAAGATATTAA
CTGCAGGGTTACTATATTTATTATTGGTTATTTTGTGAGCAAATACCAATTGCTTTATGCTTGTG
TTCATCTCCACACTCAACGGGCAAAGTTTGGCCAATAATTTTCCGAAGAATCATATTAGGGTTAT
TTCTTTTCAAATCACAATGGTTGGCACATTAGCATTACAAGATGCAATCACATGTGCTACTTTCT
TGGCACCATTGCCGTTTTTACACTTTACTTTTGGTGGAGTTTCCATAAACAATATATTCCCTTGT
CAACATTCATTGCCTTGAGAGCAATTGAAAGCAATGAAATATCAACCCTACTGATTTGGAGCAAA
TCATTGAAAACAACAATAATAAACTCTTGACGAAAGAAGGAATTGAACACTAAATACGAATACC
CCAATCTAGTTAATGATTTAGACGGGCCAATGATTGCATTGGATGGTGAAGATGTATTGATAGTTA
ATCGAGATGGTACAACGTACGGAACCACTCAATATTTAGTTTCAAGATGGGACTATTAA

YLR241W_homolog 865aa (SEQ ID NO 404)

MIDNIINNLIILQONDDNFTSPHDDVIYRPHSARVARYQVIIASTLGLTALLLFSILRLKYPKIY
VANFNHLNLSLHSTSRRLNPELPSNSLFGWIPTVYKITEQEILEHAGLDVVFLEFFKMCIRIISI
CLVFAIIIIISPIRYKFTGRVDEDPDDSDNDGSDNNNGTTIIKHIVSAGISVASKNNDGEQYQ
QFLWLTYIFTYVFTFVTYVFLFKQTNRIISMRQKYLGSQNSVTDRTVKISGIPGSLRDEVALARHI
DRLNIGEVDVSLIVKEWQNLNKLFRRRRIVRKLSESWVEYFEKNGITNKSGLISLHPQVGESYRF
SNRYTDDAESPDWGSQNSNSAQASIIDQDSESVEGDSSDTLNRLLNDESRTSLRKGWFLGFGP
KVDSINYYTDKLEVIDKEITRARTREYPATSTAFITMKTVAEAQMLAQAVLDPKVNHLITNLAPAP
HDIRWDNLSLTRQDRNTKILAVTIFIGIMSLLLVYPVRFMASFLNTKSISKIWPISLGAIESHKWA
ETLITGLLPTYLFTILNIVIPFFYVWISERQGYLSHSDEELSSVSKNFFYIFVNLFLVFTTFTGTAS
FVDTTKIAFDLARSRLDLSMFYVDLIILQGLGIFPFKLLLVGNLLRFLVNSLFRCKTPRDYLNLYK
PPVFNFLGLQLPQPIILIFITLVYSVMSSKILTAGLLYFIIGYFVSKYQLLYACVHPPHSTGKWPI
IFRRIILGLFLFQITMVGTALQDAITCATFLAPLPFLTLYFWWSFHKQYIPLSTFIALRAIESNE
NINPTDLEQIIENNNNKTLDERRELNTKYEYPNLVNDLDGPMIALDGEDVLIVNRDGTTVRKPPQY
FSSEWDY

YLR321C_homolog 1559bp public: 1..947/1189..1559, PathoSeq:

948..1188; CDS: 501..1556 (SEQ ID NO 405)

TTCCGAATTAGTAGATATTTCTGATATCAAGTTGGAGATAGGGATATCGAACTGGGATTCTATAT
TTTGTTTTATCTTGGAGAACCTGTGTTGTTGTTGGCGTTCTATCTCTTTATATATTTTCTCTATTA
ATTCAATTGAAACATTTGAAGGAAATCTTTCTTAAAAGCATCTAGTGACACATGATCTCTAATCT
CCAGTCTTTTGATTAAATATTCTTTTAGAATATCAGGTGAAGAAGTGTGGTAGTCATAGCTAGTA
GATACTGTGTGGTGTCTGGGATAATAATTATAATGTAAACAAAACAAAGTCGTGTCACTGTATATT
TTTCTTTTGTCAATTCCATCTTTTTTTTTTCTCTTGAGAAATGTATAACAGAGGATCCATCCATT
TGCTTGACAGAGAAATACAGAACTAAACAAACATTTTTTTCATTCCTTTCTGTTTGTCTGTT
ATACCCCAAAAGTTTGAATAAGTCTTCAGATATCTAGCATGGCAACTTCTCAAGAATTGACAGCAG
ACATACAAGCTCTTGCAACTAGTTTCCCAAGCGATTAGCTAATGATAGTGACAATTCATTACTTA

FIG. 2 - 44

TTAATGTTGCACCAACTGGTCGACAAGCCAAAAGACATATTCAACAGATTAATTACTCCGAAGAGT
TTGGAGATGACCTTGATTTTGATGAATTCCTCTTCGACACCCGGTACTAGAAGCTTAAATGAAA
ATAAAGCTCAAATAGAACACAAAGATATTCTCTTGGAAAAACACACCAACGCCCAAGAGAATCT
TAGAAAAACCGGTGTTATCTGAGTTGGTTGAAAAACAGTGGTGCTTATTCCTATCAAAATAATGA
TTGAGAATTTGAACACAAACCAAAAGTTGATTGATTCTTTATGTGGAACCTGAATGAAAGCTTGA
TTACACCAACTGAGTTTGCAGGAAATGTTTGCAGTGATTTAGATTACCATTTCAGTATGGCTGCAC
AAATAGCAGACTCCATTAATCAACAGATTGAAGAGTATTCCTATGCATCTAATTTACAACCTACCAA
ATAAGGGCCCTTACAATGTTACCATTGATTTATCAGTAACTTAAATAAACAATTATACCAAGATA
GATTTGAATGGGATATGAATCAAAATGAAGTTACACCAGAAATTTTGTGCTGAAATAGTTGTTGCTG
ATTTGGGGTTATCGTTAGAATTTAAGAATGCCATATCACATGCATTGCACGAAATAATTATCAGAG
TGAAAAAAGAAGTAATAGATGGTACTTTTGACAATGAAATGCACAACCTTGCATCTAGTAAAAAGGTA
TAATGTTTGAACAAGGAATTAGAATTTTCACTGAAAACAGTGTTCAAAATGGAATGACCGTTGGG
AACCTTTGGTTCGAAGTATTGACTTCTAGTGAAATCGAAAGAAGAGAAAATGAAAGGGTTAGAACT
TGAGAAGATTAAAGAGAGAGAAATATGAGAAGAGATTACGATGATCATAGTAGGAGAAGGCAAGCAG
GAAAAAGAAGGTATGATGAGTTAGAAGGAGCCTGGGTATAG

YLR321C_homolog 352aa (SEQ ID NO 406)

MATSQELTADIQALATSFPKRLANDSDNSLLINVAPTGRQAKRHIQQINYSSEFGDDLDFDEFPSS
TPGTRSLNENKAQIEAQRYSLAKNTPPKRILEKPVLSSELVEKPVVLIPIKIMIENLNTNQKLIDS
FMWNLNESLITPTEFAEIVCSDLPLPFMAAQIADSIHQIEEYSYASNLQLPNKGPYNVTIDLSV
NLNKQLYQDRFEWDMNQNEVTPEIFAEIVVADLGLSLEFKNAISHALHEIIIRVKKEVIDGTFDNE
MHNHLHLVKGIMFEQGI RIFTENSQNGNDRWEPLVEVLTSSEIERRENERVRNLRRLKRENMRRDY
DDHSRRRQAGKRRYDELEGAWV

YLR325C_homolog 737bp PathoSeq: 1..737; CDS: 501..734 (SEQ ID NO 407)

AAGAAAAGTATAGTCAAATTTGTTATACAAGCTAAGGAGCCATAAACTTTCTTTGGACATGCTAATA
TCGCTCCTGACCATTGTTTACTATATTCAACAAAACGAATTCAACAAGGCAAACGAAAGCTACATG
AAACTAAGTATCGGCAACGTCTGTTGGCCAATTGGGGTGGTCAATGTAGGTATTTCATGCAAGAAGT
GCAGCACTGAAAATAAACCAGTGCCTCTAACGTCAGTTAACATAATGCTAAGCGAGTCTACACGAAGA
TGGATTATAAGTATAAAGAGGTTGATTAGTTTTAAAGAGAGAGTATATAATAATGCACGTGATTAG
TTTAGTAATTTTTTGGCAGTTAGGGCTATAGCCCTAAGACATTCACACAATAACAAAAAGGAAGT
TCTCACGCACATAACGTGTAACCCACATAAAGAAAGAAAAAAATTTCTTTGAAAAAATTCACA
TCACGCTTTAACCCTTCAACCTATAACAACCTCAACCATGGCTAGAGAAATCAAGGATATCAAAG
AATTCGTGCAATTGGCTAGAAGATCAGACATCAAATCTGCTATTGTCAAAGTTAACGCCAAGGTCA
ATGCTAACCGTAAAAAATTCAAACAAACCAAAATTCAGGTCAGAGGTTCAAGATACCAATCACTT
TAGTTGTCAACGATGCTTCTAAAGCTAAAAAATTACAACAATCTTTACCACCAACCTTAAAAATCA
CCAACCTGTAA

YLR325C_homolog 78aa (SEQ ID NO 408)

MAREIKDIKEFVELARRSDIKSAIVKVNKVNANGKKFKQTKFKVRGSRYQYTLVVNDASKAKKLQ
QSLPPTLKITNL

YLR344W_homolog 1348bp PathoSeq: 1..1348, exon 1: 501..515, intron 1: 516..979, exon 2: 980..1345 (SEQ ID NO 409)

ATACCATGACAAGCAAGCTCAGGGTCGCGGGTTCGAGTCCCGCGGGGAGCTAATTATACCCTCATT
TTTGAACCCACCAAATTTCTTTTACATTATAATGAAATAAGAGTATTCCTGGCTTCTTTTTTTT
TTTTTTTTTGGCAATATAGAGAAGACTGTAATAAGTATAGCTCACTAAAAGTCTTTTTTTTCTATT
CGTTTTATATTTTTTTAAGAAATTTGATGTTGATTGGTAAATGCCAAATTTTAAATGTGTGTTAG
GGCTATAGCCCTAATGTACTGTATATGCAGTATCAGAAATACTTTTGTACGCACAGTTTGTCTTA
CCAAATACATTATATATATATATTTTTTTTTTTTTTGGAGTAGAGGAGCTACACTAGACCACAGTGCG
AAAAATTCATCTCTCTATACACTTACTCAATTTGAAGATATTCAAATTTTTTTTCAAAAAAAATTC
CTTTTGGATCGATACTAGATAGCATATAATCATCAAAATGGCCAAGATCAGTCAAGGTATGAAAT
AGATATTCAATTAGATATGGAGAAAGGAAGATAAAAGGAAAAAGAAAAAAGAAAGAAATAA

FIG. 2 - 45

AGGAATATATACATTGAAAAGGAGATAGAACATCAAACAACCACTTAAGAATTAAGTTTAAATAC
AGTTTCAATAAAGAGGGTTTTTTTCTCAGAACAAACCACTTGACTGAAGTACTACACCAAGAAGGTA
TAATGATTTTACGATTTACCTGAATATAAAGAACATCCTTAATATTGAATTTCAATATTAATAAATA
CAATTTGGGGATATTGATGAAATTATGTATAGGAGATTCCATTTTTCAAACCTTGTTGAATGGAAAA
CTTGAAAAATCAAATCAAATCAAATCATAACCCCTTCAATATATTCCCTTCCTTATCTTACTTTTCCT
ATTAATAACAAAGACTAAGAAACATTCAGTAAAATACTAACAAAAATTCATTTATATAGACGTTTC
TTCATCTCGTTCTAAAGCTAGAAAAGCTTATTTCACTGCTTCATCAGTTGAAAGAAGAGTTCTTTT
ATCTGCTCCATTATCCAAAGAATTAAGACAACAATACAATGTCAAATCTTTGCCAATTAGACAAAA
TGATGAAGTTTTAGTTGTTAGAGGTTCTAAAAAGGTTCTGAAGGTAAAGTTAATTTCTGTTTATAG
ATTGAAATTTGCTATTCAAGTTGATAAATTACAAAAAGAAAAATCAAATGGTGCTTCTGTTCCAAT
CAACATTCATCCATCTAAAGTTGTCATTACTAAATTACATTTGGACAAAGATAGAAAAGCTTTGAT
TCAAAGAAAAGGTGGTAAAGCTGAATAA

YLR344W_homolog 127aa (SEQ ID NO 410)

MAKISIDVSSSRKARKAYFTASSVERRVLLSAPLSKELRQQYNVKS LPIRQNDENVLVVRGSKKGS
EGKVN SVYRLKF AIQVDKLQKEKSN GASVP INIHP SKVVI TKLHLDKDRKALIQRKGGKAE

YLR393W_homolog 1631bp public: 1..1207/1209..1631, PathoSeq: 1208;
CDS: 501..1628 (SEQ ID NO 411)

TTCATCTTTTCGAAATCTTCCCTCTTGGAACGACCAAGAGTTGGATTTCGGTGCCCTTGACTAGCAC
AACTTTGTTCAAATCTTTATTGAATAATGCAACACCACGAACCGGTATGGTCGATTTATATTTTCC
GAATTTAGATAATGCTTCTCTGTGGGTCACCCCATTTCCAAATAAGCGGGCATTTCTCTAAAATCTT
TGTACTGAACGTCTTTCATCTTCATGCTTTTGCAAATCGGGATTCAACTGACGAACAAAGTCAGCATA
AAACCATTGTGCTTCTCAATCTGAAACATTATTCTTTCAATGGAAGATAAATCCTCTTCGGGAAC
ATTACCACAAATCTAATAACAAATCTTCCAACACCCGATCTAGAGTTTGATTAGCTAAACCATT
GCGTAATTGGATCGACATATCTTGTATTCTTCTATGATTAATCTTTCTTTTTCTTTCTTTTCAC
TGAATATTCGTAATTAATAATTGATTCAAATTTGATTGATGTTTGTATACTGGATAAAACAATTTGT
GTGAGATCATTCAATGTATTGCTGGCGGAGAAGGAGGCAAGGACGAACTTTTTCTCTCATACT
TTTTTTTTTCTCTCTCTCTTTCTTTTCAGTCACATTGTCTGAGTGTTAAAGGCTGGCTTTCTGTG
CTGAACCTTGTGGACTGGTAAACGCACGACATAGAGTAATATTTGGAGAAACCAAGAATTTTGA
AAAACCGTGGTTTGAATTCGACCACAGATTGGTTGGACGACAAAATGCAAAGTGATTATCCGGA
CTTTTGCTACCTCAAGAATAGAGTTCCAGCGGTACCAGCCGCTTTTGTAAATACCATTAAAGAAA
CGGTCAAATCGGCACAAGAAAAGTCGTACAGTATTACTAGACCATTGGGGTTGTCAAAACCAGTTT
TGTTAAATCATAAATTGTCAGACACATACTCATTGTCCAATATATACGAGGAGTTGTTTGGTCAAA
AATCCAAAAGAAAAGACAGAAAACAAC TAGACTACGATTGAAACACTCGCCAATTTATGAAGTCA
AGTCATTTGAGAATACAAAGGGGAAAATATTTACTCCTCTCTGTTTCGTACTTTTCGACAAGACAAAT
CTTTGTATTTCCCGGATTTTATAGCGAAAACATTGGCAGGTAATCAGAGAAGTTTGTACGACTCAT
TAGACAATAGATTAAAGCATAGTCAAATTGTTTTCTTCTGTTGCTGGTGAGCAGTGACCCGTTTCGT
ACTTTAAGGTTGAAAACAAAGATTACTATTCCAGGATTATGATACCTTTGTGGAGGAATATCCCC
ATACCCAGATACTTGATGTGAATATGCCGCAAAGTTGGATCAAGGGGTTTGTGACAACTTGAGCA
CAGGAAATTTAAGAAAGACTTTGAAGCCAGCTCTGAGATACGAGAATTATTTTCTCTTGCTGGCC
ACATAATGTGACGGGAAATTAGAGAACAGTTGTACTGTGATAATCAATGTTCCGGGTATATTTATA
TTGTTGATTGATGGGGAAGATAAGATGGGCGACAAGTGGGTATGCAACTCCTGAGGATTTGAAAT
TGATGTGGAAGGTTGTGAAAGGGGTGCAAAGAGAAATGACCAAGTAA

YLR393W_homolog 376aa (SEQ ID NO 412)

MFVYWINNLCEIIQCICWRRRRQGR TFFPSYFFSLFFQSHCSSVKGWLFCAEPCGSVNARHRV
IFGETKRILKNRGLNSTTDWLDDKM QS VFIRTFATSR IEFQRYQPRFVNTIKETVKSAQEKSYSIT
RPLGLSKPVLLNHKLSDTYSLSN IYEELFGQSKERRQKQLDYDLKHSP IYEVKSFENTKGKIFTP
PVS YFRQDKSLYFPDFIAKTLAGNQRS LYDSL NRLSIVKLFSSVAGEQCTRSYFKVENKDYYSQD
YDTFVEEYPHTQILDVNMPQSWIKGFVTNLSTGNLRKTLKPASRYENYFILPGHIMS AEIREQLYC
DNQCSGYIYIVDSMGKIRWATSGYATPEDLKL MWKVVKGVQREMTK

FIG. 2 - 46

YML063W_homolog 1271bp PathoSeq: 1..773, public: 774..1271; CDS: 501..1268 (SEQ ID NO 413)
CCAGTGCCTTTTGTGTTTCCACATCATACTTCACTGAACTAAATAAGTTTGTGTTACATTTT
GAGACTTCAGGTACGACCCAGGGTTGCGACAAAGTTTAGGTAGTTTGTCTGCTGAATGTCGCAACA
AAATAGGCTGTAGCCCTAGTCATGTGATGTGAATTAACATAACAAGAAGATTGCTGGTGCACAA
AAAGATTATGTGATTTTATGTGCGTTGTTATCCTGCACACTAAAATTGAGCAGTGACACACACA
CATATTGGGCTGTATTTTATTCTTGTGTTTCTGCTGTTCTCTCACTGTTAAGCTCTAAGTGAATT
TGTGTGTGCTGTAATAGTGTGTGTGTTCCAAGTCCCAGCTCTCACAGATACTCACGCACGCCATA
CTACTGAAAATTTCTGACTTTCTGTATCTAAAAATTTTTTACTAGGAATTTTTTTCTTTTACGTT
TTTCACTTGTTCATATAATCACCAACTCAAGTACAACATGGCTGTCCGTAAGAAACAAGAGATTGT
CCAAAGGAAAGAAAGGATTAAAAAGAAGGTCGTTGACCCATTACCAGAAAAGATTGGTTTGACA
TCAAAGCTCCAACCACTTTTGAAAACAGAAATGTTGGTAAAACTTTGATCAACAGATCTACCGGTT
TAAAGAAATGCCGCTGATGGCTTGAAAGGTAGAGTTTTCGAAGTTTGTGTTGGCCGACTTACAAGGTT
CCGAAGACCACTCTTACAGAAAAATCAAATTGAGAGTTGATGAAGTTCAAGGTAAAAACTTGTGTA
CCAACCTCCATGGTTTGGATTTCCTTCTGACAAATTAAGATCATTGGTCAGAAAATGGCAATCAT
TAGTTGAAGCTAATGTCACTGTTAAAACCTCCGACGATTACGTTTTGAGAGTTTTTGCCATTGCTT
TCACCAAAAGACAACCAAAACCAATCAAGAAAACCTACTTACGCTCAATCCTCTAAATTGAGAGAAG
TCAGAAAGAAGATGATTGAAATTATGCAAAGAGAAGTTTCCAACCTGTACTTTAGCTCAATTAACCT
CCAAATGTATCCAGAAGTCATTGGCCGTGAAATGAAAAATCCACCAAAACCACTTTCCCATTTAC
AAAATGTCCACATCAGAAAAGTCAAATTTGTTGAAACAACCAAAATTCGACTTGGGTTCCATTATTGG
CTTTGCACGGTGAAGGTTCAACCGAAGAAAAGGTAAGAAAAGTTTCTTCTGGTTTCAAAGATGTTG
TTTTAGAATCTGTTTAA

YML063W_homolog 256aa (SEQ ID NO 414)
MAVGKNKRLSKGKKGLKKKVDPFTRKDWFDIKAPTTFENRNVGKTLINRSTGLKNAADGLKGRVF
EVCLADLQGSSEHSYRKIKLRVDEVQGNLLTNFHLDFTSKLRSLVRKWQSLVEANVTVKTSDD
YVLRVFAIAFTKRQPNQIKKTTYAQSSKLREVRKKMIEIMQREVSNCTLAQLTSKLIPEVIGREIE
KSTQITIFPLQNVHIRKVKLLKQPKFDLGSLLALHGEESTEEKGKKVSSGFKDVLVLESV

YML128C_homolog 1517bp public: 1..1499, PathoSeq: 1500..1517; CDS: 501..1514 (SEQ ID NO 415)
TGATATGGATTTTCAAACATAAGAAACAATACCAACTACAACAACAAGAAACATAAGTGTTTGCT
TAATTCATGACCTCGAGTCATATCCCACGTTTAAAGTATGAGTGTTTTACGAAGTTGTGGATCC
TATTTTAAATAAAACAATAATAGTAATAAAAAAAAAAACCTTCTTTGCTTTTCGAGAATTTGTAAC
ACATTGTTTCTTTCTTCCCACAGCAACCAATTTTATTTTATTTTTCTTTTGGGACTTACCCACA
GTTGCTCAATTATGTATAACAAGGGTAGAACTCTGTGGGATTCCTCCTTAAAAATATAGCAATC
CTTTTCTTCAACGATTGCTATATGACCCCCCCCCAAGCATTCAATGCTTTTATATATATTTA
ATAATGTATTTCTTGTTCAGGATAATTATCACTATTTGTGACGTTTAAATTTTACATTTCTTCT
TCTTCTTCTTCTTATTTCAACATTAAAGAACATTTAATATGTATTTCCCAATCATTTGTATGGTTAT
ATGTATCTATCACTTTTGTGGTTGCCAATTATGGTTTTGATCAATGGACAAATGATGATTTAAAC
AATTTTAAAGAAGCTAAAGTTGCATTCAATGATGCCTTGAGAGATCCAAAATTAATTAGTTTGG
CTAATGAAGAAGCTAAGAAATTAGAAAAAGGTTACAAGAAAGTTACTGAAGAATTAATAACAATT
TGAATCCTCCAGATGATTCATTAATGATTATTTGAATTTTGATTACTTATTTGGGAAAAGAAAAG
AAAATTATTCAATTAAGAATGGATTTTGAAGTTGGCCAGTAACCAAGTTGCAAACTTTTTTAA
CTCAAAATAATATCCAATATAGTGCAAAGGATACCAAGATGATTTAATCAATAAGGTTAAAGATC
AATTTGATTCTATTTCTAAGAAAAATCATGGGTCTAGTTTTTATCCTGGCAATTGGTTATATGAAT
CTTGGTCAGAAAATGATTTGAAAGATTGGTTGAAATCTTATGGCATTGAATTTAATCCTAGTTCAA
CAAAGGATCAATTGGTTGAAAAATTAAGAATTTAGTTATCAAGCCACTCATTCATTAAGAGATT
CCAAAGAATCTTTATTTGATTCAATGGATTTATTTGATAAAACCATTTTGTATAAAAAAGGTCAAA
TTGAAGATGAATTTTCCAACTTGGTCATATTCTCAATTACGTGAATGGCTTTATTTACATGGAT
TTATTGACACTAAACCAGGAATTTACGTTGAAGATTTGGATAAGGAAAAATTAGTCAAGATTGGCC
AAAGTTATAAGAAATGTTTGTGAGTGACATTCATACTTGGTTGGCAACACTGAAAAGAAGTCTC
AACCTTGGATCACAAGGGAGAACAAAAGTCTCAGAAAAAGAAGGGTAGTAATTTGATTAATGATA
CATTCTTTGTTGGTATTAATAATTGGTCCAAGGATAAATGCGTGAATTGGGCAATCTTGACTAA

FIG. 2 - 47

YML128C_homolog 338aa (SEQ ID NO 416)

MYFPIIVWLVSITFVVANYGFDQWTNDDLKQFLKERKVFNDALENPKLISLANEEAKKLEKGYK
KVTEELNNNLNPPDDSLNDYLNFDYLFGRKENYSIKEWIFESWPVTSLQTFLTQNNIIOYSKDTK
DDLINKVKDQFDSISKKNHGSFYPGNWLYESWSENDLKDWLKSYGIEFNPSSTKDQLVEKLKEFS
YQATHSIRDSKESLFDSDLDFDKTIFDKKGQIEDEFFQTWSYSQLEWLYLHGFIDTKPGIYVEDL
DKEKLVKIAQSYKKCLLSDIHTWLANTEKKSQPWITKGEQKSQKKKGSNLINDTFFVGINNWSKDK
LRELGNLD

YML130C_homolog 2243bp public: 1..829, PathoSeq: 830..2243; CDS:
501..2240 (SEQ ID NO 417)

ATGAGTTCATAGATGATCTGTTTCACTTTCAAATAACGTGTCAACAAAAATAAAGTTAGAGCATAG
ATTTTGGCCGCACTTGTACAGATGGATAGAATTGAATGCAAATTCGCATAAAGATTAAAGTGAAA
AACAATTTCCGAAAAAAGAAGAAAAATCGAACACATTGAGAAAAAGAAACGAAACAAAAAGAAAAAAT
TTCAAATTGTAGTTGCATGTATATAAAATAATATAAAAGATATATCACCAGCACAACTGATTACTT
TTTATTTATATCACCTGTCAACAACAAATTTCCAAATAAATACAACTCAGAAAAACACTTACTAT
CTTTTCTTAGTTTGGTTTCTATAATCTTATTAACATTTCTTGCCTTTCATCCTTGATTATCATATT
AGATCTTATCTTTAATTTGTTTGAAAAATAATACCAATAATCTTCCCATTAGAACTTACAACACA
ACAACAAAAAACCCATTCTAAATCACTATTCTCCATTATGAAAAATTTTCAGATTATTTTCACTAC
TAATCGTACAATTTATCATAAATACCAGTGTGTCAGTATCACCTGTGTCAGCAGTTTACCAAAAC
TGAGTTTTCAGTCCATTTGATTCCACAGAATTTTGTTCACAGATCATAACTCCCCTTGTAATACAA
CTTTCACCTACATTGATGAATTGAATAAAGATATTCGTCCCTACTTGTGCGGAATTAGTCAAGACCC
TGTATTTCCGTTATTTTAAAGTCAATTTAGATAAACAATGTCGTTTGTGGAATGCTCAACATTTT
GTGCTAGTGAAACTGTGCTGTTGAAATATTGGAAGATTTCAATTGGAGTCAAGTCACCAATGAAA
GTTTGAAACCTTCAGGATTAGGTAAGATTTTCAATACCTGACAAATCATCAATTGATAATTCATTG
AAACCGAAGAAGTTCAAACCTGTGAAGATTTAGATTATAGTGAAATAGATGATGACCATCATTTGTG
TTTATGTCAACTTGGTAATAAACCAGAAAGATTTACTGGGTATGGTGGTAATCAAAGTTTGTGATG
TTTGGAAGGCTATTTACCTGGAAATTTGTTTCCCTAATACTAATCCAATGTCAGTGACAAATGATG
CCGACAATGGTGGTGAACAATGTATCGAAAAGAACTTGTTTTATCGTGTGTTAGTGGTATGCATG
CTTCAATTGCAGTACATTTATCAAGAGAATATTTGAATTCGAAACTGGTGAATTTTATCCCTAATT
TAAAGGTGTTTATGGAAGAGTAGGTATGCATAATGACAGATTATCTAATATTTATTTCAATTATG
CCTTAGTGTCCCAAGCTATAGTTAAATTGAGTGAAATTTTACCATTGAGAGAGTTCAATCAACTGG
GGTATGATGACATTTACTCCAGCTCAAAAGCAACATTTATTGGCTAATAATGATGTCGAATCAGTCG
AAGTTTATGATCGTTTGTGTTAGATGACATTATTCCTAGTTTGGGAAGCAAATGTTGTGTTTAATA
CTTCCAACCTGTTTGTGATAATAGCAATTTGAGGGATGAATTTAGATCAAGATTTAGAAACATTTCTG
CCATTATGGATTGTGTTGGTTGTGATAGATGCAGAATGTGGGGGAAATCCAAACCATTGGTTATG
GTACCGCTCTCAAGATTTTATTTGAAGATGACAACTATGATAATCACAATTTGAAATTTAGAAGAA
TTGAAATTGTTGCCTTGATTAATACTTTTGATCGTTTATCTAAATCTATTGAAAGTATTAATATGT
TTAAAGAAATGTATTTGCAACACCTTAAAGATATTGCTGAAGGATTAACCCAACCTGGTGTTTACG
ACAAAATACAAAACAACAAACCAGGTAACGGATTTGCCTTCCCATTGTAGTCCATTACCTCAGA
AAAAACCTGACCAACCAACACCCCCAAAAATCAACAACAAAAACAACCTCAAGAACTGACAAAA
AAAGACTTACATTAGAAGAAATTGCCACACAAAACCTGAAGATCGAACTTTTATTGAAGACTTCA
GATTATCCTTTGATGAAGTTTGGCAAGCATTAAAGATTTGTTTAACTAGTTATCAAAGATTCCCAG
CCGTATTGAGTAGATTACATTGGTTCAATTGAATGAATGGTGAATAAATTGCTTGGTAAACCAA
CAGTTTATGATTACCAAAGTTCTTTTGATGTTGATGCCCTACAATACAGTCAAGTCCTTGGATAA

YML130C_homolog 580aa (SEQ ID NO 418)

MKIFRLFSLLIVQFIINTTVAVSPVSAVLPKSSFSPFDSPEFCSQIITPTCNTTFTYIDELNKNDIR
PYLSELVKTSYFRYFKVNLDKQCRFWNAQHFCASENCAVEILEDNFWSQVTNESLKPSSGLGKISLP
DKSSIDNSIETEEVQTCEDLDYSEIDDDHHCYVYVNLVNNPERFTGYGGNQSFVDVWKAIYSENCFPN
TNPM SVTNDADNGGEQCIENL FYRVVSGMHASIAVHLSREYLNSETGEFYPNLKVFMERVGMHND
RLSNIFYNYALVSQAIVKLSEILPLREFIQSGYDDITPAQKQHLNNDVESVEVYDRLLLDDIIP
SLEANVVFNSTNLFDNSNLRDEFRRFRNISAIMDCVGCDCRCRMWGKIQTIGYGTALKILFEDDNY
DNHNLKFRRIEIVALINTFDRLSKSIESINMFKEMYLQHLKDIAEGLTQPGVYDKIQNNKPGNGFA

FIG. 2 - 48

FPFVSPLPQKKPDQNTNPKNQOQKQPQETDKKRLTLEEIAHTKPEDRTFIEDFRLSFDEVWQALRF
VLTSYQRFPAVLSRFTLVQLNEWNNKLLGKPTVYDYQSSFDVDALQYSQVLG

YMR022W_homolog 1004bp public: 1..507/668..1004, PathoSeq:
508..667; CDS: 501..1001 (SEQ ID NO 419)

TGTGAAAAAAATTGTGGTGTGGATGTTGTTGTCGTTGTCGTTGTCCACAACAAAAAACAAGT
AACAATTTCAAAGTTGGGCTTGGAGATCGATTTTTTTTCCCGCTCTGTGTGGCACGAGACAATTG
AGTCGACCAGTACGTTTAAATTGAATACGAGAGTCGACGCAATTACATCAATCCAACATTCCACTT
ATTCTATATCAATGTAAAGTCATTTTTTTGATAATATCGTAATTTACACATTTCTGTATATCTCGGCA
ATAGGGGGGATAAAAAATAGTATTGACTAATTAATATATCTTGTATTATCAAATCAGGAGTATAGAA
TTCCACCCAACAACCTAGATTTTCCGAATGCGAAACGACGAGGACGACACAACAACGACTAAAGAAG
AAGAAGAAAAAAATATAAATAAATTGATCAGCACACATTAGAAACACAATATTGGATCACTTTT
TTCTGATAATACTACCACCACACAGCTCATTCAACCATCATGCCCGAAGTTCTACTGCTCAAAGC
TTTTACTAACAGAGTATCAACAATTATCGAGGGACCCACCACCTGGGATAATCGCAGGACCAGTGA
GTGAAGATAATTTATACAAATGGGAATGTTTATTAGAAGGACCATCCGATACTCCATATGCAAATG
GAGTATCCCAGCAGTATTGACTTTCCCTAAAGATTACCCATTATCACCACCTACATTAAAGTTTG
ATCCACCATTGTTACATCCAAATATTTATGCTGATGGAACCGTTTGTATTTTCGATTTTACATCCTC
CTGGTGAAGATCCAAATCAATATGAACGACCAGAGGAAAGATGGTCACCTGTGCAAAGTATTGAAA
AGATCTTGTGTGAGTGTCTATGCTTGCAGAACCTAATCCTGAAAGTGGGGCTAATATCGATG
CTTGTAATTTATGGAGAGATAATCGTGTGAATATGACCGACAAATTAGACAACATGTCAAGGAGT
CATTAGGATTATGA

YMR022W_homolog 167aa (SEQ ID NO 420)
MPRSSTAQKRLLEYQQLSRDPPPGIAGPVSEDNLYKWECLLEGPSDTPYANGVSPAULTFPKDY
PLSPPTLKFDPLLHPNIYADGTVCISILHPPGEDPNQYERPEERWSPVQSIEKILLSVMSMLAEP
NPESGANIDACKLWRDNRAEYDRQIRQHVKESLGL

YMR118C_homolog 1031bp PathoSeq: 1..1031; CDS: 501..1028 (SEQ ID
NO 421)

CTACACAAAGCTTCGAGAGTTTTTTTTTCGTTGCAGGGGTGGGACAGGTGAGTAACGAATAAAACGT
CGATTGTCTTTTCTTTATGATTGTTCTTTAACGGAATTGTGTTCTTTAAACAAAATCAGTTCTGC
ACGTGATATAAATCTCCTATCGCTAGTAGTAAGTTTAAATTTTTTTGATCAAAGTACACTCATCAG
TCTATTGTCTGATGTTTCGCATACCTTGTGATAATATCTGGTGTGTACACTACTTTTTTGGTTTGT
TTGTAAATTACAATTTTTCTATTGGTTAAATGATAATTGTTAACAAGTCTTTTTTTTTCCCGGGA
TTGAATCCGGAACTACCATTAATTCACCTATTCTACTCACTCACCTTACACCCTCACTCACTCAA
ACAATTATATCAACCAAAAAAAAAAATCTTCACTACACCAATAACAAAGAACCAATAGTTCAAT
CTAATAAACCATCTTCCCCCTAGCCTGCCACAACAACATGATTTCTCGTATTGGATTATTGAAAA
GACCTACCGTGTCCACTTTAAACAACATATGTCAAATTACAATCGACATTAGCCCTTAAAAGATACA
CATCAACCGTACCAGCAACTTCAAATCAAGAACAAGAAATATTGGTTGCCCAACGTAAAAATAGAC
CTACATCACCTCATTTACAAATTTATGAACCACAATTAACCTGGATCATGTATCATATTCCATAGAA
TCACTGGTGTGTGCTATGGCCGGTGCCTTTTATGCTTTAACTTGTGGATTGTGCTGCTACTTCAATTT
TAAATATTCCATTTGATACTACTACTTTAGTATCTGCATTCACCACATTACCAACATTTGCTCAAT
ATGGTATCAAAGCTATTTGTGCTTATCCATTTGTTTATCATATTGGTAATGGGATTAGACATTTGG
TTTGGGATTTTGGTAAAGAATTAACCATCCCTGGTGTATAGAACTGGGTATGCTGTTTGGCTG
CTACTGCTGTCTATTGGAAGTTATTTAGCTTTCTTATGGTAA

YMR118C_homolog 176aa (SEQ ID NO 422)
MISRIGLLKRPTVSTLNNYVKLQSTLALKRYTSTVPATSNQEQEILVAQRKNRPTSPHLQIYEPQL
TWIMSSFHRTGVAMAGAFYALTCGFAATSILNIPFDTTTLVSAFTTLPTFAQYGIKAICAYPFVY
HIGNGIRHLVWDFGKELTIPGVYRTGYAVLAATAVIGSYLAFLW

YMR230W_homolog 1176bp public: 1..1176; exon 1: 501..551, intron
1: 552..870, exon 2: 871..1173 (SEQ ID NO 423)
AAAAGCAAGAAGAGAAGGACTCGTTGGCCAATTTCTTCGGCAATTTCAAGAAGAAAAGAGTAGCTG

FIG. 2 - 49

TTTAGAACTATATATATATGTACTCGCGCTTTAATGTTTATAGCAATAATGAAATGTTTAAATAAT
TATTTAATCAAACCTGGTTGTAACCTTATGATTATGGTAGTGATCTAAGAACACAACCTTGCAAAGCA
ATGGTAGTTTCTTTGATTTTGTGTTTCTATTAGATTCTGTTTCTATTAGATTCCCGCTTTTTTTT
TTTTTGCAGACATTAAACCTCAGGGCTATAGCCCTAATGGCAAAACATGCACGTGTATGTTTCTTG
ATTTTTCTACACTACTAGTAAAAAATTTTCTTTCCGCTCACTATTCACACATACACTCTTTTTTCG
CACAATTACAGTCTACCAACAGGAAAAGAAAAAAGGAATCTGGTAATTGAAAAATTGAAGTT
TGGTTCTTTAATACTATCAATCAACTAGAGTCACAGCATGTTAATTCAAAAGAAGACAGAAAAGA
AGATCCACCAATACCTCTTCCAAGGTATGTAAATATGAATTATAAACTGGAACAGAATATGGCATT
TCAAGGGATGCACGATAAGTCAAGAGTTCATGAAAAAGCACAGATTATAACAGTCGTAAAGAAAAA
TTTCACTACCAACAACAATAAGAAGATATCAAAGAGATTCAAGTAATCACTACTTACAAGAAACATA
TAACATCATGGAGAGTTTAATTTGAAATACGAATGAATATACAAATGAACTATACCCTTTTTATGG
CCATATCACGTTTCAAGAAATATTTAAACAAAAATAAAATGAAGAATAAACTTGGATATACTAAC
ACATGTATTATAGAGGGTGTCTGTTGTTGCTAAGAAAGACTTCAACCAACCAAGCACGATGAAATT
GATACTAGAAACTTGTTCGTCATCAAAGCTTTACAATCTTTGACTTCTAAAGGTTACGTCAAGACT
CAATTCTCATGGCAATACTACTACTACACCTTGACTGATGAAGGTGTTGAATCTTGAGAACCAGAA
TTGAACATTCCAGAAGGTATCTTGCCATTGACCAGATTGAAGAATGCTCCAGCTGAAAGACCAAGA
CCATCAAGAGGCGGTCCAAGAAGAGGTGGTTACAGAGGTAGAGCTAGAGACTAA

YMR230W_homolog 118aa (SEQ ID NO 424)

MLIPKEDRKKIHQYLFQEGVVVAKKDFNQPKHDEIDTRNLFVIKALQSLTSKGYVKTQFSWQYYYY
TLTDEGVEFLRTELNIPEGILPLTRLKNAERPRPSRGGPRRGYRGRARD

YNL054W_homolog 2840bp public: 1..2197/2199..2840, PathoSeq: 2198;
CDS: 501..2197 (SEQ ID NO 425)

TGTTGGGAGTATTCTGGCACAACAACTACTTTTAGGTTACTAACATTATTTTTCTTCAGCTA
ACTAATTATCTAGTTTATATCTATATCCATTATTGTTGAAATCACTATCGTGAGGTAAATAACAAC
TACAGAGTTGTACAGTATCCAAAAAACTTTGTACCTATCAATACATTTTAAAGCAATAGGTCAT
TTATTGCTGTAATCAAGTGTACCAGTATCTCTAGTTAATGTTGAGTTTATACCTAAAACATGAAC
TATATCAACTTTAAATGCCCTAATCACGTGATACAGCACATGGGAATTTGCTGCTTTGCTTCCT
TGCACGTACACGGCACATGTACACGACTTTTTTTTTCTAAATATTTTTTTTTTTGTTGTTGTTA
TTAAACAATATTATTTTCATATATATAATTGCTTAGTTTACTTGCTTCTTACACCCTTTGCATATT
TTTTTTTTTTTCTTTTCTGCCAACTTGATCAAATTCGATGCTACATCCTAATAATTCAGTAGTCG
ATATGTCTAGCACTGGAAACATGAATGAAATACAGATGCTCCACCGAAACAGCAGACGAAAAAGA
AAATATCAAAACAGAATTCAACCAAAACCGATTTTTTTGCTGCACGATTGGCTAGTGCGGTTGACG
ATATAGAAAGCAGTGATAGTGATGAAACGTTTATATATGAGAATAATGATACCTGAACTTGATGATA
ATGCTAGTAATATTAACAATAACAACAATAACAGCACCAATAACATTATCAATTTAGATAATGCTA
GTGTTAACGGAAGTATGATTGCTTCATCCAATGCAATGGTGAAGTCCCTCCCGGAACATCGATAG
CGTTAGGATCGGGCCTTCGATCGCCATCCATACTAGAGGGGAACAGCTTCAATATTTTCATGACC
CAGTGAGGCAACAACAGTTCAAACCTTCCTTCTACCAAGGCTCCGTCAATTTCCAACCTCCATCAGCA
GTTCAAATAATATAGATTCAATACTTAAACGACCTGTACATCTACGTGAGGCATCAACGTATTTCAG
TGAATGATAATGACCACCGAAATCTTGTTGCTACCAAACTCAACTGAAAGGTTTACTGCTTCACCTT
CGAACAATATTGGTAATGAAAAATATACCTCAATACCAGAAAACTAGTAGTGTGCCCCTCAATCA
ATGAAGGATACAATGATGATACATTTTCATATAATGAAGTTGAGGATAATTTAATTGATGAAGATT
CCACGGACGATGGGGATTTGACAAAAAATACCATTACTAATAACAACAATCCACCAACCACGTCGA
GCCAACAGCAACCACAACCGCAACCACAGCCGCAACCACAGCAACCACAACCTACATACTCTGTCTC
CTCTAAATCAGATACAAGCAGCGACATCAGCAACACCTTCTGTGTCCACTAAAAACGCGTCTAAAA
GAAATTACAAAACCTCATCCACTTCCCTCAAAATTAAGATCAACTACATCAAAACCTTTTCGATAAAA
AAGGGTCACAACCAAGAAGATACAGTACCATTCTCTGATGATATTGACATTGAAGATTTTCGATGATG
AGCTTATATACTATGACAACACAGCTAGGTTCCCAGCGAACGAATCAACTTCATTACTAAATCAAA
ACCAAGAATCCCCCATTATAGATCACTTAATTTGAATTTCCCTCAGGTGAAGCGCCAAAGCAAGC
GTTATTTGTCAACTGGCCAACCTTTAGAGAGTTCTGATCGTGGCTCTAACAAAGATGGTACTGATA
ATGGAAACAACAGTGATCACAATATTAATTCCTTTGACTGCTAATAATAATAATAACGTCA
ATCACAACGATCATGGTGATAACAAAAAGAGTAATACCAACAACAACATTGCTAATAATAGAG
CATTTCCATTTCTTATCAAGATCAACAACATCATTATTACTACGACTACGATGATTTTGACCAAG

FIG. 2 - 50

AATCACAAATCAATGGACCCAATTTTGATTGGCCAGACCTCCCTATAAACAGATCAGCTTCACGGA
ATTTTAAACAACAATAACCCCAAAAGATTGGCGACAGTCATTTTTTCTACCAAGAAAGACAG
ATCAGTATAGTCAAAGAACAAGCTTCTAAAGTCATGCATTTATACCTTTGTTTGTATATTAATTG
TGCTTACCATAGGGTTTGTATTGGGGTTTGTTTTGGCCACAACAAAAGATTAACTGATGTAGGTA
TCACATCCATTGAGAACCCCATTTGTAGTAAAGATGAGTTAGTTTTCATGTTGTTATTGAAGCAT
TTAATCCAGGGTGGTTTCCGTTGACATCAATGAAGTAGAGTTGGATTTATTTGCAAGAAGTGGCT
ATCTACCTGATACAGATAATCTGAAAATATCTAACATGGGAGGGTCACAAAAGTAGAGACGGTTA
AATTAGGAACGATTTTGAATTTGAATCGGTTCTCAATTTCAAAGGTGGGTTTCTCTCTCGAGAAC
CGACAATTCAAAGGGAGGAATCCGATTATTATATCTCTGGCAAAAATGTTACTGCCGAGGCTAAAT
TGGTTGTAAATATGGCTGATATTAAATAGCTGCTTCCAATAGCATTGCTAAAGAAAGCACTACTA
GTAATGACACCAAGATAATGACAACCTCAAGAAGTGGGAAATCATATCAAGCAATCCATTGATT
TGATTATAACTGGAGTATTGAAGTATGATTTACCATTTTCAAGAACCCTCAAGATCAGTCGGTTA
GAAAACTGGGTATATTGATCCTACCTTATTCGTAATACCACAAGGAGAGAATAATATTTCAATTT
AG

YNL054W_homolog 779aa (SEQ ID NO 426)

MLHPNNSVVDMSSTGNMNTDAPPKQQTKKKISKQNSTKTDFFAARLASAVDDIESSDSDETFIY
ENNDTELDNDASNINNNNNSTNNIINLDNASVNGSMIASSNAMVTGPPGTSIALGSGLRSPSILE
GEQLQYFHDVPVRQQQFKLPSTKAPSISSNSISSNNIDSILKRPVHLREASTYSVNDNDHRNLVLPN
STERFTASPSNNIGNENIPQYQKTSSVAHSINEGYNDTFSYNEVEDNLIDEDSTDDGDLTKNTIT
NNNNPPTTSSQQQPQPQPQPQPQPQLHTSSPLNQIQAATSATPSVSTKNASKRNYKTSSTSSKLR
STTSKLFDDKKSQPRRYSTIPDDIDIEDFDELIYYDNTARFPANESTSLNQNQRIPHYRSLNLN
FPQVKRQSKRYLSTGQPLESSDRGSNKDGTNGNNSDHNINSPLTANNNNNNVNHNHDGDNKKSNT
NNNNIANNRAFPFPYQDQQHYYDYDDFDQESQINGPNFDLPDLPINRSASRNFNNNNNPKRFGD
SHFFLPRKTDQYSQRTSFLKSCIYTFVCLIVLTIGFVLGTVLATTGDLTDVGITSIENPIVSKDE
LVFNVVIEAFNPGWFSVDINEVELDLFARSGYLPDTDNSKISNMGGSQKVETVKLGITILNFESVLN
FKGGFLSREPTIQGGIRLLYPGKNVTAEAKLVNMADIKIAASNSIAKESTTSNDTNDNDNSKKW
EIISSNPFDLIITGVLYDLFPFSRTSRSVVVRKTGYIDPTLFVIPQGENNIS

YNL075W_homolog 1352bp public: 1..136/138..1352, PathoSeq: 137;
CDS: 501..1349 (SEQ ID NO 427)

CCCACAGACCAATAACGTTTACCAACCAAAACCTCTGATATCAATGATTCGAAAAGATTCAATCA
ACCCCGGTTAGCTGTTTGAAGTATTGGATAGCAACACTTTCAATTAGTGCAACACAATCAAATTACC
AATACTTGTTTACCTTTTCATCTGATTCTAATTGGTTCATAGCAATATAGTCTCTTCTGTTGTTTGA
TATTAATATAAAATAAACTTATTTATCACGTTGTTTAGTAGTCTCGCAAATTTGAAACCATGGATG
AGTAACTTGTTGTGTAGATGAGCTCAAATATCTGGTGGAACAATTGTGTAGTAGCTCTTTGATA
AATATCCAAGAACAGTCGTGCAAGTTTCAAATACCATCGCAAAAATCCTAACAAAAAATAAAT
TAATAAAGAAAAAGAAATAATTCTATAATAGCTCATCACAACAATTCGTCTACACTTCCCACCTGAT
TTGTTGGTTTAAATATAATAAGACAAACCTCAGAAGCTATGATAAGAAAACAGGCTAGAGAAAGAA
GAGAGTATCTTTATAGAAAGGCTTTACAGCTTCAGGAATCTTCCTAACAGAAAAAAGACAACAAT
TGAAAGCAGCTCTAGCAAGTGGAAAAATCATTATCAAAGGAGCTTGCCGAAGATGAAAAATTACAAC
GTGATTTTATTTACGATGAAAGTGAACAAATAGAAATTGATGACGAATACAGTCGGTTGTCTGGGAA
TATCTGATCCAAAAGTTGTTATTACCACATCCCGTGATCCATCTGTCAAGTTGCTACAATTCCTGA
AAGAAATCAAGTTAATGTTTCCAAATAGCTTGAAGTTGAATCGAGGAACTATATAATCTCAGATT
TGGTAAGTACCTGTAATAGAGTGCAAGTTTCCGATATGATTTTATTGCACGAGCATCGTGGTGTCC
CATCAAGTTTAACTGTAAGCCACTTTCCTCATGGCCCACTGCGATTTTACGTTACATAATGTCA
AACTAAGACACGATTTGGCAAACCTTGGGAAACGTCTCAGAGTCCTATCCTCACTTAATATTTGAGA
ATTTCCAATCCGACTTGGGTAAGCGTGTGGTTAAAATATTGCAACATTTGTTTCTCCAGGTGTCA
AGAAAGATAGCTCCAGAGTAATAACATTTGTCAATAACGATGACTACATATCGGTGAGACACCATG
TTTACGTCAAAACTAAGGATTCAGTGGAGTTGAGTGAGATTGGCCACGTTTCGAAATGAGATTGT
ATGAAATCAGACTAGGATTACCTGACAACAAAGATGCTGATGTGAGTGGCAGATGAGAAGATTCA
TAAGAACAGCTAATAGAAAGAATTACTTGTAA

FIG. 2 - 51

YNL075W_homolog 283aa (SEQ ID NO 428)
MIRKQARERREYLYRKALQLQESSLTEKRQQLKAALASGKSLSKELAEDEKLQRDFIYDESEQIEI
DDEYSRLSGISDPKVITTSRDPVSKLLQFSKEIKLMFPNSLKLNRGNYIIISDLVSTCNRVQVSDM
ILLHEHRGVPSSSLTVSHFPHGPTAIFTLHNVKLRHDLPNLGNVSESYPHLIFENFQSDLGKRVVKI
LQHLFPFGVKKDSRRVITFVNNDYISVRHHVYVKTQDSVELSEIGPRFEMRLYEIRLGLPDNKDA
DVEWMRRFIRTAIRKNYFL

YNL096C_YOR096W_homolog 1061bp public: 1..1061; CDS: 501..1058
(SEQ ID NO 429)

TCCCTTTTGTTTTTATTTTTTGCTGTGTTACTCCAGAAATGTGCATAATAATGATAATAGTAATTTGT
GACTAATATGAGATGATCGTATGTGGGTGGGTGGGGAGGAAGGGACCCGGAATTCCTAGGAACAGGA
AAAATAAAAAACGAATAAACAAAAACCCCCAATCGGCATGCATCGGAATTCCTTCAGCCCAATTAC
TTTATTTTTTGCCCACTTCTTTTTGGATTAGGGCAATAGCCCTAAAGCTCGTGTTTTAGCCCTTTATA
TGCAGCTCATTTTTATTTTTCTTTTTTTTTTGGCTGTGGTAAACTTTTTTTTTTCGCAGGTG
TTGAAAAAAAATCATTTTTACAGTTTACATTTCTCTAACCTGCAAAAAGCTCTCGTTTTTTTTGTGA
GTGAGAGTTACTCGTTCACAATAGTATACTTTACAGGGGAGTTCTTTTCTTTTGGAAATAGTCAACC
AACAGCAAATAGCCAAGGATCAAGCTTCATCATTAAATCATGTCTCTAAGATCTTATCAGAAAACC
CAACTGAATTAGAATTAAGTTGCTCAAGCTTTTCGTTGATTTGGAAATCTCAAGCTGATTTAAAAG
CTGAATTGAGACCATTAACAATCAAAATCTATCAAGAAATGTAGTTAATGGAGGTAAGAAAAGCTT
TAGCTGTTTTTCGTTCCACCAAGTTTACAAGCTTACAGAAAAGTTCAAACTAGATTAACTAGAG
AATTAGAAAAAAAATTCCCAGATAGACATGTTGTCTTTTTAGCTGAAAGAAAGAACTTACCAAAC
CAGCTAGAAAAGCTAGAAAACAACAAAAAAGACCAAGATCAAGAACTTTGACTGCTGTTTCATGATA
AAATTTTGGAAAGATTTAGTTTTCCCAACTGAAATCATTGGTAAAAGAGTTAGATACTTGGTTGGTG
GTAACAAAATCCAAAAGTCTTGTGGATTCTAAAGATTCAACTGCTGTTGATTACAAATTGGATT
CTTTCCAACAATTGTACTCAAATTGACTGGTAAACAAGTTGTTTTTGAAATCCCAGGTGAATCTC
ATTAG

YNL096C_YOR096W_homolog 186aa (SEQ ID NO 430)
MSSKILSENPTLELKVAQAFVDLESQADLKAELRPLQFKSIKEIDVNGGKKALAVFVPPPSLQAY
RKVQTRLTRELEKKFPDRHVFLAERRILPKPARKARKQQKRPRSRTLAVHDKILEDLVFPTEII
GKRVRYLVGGNKIOKVLDDSKDSTAVDYKLDSDFOOLYSKLTGKOVVFEPGESH

YNL178W_homolog 1256bp public: 1..1024, PathoSeq: 1025..1256; CDS: 501..1253 (SEQ ID NO 431)

TGTTTTGTTTTTGCAATCAACATAATAGAAGACCAAAACAAATAATTTCTATTTTTTTTGACTCTCC
CGTAGTTTTACTTCTAGCCTCTCTTGTAATATACACCTAATTGACAGTACCATTAGGACCCCA
TCTTATTGTTAAGGATAATACTTCTTCTTCTTCTTCTTCTTGTTTAATCAAATTTGCAATAAATA
AAAAAAAAAAAAAAAACAAGCCGCACAAGTTTTCTTCTAAATGACTTATTTTGTGTAACGCATTAC
GTGATCATATAATTTTTTAAATCAAAACTGAACCAATTCCTGCATATTGAGGTTGAAAAA
AGAAACAGAAATTTTTTCAATCTTGTGTTGAGGAGAGAGAGTGAAAAATTTTTCTCTCTCTTT
CTTCTTTTCATTCTCATATACCATAAACTTAAACAACTTCTTTTACTTTTTCTTTCTTTCTTT
CAAACCTCTACAACAGATCCAATTAATTAACAAAAAAATGGTTAACGCTATCTTATCTAAGAAA
AGAAATTAGTAGCTGACGGTGTCTTCTACGCTGAATTGAACGAATTCTTCACCAGAGAATTAGCTG
ACAAGGTTATGCTGGTGTTGAAGTTAGAAAACTCCATCTAAATTTGGAAGTTATTGTTAAAGCTT
CTAACACTCAAGGTGTTTTAGGTGAACAAGGTAGAAGAATCCATGAATTAACCTCATTGATGTTA
AAGATTCAAATTATCTCCAGAGGTATTGCCATTATGCTGAAGAGTTGAAGAAAGAGGTTTAT
CTGCTGCTGTTTCAAGCTGAAGCTTTTGAAGCCAAATTATGTCTGGTTTACCAATTAGAAGAGCTG
CTTATGGTGTTTTAAGATTTGCTATGGGTGCCGGTGCTAAAGGTGTTGAAGTTGTTATCTCTGGTA
AATTAAGAGCTGCTAGAGCTAAATCTCAAAAATATGCTGATGGTTTTATGATTCATTCTGGTCAAC
CACTAGAGATTTCAATTGATATTGCCATTAGACATGTTTTAATGAGACAAGGTGTTTTGGGTATCA
AGTTAAATATGAAAAGATCCAGCTGCTAATAGATTTGGTCCAAGAGCTTTACCAGATGCTGTTA
AATTTGCTGAAGCTAAAGATGAAGATGAAGTTATTCCAGCTCCAACGTGTTAAATCTTATAAACAA
CTGCTGAAGATGAAACTGAACTGATGCTCCAGTTGAAGCTGAAGCTGAAGTTGAAGCTACTGCTT
AA

FIG. 2 - 52

YNL178W_homolog 251aa (SEQ ID NO 432)

MVNAILSKKKKLVDGVFYAELNEFFTRELAEQGYAGVEVRKTPSKLEVIVKASNTQGVLGEEQRR
IHELTSILIVKRFKLSPEGIAIYAERVEERGLSAVQAEALKAKLLSGLPIRRAAYGVLRFAMGAGA
KGVEVVISGKLRAARAKSQKYADGFMHSGQPTRDFIDIAIRHVLMRQGVLGKVKIMKDPANRF
GPRALPDAVKIAEAKDEDEVIPAPTVKSYKQTAEDDETETDAPVEAEAEVEATA

YNL182C_homolog 2105bp public: 1..728, PathoSeq: 729..2105; CDS:
501..2102 (SEQ ID NO 433)

AAACTTTCTGATTGAATAAAGTGAACCTCAATCACATTCTTCGGCATATATCAAACCATTATTAGT
TTTATCACGTAAATCTTCAATATACTCAGCCACCCATTGATCATTTGGTTCTTCTAGTAAGTAATAT
TAGTTGTGCTCCTCGTTGTCCCAATTCATATGCTATTTGAGCTCCAATACCACTGGTCCCACCAGT
AATCATAAACACTTTCCCATGCATGTCTCGCTCCCACGTATTTGGTGGCACCATTGGAAATAATACCTT
GGCTCCAGCAAGAGTTAATAGAATGGGAAGAACGGTAGGTCCATATTTCTTTAATTTGGTCCCAATA
TGGAATCACCTCTGGCCCATCAAACACAACACTAGTTAAAAAATTCACCTGGCATAATTGGTATATC
AAGAGTGAAGAAAAATGCTGTATTGGAGGTTGGAATTTGTTTACAAATTGGTTGCCTTTTTATTCT
TCTTGTCTTTTTTTTTTTTCAGTGCCTAACATAATTTGGGATGTATGTATTGAAAAAAAAAATTTTG
TACAATTTCTTGTCTTGTCTCTCCACTCATCTCATCGCTCTCTTATAAATTCACAAACATGGATG
AAGTAGTATTTTACATAGCTCAAGGTGATCCAGCTGATAAACACAGTCAAGAATCATATGGATATG
TTACATCAATCCATTCTTCCAAACAATATGCATCTTATCGACAAGCAGACTCGCATATAAACGGTA
CTGCCATAACTGGTATTGGCCCAGGAGAAAGAATTTTCACTGCTGTTTCTTAACAAGGCATTAATCA
ATGTATATTTCATGGGAAAAAGAAAGTGTGATCAACGTATACCGATACCAGAAGCATTGACTTGTA
TCACGTTGATAAACCATCCAAATGGCAGTAACAACAACAGCGACAATGATGACAACCAGTTATACA
AATTACCAAATTACCGAGTTCTTGGTTGTTAGCAGGTGGATCAAAGAGTGGGAAATTTGTACATTT
GGGAATTAAGTTCAGGCAATTTATTATGTGTGTCAGAGACGCCCATTATCAGGGGATCACTACCATCA
AGGGTTCAAGCTGTGGAACATTTTAAATTACTGGAGGAGAGGATGCCAGATGTCTTGTATGGAAAT
TAGCAGAATTAATTAGTATTTATGACAAATCAGACCATCAAGTGAAACCATATTGGCAAATCACTG
ATAACACATTACCACTCACTGATCTTTGTTTAAATGATACTCATAACATTAATGATCTAAAATTAT
ATACAACCTCAGAAGACAGCACGGTCAGGATTTATGATATAGTCACAAAGAGTTTGTTAACCACAT
TTATTTTACCCAGTTCCGCTGAATGTATCACCAGGATCCAGCTAATAGAGCGTTATATGTCCGGT
TGAATAACGGTCTTGTAAGATCAATTCCTTTATATTCTATAAATAGCCATACATCAGTGTGGAAA
GTATTGGCGGCATGAATAAGATAAATCACGGTTGATGCTGATCAAAATTTAAAAGAGACATTTGTTG
CACATCAACAAAAGACGAAAACAGGAGACGATAAGCCTGTTGTTGTTACGAAATTGACAATTTCTT
TTGATGGTACAAGTATAATATCTGGTGATTCTGAAGGCAGAGTGTGTTGTCTGACATTGTAACGA
AACAGTTGTGAAATCATTCACACCTTGTAACCTCTCCAATAGCTTATATTGCTGTTGAAACTATCC
CTGATGACTTTGTCAATAACTTAGCTACTAGTACTACCACTAATAAAGCTGACAAGAAACATAGAA
TGATACCTCAATTTAAACGAGTACTAGCAAGCACCATTCTGAAGAACATCAGATATCTTTGGACA
TTCTTGGTAAAACCACCGCAACCACCAACCGCAATATTGACTTTGCAACTTGGTTACAAG
GCAAACAATCTGAAGAATTACAATTCAAAAACCTTTCTGGAATAAACTCTATTGTCAAACAAGTTG
GCAACGAGAATGTATCGGATCTCGAAGAGAGATTACAAAGAGTTTCTCAAGCATACACTGAATTAA
GAAACAAACATGAAGAATTAATTAAAGAACATGCCAAATTATTAGATAAATTAGAATAG

YNL182C_homolog 534aa (SEQ ID NO 434)

MYVLKKKNFVQFLVVLPLISSLSYKFTNMDEVVFYIAQGD PADKHSQESYGYVTSIHSSKQYASY
ROADSHINGTAITGIGPGERIFTAVPNKALINVYSWGKESVDQRIPIPEALTCITLINHPNGSNNN
SDNDDNQLYKLPNYRVFWLLAGGSKSGKLYIWELSSGNLLCVRDAHYQGITTIGKSSCGTFLITGG
EDARCLVWNLAELISIDKSDHQVKPYWQITDNTLPLTDLCLNDTHNINDLKLYTTSEDSTVRIYD
IVTKSLLTTFILPSSAECITKDPANRALYVGLNNGLVRSIPLYSINSHTSVLESIGGMNKIITVDA
DQNLKETFFVAHQKTKTGDDKPVVVTKLTISFDGTSIIISGDSEGRVFSVDIVTKQVVKSFPCNSP
IAYIAVETIPDDFVNNLATSTTTNKADKKHRMIPQFKRVLASTNSEEHQIFLDIPGKTTATTNATG
NIDFATWLQKGQSEELQFKNLSGINSIVKQVGNENVSDLEERLQRVSQAYTELNRNKHEELIKEHAK
LLDKLE

FIG. 2 - 53

YNL190W_homolog 896bp public: 1..896; CDS: 501..893 (SEQ ID NO 435)

TTTCTGCAAGTATTGCGTGTGCTGCACAACTTTTTATATCCGAAAATTTTTGGCCGGGAACGAAA
CGGCAAGAAAAACAGAAACAATACCACCAGCACGGACAAAAAGATTATAAGCTTTGTGTAATAAG
GTTATGTCATCGGGTATTACAGATTGCAGGGCCATCTTGTCTTCATCAGTTATAGCATTCAATAA
AAATAAGCCACATATGTGTACAGCGCTGAGTCTACTCAACATGTGTAAATAGAATAAATCAATTGA
CACAGTCTTTTGGAGATCTGTTATTCTGGCCTATAGCGTTTTAGGAAATTGCGGTATTTCTTGTCT
GTTTTCTTTTTATCTATTTTCGCACGACTTGGGGTGGTTTGTGTGACTTTTTTAGCAAATTAATTT
TGTCGGTCTTCGCAGTAAAAATAAAAAATTCAAAAAACAATTGACTTTTTTTTTTACTTT
CTTTCTTTTCTATCAACAATACTAATCACAAGCCAACCATGAAATTCCTACTGTTGCCACTGTTT
TTGCTATTTTCCTCATTAGCTGCCGCTAAAGGTGGTGAAAAAGATCACGGTAAAGCTTCTACTGTCA
CCAAATATGTCACTGAACTACCCACAGATACGGTCGTTTGTACAAAACCAGTAGATCTAAAAAGC
CAAAGGAACTGGTACTCACAGATACGGTAAATTCACAAGACTCCACGTCCAGTTACCACAACCTG
TCTTGGTCAAAGAAAGCGACCTTCCAAAGAAAAGAGATGCTGTTGTTGCTAGAGATTCTAAAAACG
CTTCTTCCAACCTTACCACCTCTAGTGGTAACAATGGTGTGCCACTGGTGTGAGCTTGGGTCTTG
CTGGTGTCTTAGCTGTTGGTGTGCTTTGGTGCATCTAA

YNL190W_homolog 131aa (SEQ ID NO 436)

MKFTTVATVFAISSLAAKGGKDHGKASTVTKYVTETTHRYGRFDKTSRSKKPKETGTHRYGKFN
KTPRPVTTTTVLVKESDLPKKRDAVVARDKSNASSNSTSSGNGVATGVSGLAGVLAVGAALVI

YNL208W_homolog 1076bp PathoSeq: 1..1076; CDS: 501..1073 (SEQ ID NO 437)

TTTTTGATCAGGCCTTTTGTTTTTTTTTTTGGGTGGTGCTGTGGTTCGTTGGGTAGTTGGCTCTTG
TTTCGGTTCCTACTTGTTCCTTTTTTTTATTCTCCTCGTTAATCCTAATTTTGTGTAACAAATTAAT
TATAGGGAGTTGGAATTAAGCTTGAAAAGAAAGAAAGAAAGAAATACCAACGTGGAATTTCT
ATTACGTAAGTCACTATACTTGCATAGAAATTTTCAAGTTTTCAATTTAAGAAAGTATTAATCAAC
TGAATTAAGCAATTGAACGAATTGAACCAGCTCAGCATTTATTTTTCTGTTTTCTTTTTTTTCAA
GGGGGTGGGTGAAAGAAAATCTAAAAATATATAAATACTCCACTTATCTCCTCTCTTCCCTCTCTT
TCTCTCTCTAACTCAATTTCAATTTTTCCCAAACCAAAATTTCTTTCTTTCTTTCTTTCTTTTATT
TTTTACTCAATTGAATCAATATTAACAATAAAAGCCATGTCAGCTAACGATTTTTTATTCATCTG
GTGATCAATCCAATTATGATCCAAAAAGATCCTCGAATCAAGGATCATCATCAATGATGAAC
AACAAGACAGAGGGTTATTATCTACTGTGCCGGTGGTGTGCTGGTGGTTATGGTGGTCACAAAT
TAGGTGAAAAGGCACAACATGGTACTTTGGGTACTGTATTAGGTGCCATTGGGGGTGCCATTGGTG
CCAATAAACTAGAAGATGCTTATGAAGACCGTAAAGAACATAAAAAACACGAGCAACAATATGGTG
GTAGTGGTAAACACGAAGGCGGAAGACATGAAGGTGGTTTTTGGTGGTGGTAGACCAGATGATCGTT
ATGAAGGCGATAGAAGAAATGATAATTACGGTGGTGGTTACAATGATAGAAGAGATGACGGTTATG
GTGGTGGTTACGGTGGTGGCAGACCAGACGATAGAAGACACGAAGGTGGTTTCGCGGTGGCAGAC
CAGATGACCGTTTTTGGTGGCGGTAGACCAGATGACCGTTTTTGGAGGTGACAGAAGAGATGATAGAA
GAGATGACCGTAGATGGTAA

YNL208W_homolog 191aa (SEQ ID NO 438)

MSANDFYSSGDQSNYDPKRSSNQSSSSNDEQQDRGLLSTVAGGVAGGYGGHKLGEKAQHGTGLGTV
LGAIGGAIGANKLEDAYEDRKEHKKHEQQYGGSGKHEGGRHEGGFGGGRPDDRYEGDRRNDNYGGG
YNDRRDDGYGGYGGGRPDDRRHEGGFGGGRPDDRFGGGRPDDRFGGDRRDDRRD

YOL031C_homolog 1745bp public: 1..1342, PathoSeq: 1343..1745; CDS: 501..1742 (SEQ ID NO 439)

TTGGTATTGAAGACACCGAAGACTTGTGAAAAGATATTGAACAAGCTTTACAAAAGGCTGCTTCTG
TTTGAGGGGATGTTTATTAGCAATGTATATAATTATTGTATATTATGACAAAGAAAGAAAAAGAA
AACCAGAAAAGTGTTTATACAGGAATATTTTAATAGAAATATCGCTTATATTGTGATAAAAAATT
TGAAAGACAATCCGAATGTAGTGTCTTGTCTTATTCTGCTTGGGAATACTGTAGTATTAGCATCAAT
TGAGGAAATTCCAGATAGCTAACGGTTTTGCGATTACGAATTTGCAACCAATAAATATGTGACA
AGGAATACACTACTGATCAAGGTATTCTTAGTACAATGGAAAAAAGAAAGCAACAAAA

FIG. 2 - 54

AAACGAGAAATTAATGAACACGACTTCACTTCTACAACCTACTGGGAAAAAAGGCAGAGAGTTA
TTGAAAAAGGATCATATCAAGTTCCTTATTGTATATTATATGAAGTTTTCTGTTTTAGTATTACTTG
CCAGTTACTTAGTTGGTGTGAATTCCTCTGATTGTTGATACTTCAGAGGAATTAATTTGTCCAGATC
CAGAAAACCCCTTTAGATTGTTATCCAAAATGTTTTGTTCCAACAAACGAGTGGCAAACCATTAAC
CAGGTCAAGATATACCACCTGGGTTACACGTTAGATTAAATATAGATACGTTGGAAAAAGAGGCCA
AGCTAATGAGTGCTGACGAAAAAGACGAGCCAGTTCAAGAAGTAGTTGTTGGTGGCGAATTGCAGG
ATCATTCGAGGGAAGCCATCACTGAGAATCTACAAAAGTTGCATGAGCTGAAACATCCTGAAGTAA
AACAGGAGCACGCTCATCGTACAAAGGTTAGCCAGGGAGATTTGAGTAATTTTGACGCAGCTTGTC
TGGAAATTGAGAGTTTCAAGCCACATGAGAGTGATGTGGAAGGTTGCATTTGGCACTAGATACTT
TAGAGGAATTAAGTCATGATATCGAATTTGGGGTGAAATTGACCTCAGACAAAGCCATATTTCAAG
GTTTTGTCAACATTGCCAATGGTGCTTCTGATCCAAAAATAACCGAAAAGGTATATCGTGTAATGG
GGTCTAGTTTGAGAAATAATCCTGAAGCGATTAGTAATATCTTGACCAACTTCGACAAGAGCTATG
TGTCAATTTGTTTGAGCAATTAGCGAATGAAAATGATGTTCTACAAAAGAGGATTTTGGGTATAA
TTCAAGCTTTAGTCCAAAATAGCCATTTTGCAAGACAATATTTTTCATTTGACCACAGTTCCGGGT
TAAATGATTTAATAGCGATTTTCCCAAACCTGGTCCAACTCAAAGTCCAGGGCAAGTAACATTT
TAGAGGATTTACAATTGTTCCCAGTAACAAACGATAGAAGATCACTTGAAGATCAAGATCCTGAAT
CACAGGTTTCAAATTTATTCAGAATTCCTTTGTTGGAATAAACTTGACGAGAAGAAATTTCAAGT
CTTATTTTGATCAACTAGTAAATTTGCATCAGCTGAATAAGAGTTTGCGACCAAGTGGTGACTTTC
TCAATTGGTTAGCTGAAGAAGTGGAGTCGCGTAAAGAGAATAAAAAAGAGACGATTATTCACAAG
AAGACAAAGACTTTGATGAGTACATGTTGCGAGCACGTCATGAAGTATTTGGCAATCCAATGGGAT
TAAGAAAGGCAATTGCCGACGAGTTGTAG

YOL031C_homolog 414aa (SEQ ID NO 440)

MKFSVLVLLASYLVGVNNSIVDTSEELICPDENPLDCYPKLFVPTNEWQTIKPGQDIPPLHVRL
NIDTLEKEAKLMSADEKDEPVQEVVVGELQDHSREAITENLQKLHESKHPEVKQEHARTRKVSQ
DLNFDAAACSEIESFKPHESDVERLHLALDTLEELSHDIEFGVKLTSDKAIQSFVNIANGASDPK
ITEKVYRVMGSSLRNNPEAISNLTNFDKSYVDNLFEQLANENDVLQKRILGIIQALVQNSHFARQ
YFSFDHSSGLNDLIAIFPKLGPNSKSRASNILEDLQLFPVTNDRSLEDQDPESQVSKFIQNSFVG
NKLDEKNFKSYFDQLVNLHQSNKSLRPSGDFLNWLAEVEESRKENKKRDDYSQEDKDFDEYMLRAR
HEVFGNPMGLRKAIADL

YOL048C_homolog 1244bp PathoSeq: 1..27/985..993, public:

28..984/994..1244; CDS: 501..1241 (SEQ ID NO 441)

ATGATTTTTTCTCTGATTTTAGAGCTGTTAATTATACCTTTTTTGTTCCTCAAATAAGCGCTAAAA
TGATTGAAATTAAAAATACTAATCTATCCAGGTCAAAGTAAACACTATAAAACAATATATTTCAAT
AACAGGAGCAGTAATTAGCTTCAACATCAAGGTACTCTTTTATTTTTCTACCAAAAACACATCTGA
AGTAGCTCTTATCCATAGATCCAAATATTTTAACCTTTTTTTTTCTCTACTCTCATCTACTTTTTT
TTGCAACACTTACTGCTCACAACGCCAATGACCATAACCATTAATTTCAATAATCAAATCAAGAGCT
TATTTGTATCCTCTCAAGGTATGTTAATGTATTAACAACACCGATTCTATTTTACCAACTAACACG
ACAGAAAGGGGTTGTACTATTTTGTAAACACATCCCACCGTTTGGCCCTTTTACATAACCATATTGA
TACCTCAATTGGTCCTTACACTAGTCATTTACCTGATTATGTTTTATTGTTCTTCCCACCTCAAG
CTATTGTATATACATTGTTAATGGGACCATTAGGGGTGATTGGTGCGTGGTATAGTTTGATCCTGC
AAGCGAGCACATTGTCTATATTTGTTGTGCAATATCCTTAATGCCTCACATACAACGAGTGGCAT
ATGATGCAATATTGAGTAGAGAGTGTGCAATGATGTGGTACTAATGGGAAAACCTAGGAGGTATA
GAAAACCTACCCATTAGAGTAAGGGCCAGAGAATACCTTAAGGCCATTCCAGATTTTTCGATCTTTC
CCTTCTCTTTGCTCAAGCTACTTGTGTTTTTCGGTATTTACTTCATACCCTTTGTAGGTCCAATCA
TTGTATTGTTTTTCCAATCTTCCAAGCGTGGACTAAAGGCACATGCAAGATACTTTAAGTTGAAAG
GGTTTCTGCGTAGTGACATAAGAACAATCCACAAGCTAAACAGACCAGCATATATGGGGTACGGAG
TGGTTGCGCTTTGGCTCGAGCTGTTTCCATTTATCAATATGTTTTTTATGTTTACCAATACTTTGG
GAGCTGCTTTGTGGGCAGTTGATATTGAACAACAAGAGAAGGCCGTACAGAGAATGTGGCCGCAG
CTACTACCACCGCCACAGATACGAATAGCGTCAATCAACAAGGTCTAGTTATACCCGTACACAATG
AACCAGCACTAATATACCTGAGGCTACCCCAAAAACCTGCTACAAATACCATCTAA

FIG. 2 - 55

YOL048C_homolog 247aa (SEQ ID NO 442)

MFSLFFPPQAIIVYTLLMGPLGVIGAWYSLISQASTLSIFVVTISLMPHIQRVAYDAILSRECANDV
VLMGKLRRYRKLPIRVRRAREYLKAIPDFSIFPFSLLKLLVFFGIYFIPFVGPIIVLFFQSSKRGLK
AHARYFKLKGFSRSDIRTIHKLNRPAYMGYGVVALWLESFPFINMFFMTNTLGAALWAVDIEQQE
KAVTENVA AATTTATDTNSVNNQGLVIPVHNEPATNIPEATPKTATNTI

YOR027W_homolog 2270bp PathoSeq: 1..947/1781..1828, public:
948..1780/1829..2270; CDS: 501..2267 (SEQ ID NO 443)

GCATTTTACTTATTTAGATATTACTTCATATTGCTTTTATTTAGATTGATTTTGTTTAACAGTGAA
AGTTTTTATTTTTTTTTTTGTTTAAAGTTTTTATTTTTTTTTTTGTTTAAAGTTTTTGTATTATACAA
TATTTAAATTATAGTAATCATCTATAAATTTCAAAGTCAAAAGACAGATCTTAAGGTCTAATTAA
TAACCTCTATGGCCTTCTGTGTCAAAATTGTTGTCGTTTGATAACAAGTTTGGAAACGGTAATGGTT
GAAATTAGAAAAGAAAAAATTACACATGGTAGCAGCTGATGTATAGAACTTTCTAGCAAAAAA
AAAGAAAGAATTTTTTTTTTCTTCCATTTTTCAAATTTGAGAGATCGAAATAATTTTCTTGAATTTA
TTAAAAGGGAACCCCTTCCCGAAAAATCCAAAACCAAACCTTCCACCCAAATATCAAATAACTAAC
TTATCATTTCCAACAGATAATATCCCACTTCAATAACAATGACAACAGCTGACGAATACAAAGCAG
AAGGTAACAAATATTTTGTCTGCTAAAGATTTTGAAGGCGATTGAAGCATTCACTAAAGCAATTG
AAGCATCACCTGAACCAAAACCATGTTCTTTATTCAAATCGTTCTGGATCTTATGCCTCTTTAAAG
ATTTTAACAACGCATTAAAAGATGCTCAAGAATGTGTCAAGATCAATCCTAGTTGGGCCAAAGGGT
ATAATAGAAATTGCTGGGGCTGAATTTGGTTTAGGTAATTTTGATCAAGCCAAATCCAATTATGAAA
AATGTTTTGGAGTTGGATCCAAATAATGCCATGGCTAAAGAAGGTTTAAAATCAGTTGAATCTGCTT
TATCATCTGGTGGTGGTGTATGACAAGGATTTAGGATTTGGTAAAATTTTAAATGATCCTAATCTTT
ATACTAAATTGAAAAATAATCCTAAAACAAGTGAATTTATGAATGATCCTCAATTTGTTGCTAAAC
TTGAACGCTTTAAAATAATCCACAATTGGGTAATCCTGATATGTTTAGTGATCCAAGATTATTGA
CGGCTTTTGCTGCTTTAATGGGTATTGACATGGATTTACCAAATATGGGATTCAGTCTCCAAACG
AATCACAATCCAATGCATCAGAACCAAACTGGAACCAAAATCAGTACCAGAATCTAAACCAGAAC
CAAAAGCAGAACAAAAGGAAGAAGATCAACCTCAGCCAAAGATGAAGACACTCCAATGACTGATG
CCCAAGACGACACTAATGATAATGATGCCAAAACCAAGCTGACAATGCTAAAGCTGAAGGTAATG
CCTTATACAAGAAACGTCATTTGATGAAGCAATTGCCGCCTATAATAAGGCTTGGGAATTACATA
AGGATATCACTTATTTAAACAATCGTGCTGCTGCCGAATATGAAAAAGGTGATTATGATGCTGCTA
TTGCTACATGTGAAAAGGCCATTGATGAAGGTAGAGACATGAGAGCTGATTATAAATTGATTGCTA
AATCATTTGCTAGATTAGGTAATATTTATTTGAAAAAGATGAATTACCCGAAGCAGTGAAAAAAT
TTGAAAAATCTTTAACTGAACATCGTACCCCTGATGTTTTTAAATAAATTAAGATCAACTCAACGTG
AAATTTAAACTAGAGAATTAAATGCTTATATAGATCCAGAAAAGGCTGAAGAAGCAAGATTACAAG
GTAAAGAATATTTACCAAAGGAGATTGGCCAAATGCCGTTAAGGCTTATACTGAAATGATTAAAA
GAGCACCAGAAGATGCTAGAGGATATTTAATCGTGCTGCTGCATTGGCAAAATTTGTTATCATTTT
CTGATGCTATACAAGATTGTAATAAAGCCATTGAAAAAGATCCAAATTTTATTAGAGCTTATATTA
GAAAAGCTAATGCTCAATTGGCAATGAAAGAATATAGTCATGTCATGGATACTTTAACCAGGCAA
GAACTAAAGATGTTGAATTGGGTGGTAAATCAATTCATGAAATTGATGAATTAATGAATAAAGCTA
CTTATCAAAGATTTCAAGCCATTGAAGGTGAACTCCTGAACAACTATGGAAAGAGTTTCTAAAG
ATCCAGAAATTGTTCAAATTTTACAAGATCCAGTAATGCAAGGAATTTTAGCTCAAGCTAGAGAAA
ATCCTGCTGCTTTACAAGATCATATGAAAAATCCTGAAGTTTATAAAAAAATTAATATGTTGATTG
CTGCTGGTGTATTTCGTACCAGATAA

YOR027W_homolog 589aa (SEQ ID NO 444)

MTTAD EYKAEGNKYFAAKDFEKAIEAFTKAIEASPEPNHVLVSNRSGSYASLKDFNNALKDAQECV
KINPSWAKGYNRIAGAEFLGNFDQAKSNYEKCLELDPNNAMAKEGLKSVESALSSGGGDDKDLGF
GKILNDPNLYTKLKNNPKTSEFMNDPQFVAKLERLKTNPQLGNPDMFSDPRLLTAFALMGIDMDL
PNMGFTAPNESQSNASEPKSEPKSVPESEKPEPKAEQKEESTSAKDEDTPTMTDAQDDTNDNDAKTQ
ADNAKAEGNALYKKRQFDEAIAAYNKAWELHKDITYLNNRAAAEYKGDYDAAIATCEKAIDEGRD
MRADYKLIAKSFARLGNILYKDELPEAVKNFEKSLTEHRTPDVLNKLIRSTQREIKTRELNAYIDP
EKAEEARLQKEYFTKGDWPNVAVKAYTEMIKRAPEDARGYSNRAAALAKLLSPDAIQDCNKAIEK
DPNFIRAYIRKANAQLAMKEYSHVMDTLTEARTKDVELGGKSIHEIDELMNKATYQRFQAI EGETP
EQTMERVS KDPEIVQILQDPVMQGILAQARENPAALQDHMKNPEVYKKINMLIAAGVIRTR

FIG. 2 - 56

YOR312C_homolog 1019bp public: 1..1019; CDS: 501..1016 (SEQ ID NO 445)
CCACTAACAACTTTTTTTTGGACTATACACCACTGAAAAAAAAAAAAAAAAATTTTTGTAAAAAATCT
TAAGAATTTTCAGTTTGAAGGTATTCAACAACAACCGAAGAGTATGTTCAACATCGTTATAATAGA
ATAGAATAAGAGCATGACAACAAGGGATACAAGCTTGAAAAAAGAAAAAGGGTGGGATATCTTAA
AATTATTAAAGAGTTTTTTTTTATAACATGTCATTGAGATTGAGATTGGGAATACTGAATTCGATTT
TAAAGTCATTGGATGGGAGAGTTAATTATTCGTTTTATTATTAGGATTACCAATGAATAGTAATGA
AGTGATGGAGAGATAGAATGAAAGTATTTCAGAAGAGCATCAAGTCCCTTATAAGTTTGTGAGACAT
AATATGTCTACCCCTTGTCAACTTGTCTATAAATTTTATTGCTCGTCTCTTAAAAGAAATGAATAA
AAAGATTTACTAACTTAATTTCAATTATTTATAGAAAGATGTCTAGATTAAACGAATATCAAGTTA
TTGGTCGTAATTTACCACTGAATCCGTTCCAGAACCAAGTTGTTTCAGAATGAGAATTTTTGCTC
CAAACACCGTTTGTGGCCAAATCAAGATATTGGTATTTCTTGCAAAAATTGCATAAAGTTAAAAAAG
CTTCTGGTGAAATTGTATCTGTCAACATTATTTCTGAAGCTAAACCACTAAAGTTAAACTTTTG
GTATTTGGTTAAGATATGAATCCAGATCTGGTATTTCATAACATGTACAAAGAATACAGAGATGTTA
CTAGAGTTGGTGCTGTTGAAACCATGTACCAAGATTTAGCTGCTAGACACAGAGCTAGATTTAGAA
GTATCCATATTTTGAAAGTTGTTGAATTAGAAAAAAGTATGATGTTAAAAGACAATACGTTAAAC
AATTTTTGACTAAAGATTTGAAATTTCCATTACCACACAGAGTCCAAAAATCTAAGAAATTGTTCC
AAGCTACTGCTCCAACCACTTTCTACTAA

YOR312C_homolog 172aa (SEQ ID NO 446)
MSRLNEYQVIGRNLPTESVPEPKLFRMRIFAPNTVVAKSRYWYFLQKLHKVKKASGEIVSVNIISE
AKPTKVKTFGIWLRYESRSGIHNMYKEYRDVTRVGAVETMYQDLAARHRARFRSIHILKVVELEKT
DDVKRQYVVKQFLTKDLKFPLPHRVQKSKLQFQATAPTTFY

YOR369C_homolog 932bp PathoSeq: 1..228, public: 229..932; CDS:
501..929 (SEQ ID NO 447)
TGTTTACTTTTTCTGTAGTTTTAAAGTTTCCTAATTTAACTTCCAAAAGTTTCATTAACAACAATA
TTAACATACCTTTGTCAAGCAATTATATTGAAGTTTTTTGATACAAGTGTGTTGTTTTTTGTG
TACATGTGAGATATATAATTGTGTATATACAGTCACGTGAATAGAGCAGAAAAATTACGAAGTAGA
AATATTGGTAGCGCGTTAGGGCTATAGCCCTATTTAGTTTGTGCACCACACGACTTACAATTTTTT
TTTTTTCTTTTCTTAGAATCCTTGAGGCACTGACACTGTACTCTCTCTCTCTCTCTCTCTCTCG
TAGGTAGTGAAAAATTTCCACTAGTCTTCCCATAACCCACCTAGGTTCTTTCTTTTGAAACCACT
GAGCAGTAAATCAATTTACTTGACGAAGAAGTCTATACATAAATATAAACTTGTCCCTCCCCCCC
CTTTTTTTTTTAACTAACTAAGAAAGAAAAAATTAAAAAATGTCTGACGTTGAACAAGAACAATTG
TTGAAGAAGTTGTTGTTGAAGAACAATCCGGTGCCATCACCATTTGAAGATGCTTTAAAAGTTGTTT
TAAGAAGTTCTTTAGTCCATGATGGTTTAGCTAGAGGTTTAAGAGAAGCTTCTAAAGCTTTATCTA
AAAGAGAAGCTCAATTATGTGTTTTGTGTGACTCTGTTACTGAAGAATCAATCATCAAAATTGGTTG
AAGCTTTATGTAATGAACCAGAAGAAAAAATCCCATTTGATTAAAGTTTCCGATGCTAAATTAFTGG
GTGAATGGGCTGGTTTATGTCAATTAGATAGAGATGGTAATGCTAGAAAAGTTGTTGGTGCCTCTT
GTGTTGTTGTCAAAAAGTGGGGTGTGATTCTGATGAAAGAAACATCTTGTTGGAACACTTTTCTC
AACATAA

YOR369C_homolog 143aa (SEQ ID NO 448)
MSDVEQEQIVEEVVVEEQSGAITIEDALKVVLRTSLVHDGLARGLREASKALSKREAQLCVLCDSV
TEESIIKLVEALCNEPEEKIPLIKVSDAKLLGEWAGLCQLDRDGNARKVVGASCVVVKNWGADSDE
RNILLEHFSQQ

YPL047W_homolog 881bp public: 1..811, PathoSeq: 812..881; CDS:
501..878 (SEQ ID NO 449)
AAAAATTTCCAATCTTGAATTTTCATCTTCAACGTCATAAACTTGTTCTGTTTGAAATTTATCGTCTC
CATTATCGTTGTCATTTTCATTGTCTATTGTCAATATTACGGTTACGATTTTGTGTTTCCCTTTGAAG
TCTTTGACTCTAGCTGTTTCATCTGTCTATTACCTTTGGCTTGGTTTGTCTTACTGTTGAGCGATGAG
ACAAACTTTTTGATTGATTGCAACTGAACAAAAAATACGACAGACACACACACACACACACAC
ACACAATTTTCAGCTCCTTCCAAGTCGTGTTTTTTTTTGGAAGAAAAAACAACCTTGGCCCTAAA

FIG. 2 - 57

TTCTGTTGATAAACTCGAGCACGATCCGCAACAGCAGATTTCCTTCAAGAAGACCTAAACGAGGTAA
TGTTTTTAATTCCACAGGACATCAATGCACCACCTCCAAGACTATGTCTTGGGATTTTCAGTTAATGA
ACCAAATAATAAAGATGACGGTAAATCACACAACCATTCCAAATATAGTGATCATGAAATTGCATT
AGCTGAAGATGCTCAACGCCGAGCAATTATTGAAGCAGAAAAACATGCTCAAGAAGCTCATCGACA
AGCCAAAAAGATTGCTCAAGAAGTTTCTGGGTATAGATCACATAGATTTCATATCCATTAAAGAAGG
TGGTAGTGTTGGTAATTCTAACACCAACGGCAACGACAATGACGAAGATGATGATGAGGTTGAAGA
AGCAGTTGATAAGAAATTGGCAAATGATGTTTCTGTGGATGGACCGTTGCATGTCCACGAACAACA
TTTCGAAGAAGAAATTGAAAGCAAAACAGGTGAAAAGACCATTTCATTGGAAACAATCTATACAAG
ATGTTGTCATTTACGAGAAATTTTACCAATCCCAGCAACATTGAAACAAATTGAAAAATAAGACAGC
ACCGTTGGAAGTGTTAAAGATGCTCAACCCAAAACCAACTTTAATTGATGTGTTATCTTTTTTCAGA
TTTTATTGCCATTACACCTATTAACACGGTCATTTTTGATAACGTGACTATGACAACAGAGATGTT
GAAAAACTTTCTTGGATCGTTGACATATAATAAACAATTGGAAAAGTTATCGTTGAGAAATGTTTC
CATGATGAGTTGGGATGGAAGTATTTGTGTGAATTTTTGGCAACAAATAAAACAGTTAAGAAATT
GGATATATCACAACAACGTATCAAGCCAGATACCCAGACACAAGCATTCTGGTGAATATGAACTG
GGACTTATTTATTCGATCATTAATTTTGCCTGGTGAATAGAAGAATTGGTTATCAATGGATGTAA
ACTATCCGATGCAATATTTGAAAAGTTCATCAATCAAGCGGTTAAGAAGTCAACCTATCGATTAGG
TATTGCTGGTATTGATTTGAATGTTAAAAAATCAGAAATGGTCACATCGTGGTTAACTGATGGTAA
TTCTCAATGTGTGGTGTGATATTGCTTTTAATGATTTGAGCAAGGGACAATTACGTCCATTTCAT
TAATGCGTTTTAACACTGGCAAGTCAACAATTTAGTGTTTTTTTCATTGAATTCAACCAATTTACT
GAACATTGAAGAACTTCTGACTTGATCAAGTCATTAATTAATGTAAAACATTACGATTTTTAGA
TTTAAGTTCCATACCTAATATCTTCCCAGAAAATAATTACCCATTTGGACAAATACTTGCCAGATA
TCCTAATCTTCGAAGAATACATTTTGATCTTAATGAATTAACCGCACAGCTATTGGGTCATTGGC
GGGGTGTTTTACTGAAAATGCCCAATTAGTTCATGTCTCGTTATTGGGTAATAGAAATTTGTCAAC
TACGTCAGCAGCTACATTATACGGAGCAGTTAAACAATCCAAGACCTTGTTTGCTCTTGATTTGGA
CTACGATTTAATACCTGATCAATTATCACAACGTATTGCCTTTTATTTGATGAGAAACTTGGAATA
CACTTTGAAGCCATCTCATGGCGGCAATATTGAAAGCAATCCAGAAAAACCAGAGGATTTGATGTA
TGATGGATCGTTATTAATGGAACAGCTGAAAAATTATTAGTTGAAATAGAAAAGGGTAAGAAAGA
GGATATCAAAATGCAAAGAATTATATCCGATTCAAGTATTGGAAAGACAAGATCGATTCTGTAAGGA
TATTCACAAAACCATTGATACATTATTCGAACAAAGAAATTTAGGTAAATTATCATTTGAAGGTAA
AGAGAATTTAGTTCGATTTTGTATTATTAGATTTCGTCTTTAGAAAAATTTGGTTGTTATGGTTGAGGA
ACATGCCAACGGATTATTATTAACACCAACGACCTCCACGGACGATCTCAGAAGTAGAGCCATGTC
GCCATCGGTCACTGTTGATACAAATCCATGAAAGTGCAATGAGTTGATTACTGCTGGACCAATTTT
ATCACCACATGTCAATAGGAAAGCAGAACAAAGCTCGTATTTCCCAGTGTTTGCCAATAATGATAA
TTTGACCCCTCATCAAGTTGTCTGTTGAGTCAATGATGAAGGTAGAGATGTTCCAATAGATAAAAT
GACAGGACGACAGTTTGTATTCGATCAATTAGTCAAACCTCTGTGCATGCAAAAGAGCAAGAAAT
TGAAGAAGGGGAGCTTCATAAATTTGGATTCTTTATTCAACAAAAAGAGAGACAAAAACAACA
ACAACAACAACAACAAGAACTCACACCACGACCAACACCGGCCAGCTGATCCAACAAGAAAA
CCAGCTGCCGCTGCCACAACAAGGAAAATATGAAGATTTACCGATATTAAATACATTACCGTCAGG
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FIG. 2 - 59

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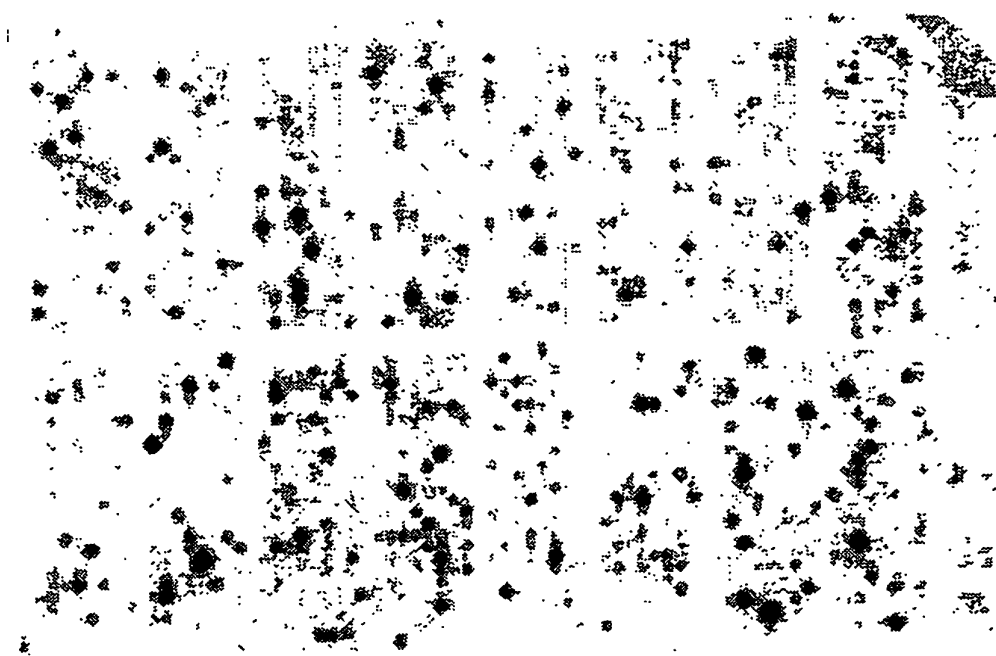
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FIG. 2 - 60

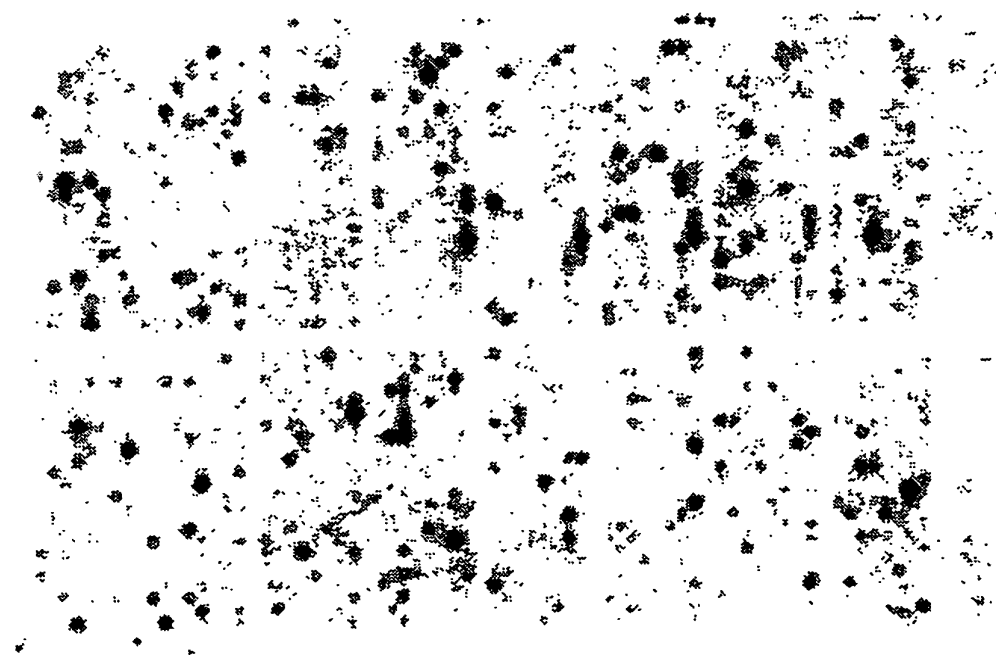
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YPL218W_homolog 190aa (SEQ ID NO 456)
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FIG. 2 - 61

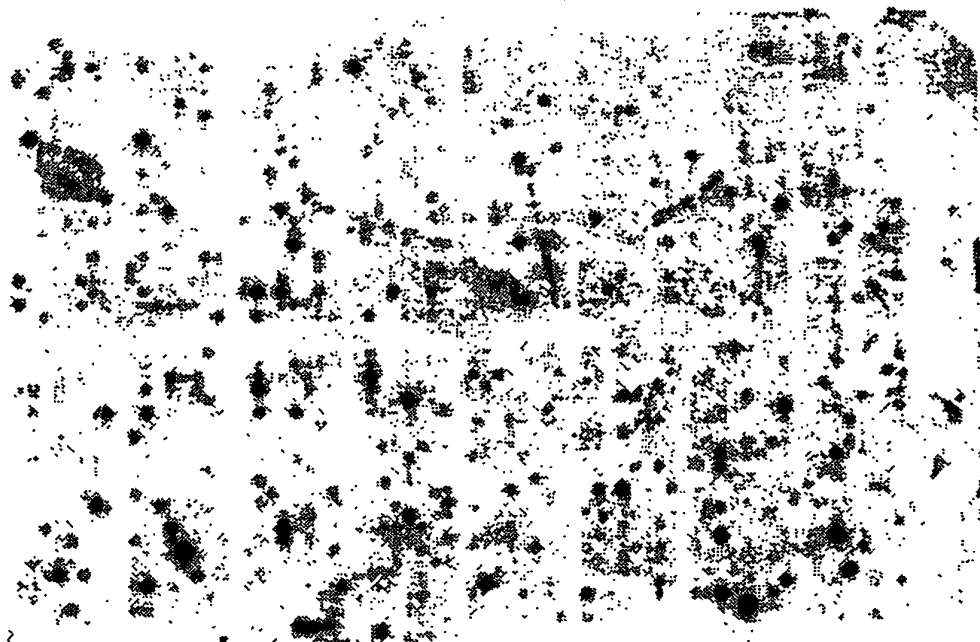


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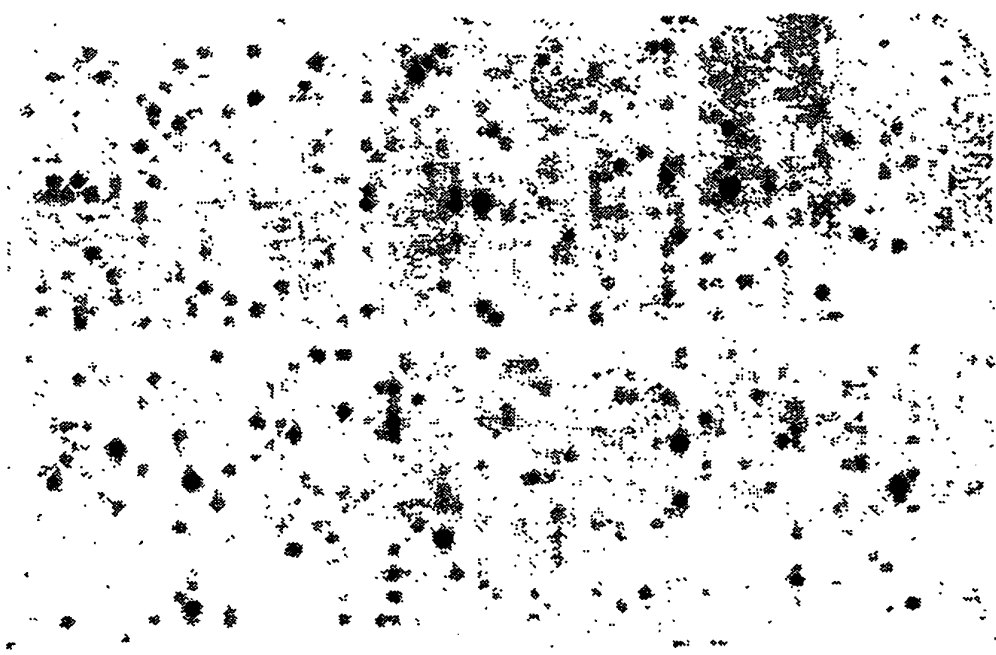


Filter II

FIG. 3A



Filter I



Filter II

FIG. 3B

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<120> Cell death related drug targets in yeast and fungi

<130> JAN-02-RC/CAND

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35 40 45

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Phe Ile His His Asn Cys Thr Pro Glu Asp Gln Ala Asp Met Val Arg
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<210> 8

<211> 668

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 8

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 35 40 45
 Gln Thr Glu Thr Gly Glu Asn Ser Ala Lys Asn Ala Glu Gln Asn Val
 50 55 60
 Ser Ser Thr Asn Leu Asn Asn Ala Pro Thr Asn Gly Ala Leu Asp Asp
 65 70 75 80
 Asp Val Ile Pro Asn Ala Ile Val Ile Lys Asn Ile Pro Phe Ala Ile
 85 90 95
 Lys Lys Glu Gln Leu Leu Asp Ile Ile Glu Glu Met Asp Leu Pro Leu
 100 105 110
 Pro Tyr Ala Phe Asn Tyr His Phe Asp Asn Gly Ile Phe Arg Gly Leu
 115 120 125
 Ala Phe Ala Asn Phe Thr Thr Pro Glu Glu Thr Thr Gln Val Ile Thr
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 Ser Leu Asn Gly Lys Glu Ile Ser Gly Arg Lys Leu Lys Val Glu Tyr
 145 150 155 160
 Lys Lys Met Leu Pro Gln Ala Glu Arg Glu Arg Ile Glu Arg Glu Lys
 165 170 175
 Arg Glu Lys Arg Gly Gln Leu Glu Glu Gln His Arg Ser Ser Ser Asn
 180 185 190
 Leu Ser Leu Asp Ser Leu Ser Lys Met Ser Gly Ser Gly Asn Asn Asn
 195 200 205
 Thr Ser Asn Asn Gln Leu Phe Ser Thr Leu Met Asn Gly Ile Asn Ala
 210 215 220
 Asn Ser Met Met Asn Ser Pro Met Asn Asn Thr Ile Asn Asn Asn Ser
 225 230 235 240
 Ser Asn Asn Asn Asn Ser Gly Asn Ile Ile Leu Asn Gln Pro Ser Leu
 245 250 255

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Ser Ala Gln His Thr Ser Ser Ser Leu Tyr Gln Thr Asn Val Asn Asn
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Gln Ala Gln Met Ser Thr Glu Arg Phe Tyr Ala Pro Leu Pro Ser Thr
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Ser Thr Leu Pro Leu Pro Pro Gln Gln Leu Asp Phe Asn Asp Pro Asp
      290                      295                      300

Thr Leu Glu Ile Tyr Ser Gln Leu Leu Leu Phe Lys Asp Arg Glu Lys
      305                      310                      315                      320

Tyr Tyr Tyr Glu Leu Ala Tyr Pro Met Gly Ile Ser Ala Ser His Lys
      325                      330                      335

Arg Ile Ile Asn Val Leu Cys Ser Tyr Leu Gly Leu Val Glu Val Tyr
      340                      345                      350

Asp Pro Arg Phe Ile Ile Ile Arg Arg Lys Ile Leu Asp His Ala Asn
      355                      360                      365

Leu Gln Ser His Leu Gln Gln Gln Gly Gln Met Thr Ser Ala His Pro
      370                      375                      380

Leu Gln Pro Asn Ser Thr Gly Gly Ser Met Asn Arg Ser Gln Ser Tyr
      385                      390                      395                      400

Thr Ser Leu Leu Gln Ala His Ala Ala Ala Ala Asn Ser Ile Ser
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Asn Gln Ala Val Asn Asn Ser Ser Asn Ser Asn Thr Ile Asn Ser Asn
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Asn Gly Asn Gly Asn Asn Val Ile Ile Asn Asn Asn Ser Ala Ser Ser
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Thr Pro Lys Ile Ser Ser Gln Gly Gln Phe Ser Met Gln Pro Thr Leu
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Thr Ser Pro Lys Met Asn Ile His His Ser Ser Gln Tyr Asn Ser Ala
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Asp Gln Pro Gln Gln Pro Gln Pro Gln Thr Gln Gln Asn Val Gln Ser
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Ala Ala Gln Gln Gln Gln Ser Phe Leu Arg Gln Gln Ala Thr Leu Thr
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Pro Ser Ser Arg Ile Pro Ser Gly Tyr Ser Ala Asn His Tyr Gln Ile
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 Ser Gln Ile Pro Ile Asn Ser Gln Thr Leu Ser Gln Ala Gln Pro Pro
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 Ala Gln Ser Gln Thr Gln Gln Arg Val Pro Val Ala Tyr Gln Asn Ala
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 Ser Leu Ser Ser Gln Gln Leu Tyr Asn Leu Asn Gly Pro Ser Ser Ala
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 Asn Ser Gln Ser Gln Leu Leu Pro Gln His Thr Asn Gly Ser Val His
 595 600 605
 Ser Asn Phe Ser Tyr Gln Ser Tyr His Asp Glu Ser Met Leu Ser Ala
 610 615 620
 His Asn Leu Asn Ser Ala Asp Leu Ile Tyr Lys Ser Leu Ser His Ser
 625 630 635 640
 Gly Leu Asp Asp Gly Leu Glu Gln Gly Leu Asn Arg Ser Leu Ser Gly
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<210> 9

<211> 3674

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 9

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<210> 10

<211> 1057

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 10

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Phe Pro Ser Lys Lys Gln Arg Ile Ser His His Asp Asp Ser His Gln
 35 40 45

Ile Asn His Arg Pro Val Thr Ser Cys Thr His Cys Arg Gln His Lys
 50 55 60

Ile Lys Cys Asp Ala Ser Gln Asn Phe Pro His Pro Cys Ser Arg Cys
 65 70 75 80

Glu Lys Ile Gly Leu His Cys Glu Ile Asn Pro Gln Phe Arg Pro Lys
 85 90 95

Lys Gly Ser Gln Leu Gln Leu Leu Arg Gln Asp Val Asp Glu Ile Lys
 100 105 110

Ser Lys Leu Asp Thr Leu Leu Ala Asn Asp Ser Val Phe Val His Leu
 115 120 125

Leu Gln Gln Ile Pro Met Gly Asn Ser Leu Leu Asn Lys Leu Asn Leu
 130 135 140

His Pro Thr Pro Thr Pro Gly Thr Ile Ile Pro Asn Pro Asp Ser Ser
 145 150 155 160

Pro Ser Ser Gly Ser Pro Thr Ser Ser Ala Ala Gln Arg Asp Ser Lys
 165 170 175

Val Ser Val Gln Thr Tyr Leu Ser Arg Glu Pro Gln Leu Leu Gln Ala
 180 185 190

Asn Gln Gly Ser Asn Thr Asn Lys Phe Lys Ala Asn Asn Glu Ala Ser
195 200 205

Ser His Met Thr Leu Arg Ala Ser Ser Leu Ala Gln Asp Ser Lys Gly
210 215 220

Leu Val Ala Thr Glu Pro Asn Lys Leu Pro Pro Leu Leu Asn Asp Ser
225 230 235 240

Ala Leu Pro Asn Asn Ser Lys Glu Ser Leu Pro Pro Ala Leu Gln Met
245 250 255

Ala Phe Tyr Lys Asn Asn Ser Ala Gly Asn Thr Pro Asn Gly Pro Phe
260 265 270

Ser Pro Ile Gln Lys Thr Tyr Ser Pro His Thr Thr Ser Thr Thr Val
275 280 285

Thr Thr Thr Thr Asn Gln Pro Pro Phe Ala Ala Thr Ser His Val Ala
290 295 300

Thr Asn Asn Asn Ala Asp Arg Thr Lys Thr Pro Val Val Ala Thr Thr
305 310 315 320

Thr Thr Met Pro Leu Leu Pro Ser Pro His Ala Asn Val Asp Glu Phe
325 330 335

Val Leu Gly Asp Ile Ser Ile Ser Ile Glu Lys Ala Asn Arg Leu His
340 345 350

His Ile Phe Val Thr Arg Tyr Leu Pro Tyr Phe Pro Ile Met Tyr Ser
355 360 365

Asn Asn Ala Thr Glu Leu Tyr Ser Gln Ser Gln Leu Leu Phe Trp Thr
370 375 380

Val Met Leu Thr Ala Cys Leu Ser Asp Pro Glu Pro Thr Met Tyr Cys
385 390 395 400

Lys Leu Ser Ser Leu Ile Lys Gln Leu Ala Ile Glu Thr Cys Trp Ile
405 410 415

Arg Thr Pro Arg Ser Thr His Ile Ser Gln Ala Leu Leu Ile Leu Cys
420 425 430

Ile Trp Pro Leu Pro Asn Gln Lys Val Leu Asp Asp Cys Ser Tyr Arg
435 440 445

Phe Val Gly Leu Ala Lys Ser Leu Ser Tyr Gln Leu Gly Leu His Arg
 450 455 460

Gly Glu Phe Ile Ser Glu Phe Thr Arg Thr Gln Thr Ser Met Pro Asn
 465 470 475 480

Ala Glu Lys Trp Arg Thr Arg Thr Trp Leu Gly Ile Phe Phe Ala Glu
 485 490 495

Leu Cys Trp Ala Ser Ile Leu Gly Leu Pro Pro Thr Ser Gln Thr Asp
 500 505 510

Tyr Leu Leu Glu Lys Ala Leu Ser Cys Gly Asp Glu Glu Ser Glu Glu
 515 520 525

Asp Asn Asn Asp Ser Ile Asp Asn Asn Asn Asn Asp Lys Arg Asn Lys
 530 535 540

Lys Asp Glu Pro His Val Glu Ser Lys Tyr Lys Leu Pro Gly Ser Phe
 545 550 555 560

Arg Arg Leu Leu Ser Leu Ala Asn Phe Gln Ala Lys Leu Ser His Ile
 565 570 575

Ile Gly Ser Ser Thr Ser Ser Pro Asp Gly Leu Leu Glu Pro Lys Tyr
 580 585 590

Arg Ala Glu Thr Leu Ser Ile Leu Gly Lys Glu Leu Asp Leu Leu Ala
 595 600 605

Lys Thr Leu Asn Phe Gln Ser Asp Asp Thr Val Asn Ile Tyr Phe Leu
 610 615 620

Tyr Val Lys Leu Thr Val Cys Cys Phe Ala Phe Leu Pro Glu Thr Pro
 625 630 635 640

Pro Thr Asp Gln Ile Pro Tyr Val Thr Glu Ala Tyr Leu Thr Ala Thr
 645 650 655

Lys Ile Val Thr Leu Leu Asn Asn Leu Leu Glu Thr His Gln Leu Ile
 660 665 670

Glu Leu Pro Ile Tyr Ile Arg Gln Ala Ala Thr Phe Ser Ala Leu Ile
 675 680 685

Leu Phe Lys Leu Gln Leu Thr Pro Leu Leu Pro Asp Lys Tyr Phe Asp
 690 695 700

Ser Ala Arg Gln Ser Val Val Thr Ile His Arg Leu Tyr Arg Asn Gln
705 710 715 720

Leu Thr Ala Trp Ala Thr Ser Val Glu Asn Asp Ile Ser Arg Thr Ala
725 730 735

Ser Met Leu Glu Lys Leu Asn Phe Val Leu Ile Met His Pro Glu Val
740 745 750

Phe Val Glu Glu Asp Gly Ile Ile Ser Arg Met Arg Ser His Leu Thr
755 760 765

Gly Ser Leu Phe Tyr Asp Leu Val Trp Cys Val His Glu Ala Arg Arg
770 775 780

Arg Glu Met Asp Pro Glu Tyr Asn Lys Gln Ala Leu Glu Lys Ala Ala
785 790 795 800

Lys Lys Arg Lys Phe Ser Ser Asn Gly Ile Tyr Asn Gly Thr Ser Ser
805 810 815

Thr Gly Gly Ile Thr Asp Arg Lys Leu Tyr Pro Leu Pro Leu Tyr Asn
820 825 830

His Ile Ser Arg Asp Asp Phe Glu Thr Val Thr Lys Thr Thr Pro Ser
835 840 845

Gly Thr Thr Val Thr Thr Leu Val Pro Thr Lys Asn Ala Leu Lys Gln
850 855 860

Ala Glu Lys Leu Ala Lys Thr Asn Asn Gly Asp Ser Asp Gly Ser Ile
865 870 875 880

Met Glu Ile Asn Gly Ile Pro Leu Ser Met Leu Gly Glu Thr Gly Ser
885 890 895

Val Lys Phe Gln Ser Leu Phe Ala Asn Thr Ser Asn Ser Asn Asp Tyr
900 905 910

Asn Asn Asn Arg Thr Leu Leu Asp Ala Ser Asn Asp Ile Ser Ile Pro
915 920 925

Ser Asn Ser Ile Tyr Pro Val Ala Ser Val Pro Ala Ser Asn Asn Asn
930 935 940

Pro Gln Ser Thr Lys Val Asp Tyr Tyr Ser Asn Gly Pro Ser Val Ile
945 950 955 960

Pro Asp Leu Ser Met Lys Arg Ser Val Ser Thr Pro Val Asn His Phe
 965 970 975

Pro Ala Ser Val Pro Gly Leu Arg Asn His Pro Val Gly Asn Leu Ser
 980 985 990

Asn Asn Val Thr Leu Gly Ile Asp His Pro Ile Pro Arg Glu His Ser
 995 1000 1005

Asn Leu Gln Asn Val Thr Met Asn Tyr Asn Asn Gln Phe Ser Asn Ala
 1010 1015 1020

Asn Ala Ile Gly Arg Ser Gln Ser Ser Met Ser His Ser Arg Thr Pro
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Leu Phe Arg Ser Ile Tyr Asp Ser Trp Ile Pro Arg Pro Thr Pro Val
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<210> 11

<211> 854

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 11

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<210> 12

<211> 117

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 12

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Cys Glu Lys Ala Glu Lys Ser Asp Ile Pro Glu Ile Asp Lys Arg Lys
 35 40 45

Tyr Leu Val Pro Ala Asp Leu Thr Val Gly Gln Phe Val Tyr Val Ile
 50 55 60

Arg Lys Arg Ile Met Leu Pro Pro Glu Lys Ala Ile Phe Ile Phe Val
 65 70 75 80

Asn Asp Thr Leu Pro Pro Thr Ala Ala Leu Met Ser Ala Ile Tyr Gln
 85 90 95

Glu His Lys Asp Lys Asp Gly Phe Leu Tyr Val Thr Tyr Ser Gly Glu
 100 105 110

Asn Thr Phe Gly Arg
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<210> 13

<211> 1145

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 13

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<210> 14

<211> 214

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 14

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Tyr Ala Pro Arg Arg Gln Leu Ala Asn Thr Pro Ala Lys Asp Ser Thr
 35 40 45

Gly Lys Glu Val Ala Arg Pro Asn Asn Tyr Ala Gly Ala Leu Tyr Asp
 50 55 60

Pro Arg Asp Glu Thr Leu Asp Asp Trp Phe Asp Asn Asp Leu Ser Leu
 65 70 75 80

Phe Pro Ser Gly Phe Gly Phe Pro Arg Ser Val Ala Val Pro Val Asp
 85 90 95

Ile Leu Asp His Asp Asn Asn Tyr Glu Leu Lys Val Val Val Pro Gly
 100 105 110

Val Lys Ser Lys Lys Asp Ile Asp Ile Glu Tyr His Gln Asn Lys Asn
 115 120 125

Gln Ile Leu Val Ser Gly Glu Ile Pro Ser Thr Leu Asn Glu Glu Ser
 130 135 140

Lys Asp Lys Val Lys Val Lys Glu Ser Ser Ser Gly Lys Phe Lys Arg
 145 150 155 160

Val Ile Thr Leu Pro Asp Tyr Pro Gly Val Asp Ala Asp Asn Ile Lys
 165 170 175

Ala Asp Tyr Ala Asn Gly Val Leu Thr Leu Thr Val Pro Lys Leu Lys
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Pro Gln Lys Asp Gly Lys Asn His Val Lys Lys Ile Glu Val Ser Ser
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Gln Glu Ser Trp Gly Asn
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<210> 15

<211> 3377

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 15

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<211> 958

<212> PRT

<213> *Saccharomyces cerevisiae*

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Thr Gln Met Gln Ile Pro Lys Tyr Glu Asn Lys Pro Phe Lys Pro Pro
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Arg Arg Val Gly Ser Asn Lys Tyr Thr Gln Leu Lys Pro Thr Ala Thr
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Ala Val Thr Thr Ala Pro Ile Ser Lys Ala Lys Val Thr Val Asn Leu

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Leu Ile Asp Met Leu Val Cys Asp Glu Gly His Arg Leu Lys Asn Gly		
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Ala Ser Lys Ile Leu Asn Thr Leu Lys Ser Leu Asp Ile Arg Arg Lys		
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Phe Lys Arg Arg Phe Ile Ile Pro Ile Thr Arg Ala Arg Asp Thr Ala		
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580

585

590

Lys Pro Tyr Ser Gln Gln Ile Leu Ala Phe Lys Asp Ile Leu Gln Gly
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Asp Leu Lys Asp Leu Phe Ser Val His Thr Asp Thr Lys Ser Asn Thr

835

840

845

His Asp Leu Ile Cys Ser Cys Asp Gly Leu Gly Glu Glu Ile Glu Tyr
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Thr Thr Thr Trp Thr Ser Ala Leu Asp Leu Gln Lys Lys Met Asn Glu
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Ala Ala Thr Asn Asp Asp Ala Lys Lys Ser Gln Tyr Ile Arg Gln Cys
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Leu Val His Tyr Lys His Ile Asp Pro Ala Arg Gln Asp Glu Leu Phe
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<211> 3341

<212> DNA

<213> *Saccharomyces cerevisiae*

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<211> 946

<212> PRT

<213> *Saccharomyces cerevisiae*

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 Ser Tyr Ala Phe Ile Arg Ile His Gln Asp Asn Ala Lys Pro Leu Phe
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 Asp Thr Glu Leu Ser Asp Asp Leu His Lys Leu Ile Ser Ile Ser Lys
 85 90 95
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 100 105 110
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 115 120 125
 Asn Tyr Ile Lys Trp Leu Ile Pro Phe Ser Phe Phe Gly Leu Ser Ile
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 Tyr Glu Pro Phe Trp Ser Asp Arg Leu Ser Lys Tyr Ser Ser Phe Ser
 180 185 190
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 195 200 205
 Ser Val Ile Met Leu Lys Lys Cys Cys Phe Ile Pro Val Ala Leu Leu
 210 215 220
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 Ile Phe Tyr Lys Gln Ile Tyr Asn Gly Pro Met Ile Ser Ile Leu Ser
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 Phe Leu Pro Thr Ile Leu Ile Cys Thr Phe Thr Pro Val Leu Thr Val

260

265

270

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Tyr Leu Pro Met Gly His Leu Leu Thr Ala Glu Ile Arg Thr Lys Val
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Phe Asn Ala Phe Ser Ile Leu Ala Arg Leu Pro Thr His Asp Ser Asp
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Phe Ile Ile Asp Thr Lys Arg Tyr Glu Asp Gln Phe Phe Tyr Phe Ile
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Val Ile Asn Gln Leu Ile Gln Phe Ser Met Glu Asn Phe Val Pro Ser
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Leu Val Ser Ile Ala Gln Gln Lys Ile Asn Gly Pro Asn Pro Asn Phe
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Val Lys Ala Glu Ser Glu Ile Gly Lys Ala Gln Leu Ser Ser Ser Asp
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Cys Leu Ile Val Asn Leu Ile Val Tyr Gln Val Asp Leu Arg Lys Ala
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Val Leu Tyr Ser Lys Pro Glu Tyr Phe Pro Phe Pro Ile Tyr Asp Lys
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 <213> *Saccharomyces cerevisiae*

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tctcttga aaatcaatgac ttctacgact atgctgaaaa gagagtagcc ggtactgact 1800
tcctaaagggt ctgtaacgct agcagcgtca gtaactctac tgaattgacc ttctactggg 1860
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```

<210> 20

<211> 467

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 20

```

Met Phe Lys Ser Val Val Tyr Ser Ile Leu Ala Ala Ser Leu Ala Asn
  1             5             10            15

```

```

Ala Gly Thr Ile Pro Leu Gly Lys Leu Ala Asp Val Asp Lys Ile Gly
      20             25            30

```

```

Thr Gln Lys Asp Ile Phe Pro Phe Leu Gly Gly Ala Gly Pro Tyr Tyr
      35             40            45

```

```

Ser Phe Pro Gly Asp Tyr Gly Ile Ser Arg Asp Leu Pro Glu Gly Cys
      50             55            60

```

```

Glu Met Lys Gln Leu Gln Met Val Gly Arg His Gly Glu Arg Tyr Pro

```

65		70		75		80
Thr Val Ser Leu Ala Lys Thr Ile Lys Ser Thr Trp Tyr Lys Leu Ser						
	85			90		95
Asn Tyr Thr Arg Gln Phe Asn Gly Ser Leu Ser Phe Leu Asn Asp Asp						
	100			105		110
Tyr Glu Phe Phe Ile Arg Asp Asp Asp Asp Leu Glu Met Glu Thr Thr						
	115			120		125
Phe Ala Asn Ser Asp Asp Val Leu Asn Pro Tyr Thr Gly Glu Met Asn						
	130			135		140
Ala Lys Arg His Ala Arg Asp Phe Leu Ala Gln Tyr Gly Tyr Met Val						
	145			150		155
Glu Asn Gln Thr Ser Phe Ala Val Phe Thr Ser Asn Ser Lys Arg Cys						
	165			170		175
His Asp Thr Ala Gln Tyr Phe Ile Asp Gly Leu Gly Asp Gln Phe Asn						
	180			185		190
Ile Thr Leu Gln Thr Val Ser Glu Ala Glu Ser Ala Gly Ala Asn Thr						
	195			200		205
Leu Ser Ala Cys Asn Ser Cys Pro Ala Trp Asp Tyr Asp Ala Asn Asp						
	210			215		220
Asp Ile Val Asn Glu Tyr Asp Thr Thr Tyr Leu Asp Asp Ile Ala Lys						
	225			230		235
Arg Leu Asn Lys Glu Asn Lys Gly Leu Asn Leu Thr Ser Thr Asp Ala						
	245			250		255
Ser Thr Leu Phe Ser Trp Cys Ala Phe Glu Val Asn Ala Lys Gly Tyr						
	260			265		270
Ser Asp Val Cys Asp Ile Phe Thr Lys Asp Glu Leu Val His Tyr Ser						
	275			280		285
Tyr Tyr Gln Asp Leu His Thr Tyr Tyr His Glu Gly Pro Gly Tyr Asp						
	290			295		300
Ile Ile Lys Ser Val Gly Ser Asn Leu Phe Asn Ala Ser Val Lys Leu						
	305			310		315
Leu Lys Gln Ser Glu Ile Gln Asp Gln Lys Val Trp Leu Ser Phe Thr						

325 330 335
 His Asp Thr Asp Ile Leu Asn Phe Leu Thr Thr Ala Gly Ile Ile Asp
 340 345 350
 Asp Lys Asn Asn Leu Thr Ala Glu Tyr Val Pro Phe Met Gly Asn Thr
 355 360 365
 Phe His Arg Ser Trp Tyr Val Pro Gln Gly Ala Arg Val Tyr Thr Glu
 370 375 380
 Lys Phe Gln Cys Ser Asn Asp Thr Tyr Val Arg Tyr Val Ile Asn Asp
 385 390 395 400
 Ala Val Val Pro Ile Glu Thr Cys Ser Thr Gly Pro Gly Phe Ser Cys
 405 410 415
 Glu Ile Asn Asp Phe Tyr Asp Tyr Ala Glu Lys Arg Val Ala Gly Thr
 420 425 430
 Asp Phe Leu Lys Val Cys Asn Val Ser Ser Val Ser Asn Ser Thr Glu
 435 440 445
 Leu Thr Phe Tyr Trp Asp Trp Asn Thr Thr His Tyr Asn Ala Ser Leu
 450 455 460
 Leu Arg Gln
 465

<210> 21

<211> 1563

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 21

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 aaataaatta tttccttact tttttttcta cagtttgcac cattaacctc ttttcttgca 180
 tccatacatc tttgaactcc atacatctta tttttttgct gttttttttc agtgtctcgg 240
 gcatacaggc cgcttatctt catgccggcc catcatccta ggaaactctt tcggtatggg 300
 ccaagggcag gcgaaatcc tatgtgcgtg gagctgatac aatctcggct ggcttggttt 360
 gtagggcacg gtcaatgaat gcctgatggg agaaaaattc atctttatga aaagtgatct 420
 taatttgaat agtgtgccct tcaaaacatt tggaagtcac taattgaaac tatccagtgt 480
 gaatagacga ctgagccatc atgaaggtat gtaatatcac ccaaactcctt agaattctaa 540
 tgaatcagca cgcgctaacc ggctgtttct gactgtttga taaacgtata cccacaaatt 600
 agtgcactat aataaaaaatt ctcaagaaca acgttgttta aacgagataa ttccctctaa 660

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tatacacgta cgcacactta ggaaaatata tcgctaagtt caaattaagg aatgaaaaag 720
gaatttacga aaagggttta gaaatatcaa tgaaaataag aaaaacctgt aacggaagaa 780
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gaaattgatg atgaacaccg tattcgtggt ttcttcgaca agagaatcgg tcaagaagtc 960
gatggtgaag ccgttggtga tgaattcaag ggctacgtct tcaagatctc tgggtggtaac 1020
gacaaacaag gtttcccaat gaagcaagggt gttttgttgc caactagaat caagttggtg 1080
ttgaccaaga acgtttcttg ttacagacca agacgtgatg gtgaaagaaa gagaaagtcc 1140
gtcagagggtg ccattggttg tccagatttg gctgtcttgg ctttggtcat tgtcaagaag 1200
ggtgaacaag aattggaagg tctaactgac actactgttc caaagagatt ggggtccaaag 1260
agagctaaca acatcagaaa gttcttcggt ttgtccaagg aagatgacgt tcgtgatttc 1320
gtcatcagaa gagaagtcac caagggtgaa aagacttaca ccaaggctcc aaagatccaa 1380
agattgggta ctctcaaaag attgcaaaga aagagacacc aaagagcttt gaaggtcaga 1440
aacgctcaag ctcaaagaga agctgctgcc gaatacgtc aattgttggc taagagattg 1500
tctgaaagaa aggctgaaaa ggccgaaatc agaaagagaa gagcttcttc tttgaaggct 1560
taa

```

<210> 22

<211> 236

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 22

```

Met Lys Leu Asn Ile Ser Tyr Pro Val Asn Gly Ser Gln Lys Thr Phe
  1                      5                      10                      15

```

```

Glu Ile Asp Asp Glu His Arg Ile Arg Val Phe Phe Asp Lys Arg Ile
      20                      25                      30

```

```

Gly Gln Glu Val Asp Gly Glu Ala Val Gly Asp Glu Phe Lys Gly Tyr
      35                      40                      45

```

```

Val Phe Lys Ile Ser Gly Gly Asn Asp Lys Gln Gly Phe Pro Met Lys
      50                      55                      60

```

```

Gln Gly Val Leu Leu Pro Thr Arg Ile Lys Leu Leu Leu Thr Lys Asn
      65                      70                      75                      80

```

```

Val Ser Cys Tyr Arg Pro Arg Arg Asp Gly Glu Arg Lys Arg Lys Ser
      85                      90                      95

```

```

Val Arg Gly Ala Ile Val Gly Pro Asp Leu Ala Val Leu Ala Leu Val
      100                      105                      110

```

```

Ile Val Lys Lys Gly Glu Gln Glu Leu Glu Gly Leu Thr Asp Thr Thr
      115                      120                      125

```

Val Pro Lys Arg Leu Gly Pro Lys Arg Ala Asn Asn Ile Arg Lys Phe
 130 135 140

Phe Gly Leu Ser Lys Glu Asp Asp Val Arg Asp Phe Val Ile Arg Arg
 145 150 155 160

Glu Val Thr Lys Gly Glu Lys Thr Tyr Thr Lys Ala Pro Lys Ile Gln
 165 170 175

Arg Leu Val Thr Pro Gln Arg Leu Gln Arg Lys Arg His Gln Arg Ala
 180 185 190

Leu Lys Val Arg Asn Ala Gln Ala Gln Arg Glu Ala Ala Glu Tyr
 195 200 205

Ala Gln Leu Leu Ala Lys Arg Leu Ser Glu Arg Lys Ala Glu Lys Ala
 210 215 220

Glu Ile Arg Lys Arg Arg Ala Ser Ser Leu Lys Ala
 225 230 235

<210> 23

<211> 893

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 23

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 agtgtattac caacttgcgc atgcaaggat atcacactcc tgtttctgcc tcatgtcttt 180
 taaaacgctt ccacgggaca tgggttctaa ttatggagaa gatcaagctt tgaaatggcc 240
 cgtttacaca ttttgataca accgtagacg gcgtctcgtt tcaaagaccg tgtggttgtc 300
 tatcagtata tactcattgt gtttttcaaa aaatctctgg gttgtttaga tgccactata 360
 tttctattcg tatttatttt tatgtatact tattttgctt atttttctta tactcaggaa 420
 acgtcacttg gcttgatata ctgcacgctt tattctgcaa attcaggtct caaatctgaa 480
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 atcatggcca atgtcaaaat cactgtactt ctccaaacac tgtacgacaa aacaaaacaa 600
 acaaactctt gttagtaaaa aagaaagga aactagtaat atggagacac atcgtaaaaa 660
 aaatgttgca catacgcttg gttgttcttt ggagccatta tccagaacag cacggacatg 720
 gcactaacca ctatgaatac accaacaaca gtatagctaa attggacgcg cagagagtta 780
 gtagaagaag aaggaagaaa agggaagcgg agagaagaga ttatgacaca taaaactac 840
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<210> 24

<211> 130

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 24

Met Glu Leu Ala Lys Glu Arg Asn Gly Pro His Gln Lys His His Gly
 1 5 10 15

Gln Cys Gln Asn His Cys Thr Ser Pro Asn Thr Val Arg Gln Asn Lys
 20 25 30

Thr Asn Lys Leu Leu Leu Val Lys Lys Lys Gly Lys Leu Val Ile Trp
 35 40 45

Arg His Ile Val Lys Lys Met Leu His Ile Arg Leu Val Val Leu Trp
 50 55 60

Ser His Tyr Pro Glu Gln His Gly His Gly Thr Asn His Tyr Glu Tyr
 65 70 75 80

Thr Asn Asn Ser Ile Ala Lys Leu Asp Ala Gln Arg Val Ser Arg Arg
 85 90 95

Arg Arg Lys Lys Arg Glu Ala Glu Arg Arg Asp Tyr Asp Thr Tyr Lys
 100 105 110

Leu Leu Ile Thr Leu Cys Ser Leu Leu Phe Val Gly Pro Leu Phe Leu
 115 120 125

Lys Val
 130

<210> 25

<211> 1429

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 25

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 aggcgggttta ttatctttgt ccctttatac tgttgtgttt cttgcttatt gcttcagtag 180
 gcagcgata gtataaccag aaaaaagtga aaaataaact aaaaaagcac tatgagatga 240
 acggtaaaaa tccaccagag atttgctcac taataatcct gtaccatgtc catcaacctta 300
 cattccgcac ccgagtatga tccatcttat aagctgatcc agttgacacc agagttactg 360
 gatataatac aggatccggt tcaaaatcac cagttaaggt ttaagtcatt ggacaaagac 420
 aagtctgaag ttgtactgtg ttcgcacgac aagacttggg tgctgcaagc agcgcaaaca 480
 ttcaaacaca gttctactaa tgagagaatt tgttcctgaa caacctatta ctttcgacga 540


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aacgctcttg tttggactgt ccaagccgta catggacgtc gtgggattcg ccaagactga 600
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caacggagaa ctggatttct cgcacaaaat catgaagagg tcatctacaa aggttatcgg 720
gaccctggaa gaactacttg agaactcacc atgttctgcg ctagaaggta tatcaaaatg 780
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gcctctaatt gaagaactaa attcaagagg tatgaaaata gacagtttca tcatgaagta 1380
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<210> 26

<211> 309

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 26

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Met Arg Glu Phe Val Pro Glu Gln Pro Ile Thr Phe Asp Glu Thr Leu
  1              5              10              15

Leu Phe Gly Leu Ser Lys Pro Tyr Met Asp Val Val Gly Phe Ala Lys
      20              25              30

Thr Glu Ser Glu Phe Glu Thr Arg Glu Thr His Gly Glu Leu Asn Leu
      35              40              45

Asn Ser Val Pro Ile Tyr Asn Gly Glu Leu Asp Phe Ser Asp Lys Ile
      50              55              60

Met Lys Arg Ser Ser Thr Lys Val Ile Gly Thr Leu Glu Glu Leu Leu
      65              70              75              80

Glu Asn Ser Pro Cys Ser Ala Leu Glu Gly Ile Ser Lys Trp His Lys
      85              90              95

Ile Gly Gly Ser Val Lys Asp Gly Val Leu Cys Ile Leu Ser Gln Asp
      100              105              110

Phe Leu Phe Lys Ala Leu His Val Leu Leu Met Ser Ala Met Ala Glu
      115              120              125

Ser Leu Asp Leu Gln His Leu Asn Val Glu Asp Thr His His Ala Val

```

130 135 140
 Gly Lys Asp Ile Glu Asp Glu Phe Asn Pro Tyr Thr Arg Glu Ile Ile
 145 150 155 160
 Glu Thr Val Leu Asn Lys Phe Ala Val Gln Glu Gln Glu Ala Glu Asn
 165 170 175
 Asn Thr Trp Arg Leu Arg Ile Pro Phe Ile Ala Gln Trp Tyr Gly Ile
 180 185 190
 Gln Ala Leu Arg Lys Tyr Val Ser Gly Ile Ser Met Pro Ile Asp Glu
 195 200 205
 Phe Leu Ile Lys Trp Lys Ser Leu Phe Pro Pro Phe Phe Pro Cys Asp
 210 215 220
 Ile Asp Ile Asp Met Leu Arg Gly Tyr His Phe Lys Pro Thr Asp Lys
 225 230 235 240
 Thr Val Gln Tyr Ile Ala Lys Ser Thr Leu Pro Met Asp Pro Lys Glu
 245 250 255
 Arg Phe Lys Val Leu Phe Arg Leu Gln Ser Gln Trp Asp Leu Glu Asp
 260 265 270
 Ile Lys Pro Leu Ile Glu Glu Leu Asn Ser Arg Gly Met Lys Ile Asp
 275 280 285
 Ser Phe Ile Met Lys Tyr Ala Arg Arg Lys Arg Leu Gly Lys Lys Thr
 290 295 300
 Val Val Thr Ser Arg
 305

<210> 27
 <211> 1952
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 27
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 gaccctgagg aaggagccga tgaggccact ctgcaacgca ggaggcagtt ggaacagatc 120
 attacgggag acaacgctga ggaggagttg gaaaggtaca tccgtgctat ggtcagagag 180
 cagatgctgg gccagggctc catggcgggt tccggggacg aaccagattc caagagaaga 240
 aaataacgac ccagcacaaa ggctcttaca gcttgctaaa agaaattgaa cgcgacgcta 300

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catgaactac ttctttctct tacatagtct tttcccttat gtatcttttc tgtacattaa 360
tagacgttct tacaaggtaa aatttcaccg cgttttttaa tagaatgaaa aaaacgttgt 420
agagtgaaag aaaagcaaca aatatacagt tcacaaggca gcttcgtata gtaatacagc 480
acgaaaaaca gtcctatagaa atggtaacac agaccaatcc ggtccctgtt acatatccaa 540
cggatgctta tatccccacg tatctgcccc atgataaggt ctccaatctg gcagatttga 600
aaaaattgat agaaatggat tccagactag atttgtatct gacaagaagg aggctggata 660
cgtccatcaa ttacctaca aacaccaaga ccaaggacca tcccccaat aaagagatgc 720
tgaggattta cgtctacaac actacggaaa gcagccctcg cagcgattct ggcaccccag 780
cggactcagg caagactaca tggacactga gaatagaagg taagcttctg cagcagtcgc 840
caaacggaaa gcacccattt agtgagtttt tggaagggtg cgcggtcgac tttaaaagac 900
tgaaaccgct gggcatgggc aagaagagga aacgcgattc gtcattgagc cttcctttga 960
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actacgatga aaacaacggt gtggagtttg atggtatcga catcaagagg caaggcaagg 1140
ataatttgcg atgcagtata accatccagt tgaggggtgt cgacggtgga aaagtacagt 1200
actcgcccaa cttagctacc ttgataggta tgcaaacggg ctccgttaat gacgcggttt 1260
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caattgatct ttccaaagat accacctatg gtgctaccac cttggatgta gatgtgtcgc 1620
acattctcca ccagcctcaa cccagccaa atttacaata agaggaagaa acagatgctg 1680
aagacacagc aaaactacgt gaaatcacia agcttgcttc gcagttgaac tctagtgtc 1740
aaaaatacca gtttttccac gaactgtctt tgcattcaag agaaacgctg actcactact 1800
tatggtcttc caagcaaac gagcttggtc tgcagggcga ccaatacttc aatgaagatg 1860
ctgcaagaac gagtgacata tacagtaaca acaacaatga caggtcacta atgggcaata 1920
tctcactact gtactccaa ggaagactat aa 1952

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<210> 28

<211> 483

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 28

Met Val Thr Gln Thr Asn Pro Val Pro Val Thr Tyr Pro Thr Asp Ala
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Tyr Ile Pro Thr Tyr Leu Pro Asp Asp Lys Val Ser Asn Leu Ala Asp
20 25 30

Leu Lys Lys Leu Ile Glu Met Asp Ser Arg Leu Asp Leu Tyr Leu Thr
35 40 45

Arg Arg Arg Leu Asp Thr Ser Ile Asn Leu Pro Thr Asn Thr Lys Thr
50 55 60

Lys Asp His Pro Pro Asn Lys Glu Met Leu Arg Ile Tyr Val Tyr Asn
 65 70 75 80
 Thr Thr Glu Ser Ser Pro Arg Ser Asp Ser Gly Thr Pro Ala Asp Ser
 85 90 95
 Gly Lys Thr Thr Trp Thr Leu Arg Ile Glu Gly Lys Leu Leu His Glu
 100 105 110
 Ser Ala Asn Gly Lys His Pro Phe Ser Glu Phe Leu Glu Gly Val Ala
 115 120 125
 Val Asp Phe Lys Arg Leu Lys Pro Leu Gly Met Gly Lys Lys Arg Lys
 130 135 140
 Arg Asp Ser Ser Leu Ser Leu Pro Leu Asn Leu Gln Gln Pro Glu Tyr
 145 150 155 160
 Asn Asp Gln Asp Ser Thr Met Gly Asp Asn Asp Asn Gly Glu Asp Glu
 165 170 175
 Asp Ser Ala Glu Ala Glu Ser Arg Glu Glu Ile Val Asp Ala Leu Glu
 180 185 190
 Trp Asn Tyr Asp Glu Asn Asn Val Val Glu Phe Asp Gly Ile Asp Ile
 195 200 205
 Lys Arg Gln Gly Lys Asp Asn Leu Arg Cys Ser Ile Thr Ile Gln Leu
 210 215 220
 Arg Gly Val Asp Gly Gly Lys Val Gln Tyr Ser Pro Asn Leu Ala Thr
 225 230 235 240
 Leu Ile Gly Met Gln Thr Gly Ser Val Asn Asp Ala Val Tyr Ser Ile
 245 250 255
 Tyr Lys Tyr Ile Leu Ile Asn Asn Leu Phe Val Thr Glu Gln Thr Glu
 260 265 270
 Ala Gln Asp Gly Ser Asn Asp Ala Glu Asp Ser Ser Asn Glu Asn Asn
 275 280 285
 Asn Lys Asn Gly Ala Gly Asp Asp Asp Gly Val Glu Gly Ser Thr Pro
 290 295 300
 Lys Asp Lys Pro Glu Leu Gly Glu Val Lys Leu Asp Ser Leu Leu Gln
 305 310 315 320

Lys Val Leu Asp Thr Asn Ala Ala His Leu Pro Leu Met Asn Val Val
 325 330 335
 Gln Thr Val Asn Lys Leu Val Ser Pro Leu Pro Pro Ile Ile Leu Asp
 340 345 350
 Tyr Thr Ile Asp Leu Ser Lys Asp Thr Thr Tyr Gly Ala Thr Thr Leu
 355 360 365
 Asp Val Asp Val Ser His Ile Leu His Gln Pro Gln Pro Gln Pro Asn
 370 375 380
 Leu Gln Lys Glu Glu Glu Thr Asp Ala Glu Asp Thr Ala Lys Leu Arg
 385 390 395 400
 Glu Ile Thr Lys Leu Ala Leu Gln Leu Asn Ser Ser Ala Gln Lys Tyr
 405 410 415
 Gln Phe Phe His Glu Leu Ser Leu His Pro Arg Glu Thr Leu Thr His
 420 425 430
 Tyr Leu Trp Ser Ser Lys Gln Asn Glu Leu Val Leu Gln Gly Asp Gln
 435 440 445
 Tyr Phe Asn Glu Asp Ala Ala Arg Thr Ser Asp Ile Tyr Ser Asn Asn
 450 455 460
 Asn Asn Asp Arg Ser Leu Met Gly Asn Ile Ser Leu Leu Tyr Ser Gln
 465 470 475 480
 Gly Arg Leu

<210> 29

<211> 911

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 29

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 gtcgtctttg acgaaggaga cgaaaacctc ttctaaaacg ttgggagaga gataattaca 180
 tggccagaac aatactgcaa cgtgcatata gtcgttagtc tgtgcttgca catccacggc 240
 agccgcagtg gacgcactga tggaaggaca cctgtgtgcc ctttttgctg gttcttctct 300
 ctaactgtgc acgaggcacc ctgcagatgc aagtgtctacc gttgttagtt tcgttctttt 360
 gaatgcagcg cagacagcac agttttttcat acccggtttt gcgccatttg gcaattagca 420

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atttatcagc atacttttcc tttatcaacc aatcgtaaag gtctttggag atggcctttc 480
tctttagta cagagtatat atgtatctag agcgctggtg gtggagttgc attatctccc 540
agagctgctc attggacttt gctgcgagct tagacgactt gtccttttgg gcatctctga 600
gttggatttc gaaatctgtg agggttggct tgattttttc gaaccctgca ggtgcaggct 660
tggtatcttct ggtcttttatg cgcggcatgt cgttttgtga ggtgagcttt gctagtcttg 720
acggctgtag agtggtttac attgatgatg agtccctaag aaaatttttc tttttttttc 780
agtatttcac tttccgttgt gaacgacaaa tgtactatgc gttcaagagc caacgcagta 840
tcacgtcaa agttcctacc acaacgcgtg tgattgatct tgtactgggt gtaaagtgc 900
taagtctgtg a 911

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<210> 30

<211> 136

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 30

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Met Tyr Leu Glu Arg Trp Trp Trp Ser Cys Ile Ile Ser Gln Ser Cys
  1                      5                      10                      15

```

```

Ser Leu Asp Phe Ala Ala Ser Leu Asp Asp Leu Ser Phe Trp Ala Ser
          20                      25                      30

```

```

Leu Ser Trp Ile Ser Lys Ser Val Arg Val Gly Leu Ile Phe Ser Asn
  35                      40                      45

```

```

Pro Ser Gly Ala Gly Leu Asp Leu Leu Val Phe Met Arg Gly Met Ser
  50                      55                      60

```

```

Phe Cys Glu Val Ser Phe Ala Ser Leu Asp Gly Cys Arg Gly Val Tyr
  65                      70                      75                      80

```

```

Ile Asp Asp Glu Ser Leu Arg Lys Phe Phe Phe Phe Phe Gln Tyr Phe
          85                      90                      95

```

```

Thr Phe Arg Cys Glu Arg Gln Met Tyr Tyr Ala Phe Lys Ser Gln Arg
        100                      105                      110

```

```

Ser Ile Ile Val Lys Val Pro Thr Thr Thr Arg Val Ile Asp Leu Val
        115                      120                      125

```

```

Leu Val Val Asn Val Leu Ser Leu
        130                      135

```

<210> 31

<211> 1448

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 31

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ttttcaccta caaggaacta ccttttatag ccaccctaag taaaacaaca ttagcttagc 180
atcctcaatt cttatcgtat gttgttgctg ctatttttat cctattgttc ctggcatcgc 240
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agggttaata cgaaatatgt taaggcttag tttccaaaaa atgaagaaaa tgtgattaga 360
catcctgggg aaattaggtt taaatagggc gggcgctaca ggggttttcc taacaaat 420
caatgataat agtggcatca tcacgtcat atccagtgtta ggtatggact agaacagaaa 480
gcaatttgca gcaagacaat atgactacga cggtaaccaa gatattcgcg tttcacgagt 540
tttcagacgt ggcagaggcc gtagctgacc atgtagtcca cgcgcaagac ggtgcattgg 600
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gtagtggcag tggtagcagt aagcccaaaa aggagaaacg gttcaagatt gctctctccg 780
gtgggtcatt gatcgaagt ctacacgaag gtctgctaaa acgagacgat gtacgggtgg 840
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gcctacctag cagtattgtc aacgaagggt ctgctggtcg tgtatcatgg tttgttgacg 1380
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ctatttaa
1448

```

<210> 32

<211> 315

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 32

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Met Thr Thr Thr Val Pro Lys Ile Phe Ala Phe His Glu Phe Ser Asp
 1             5             10            15

Val Ala Glu Ala Val Ala Asp His Val Val His Ala Gln Asp Gly Ala
      20             25            30

Leu Ala Pro Lys Asn Glu Arg Lys His Ser Val Pro Asn Ile Ser Met
      35             40            45

Asn Ala Leu Asp Met Thr Arg Glu Ala Ser Cys Lys Ser Thr Ala Ser
      50             55            60

```

Ala Ala Glu Gly Lys Ser Gly Ser Ser Gly Ser Gly Ser Gly Ser Ser
 65 70 75 80
 Lys Pro Lys Lys Glu Lys Arg Phe Lys Ile Ala Leu Ser Gly Gly Ser
 85 90 95
 Leu Ile Glu Val Leu His Glu Gly Leu Leu Lys Arg Asp Asp Val Arg
 100 105 110
 Trp Gly Asp Trp Asp Ile Tyr Phe Ala Asp Glu Arg Leu Val Pro Phe
 115 120 125
 Ser Ser Asn Glu Ser Asn Tyr Gly Cys Ala Lys Arg Lys Ile Leu Asp
 130 135 140
 Leu Ile Asp Thr Ala Lys Tyr Gly Thr Pro Lys Val Tyr His Ile Asp
 145 150 155 160
 Glu Ser Leu Ile Asp Asp Pro Gln Glu Cys Val Asp Asn Tyr Glu Lys
 165 170 175
 Val Leu Ile Arg Gly Phe Ala Gly Arg Asp Ser Val Lys Leu Pro Met
 180 185 190
 Phe Asp Leu Phe Leu Leu Gly Cys Ala Pro Asp Gly His Ile Ala Ser
 195 200 205
 Leu Phe Pro Asn Phe Gln Asp Asn Leu Arg Glu Lys Leu Ala Trp Val
 210 215 220
 Val Pro Val Glu Asn Ala Pro Ser Gly Pro Ser Thr Arg Ile Ser Leu
 225 230 235 240
 Thr Ile Pro Val Ile Cys His Ser His Arg Val Thr Phe Val Val Glu
 245 250 255
 Gly Ala Thr Lys Ala Pro Ile Ile Lys Thr Ile Met Glu Arg Pro Glu
 260 265 270
 Lys Gly Leu Pro Ser Ser Ile Val Asn Glu Gly Ala Ala Gly Arg Val
 275 280 285
 Ser Trp Phe Val Asp Asp Asp Ala Leu Thr Asp Val Leu Val Thr Lys
 290 295 300
 Lys Lys Tyr Lys Phe His Gln Gly Leu Ser Ile
 305 310 315

<210> 33
 <211> 1196
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 33
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 ctacagctacc gatttagtggt gttgactttt ccgcaagatc cttttctccc tctttggacc 180
 tagtcatccc tccacacaag attcgctctt aagtagtggc gcaggctgtt cgcttttaag 240
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 gcactagcag ttagttaact ttctggaacg cgcagtagcg gtcccggggc gcctgaggcg 360
 gagcggttcgc gaaatcggga aaacattata ctgggaaaga tcaactatcta ttctctaaat 420
 gaacttttaa gcaaattatc gtaagataga aaagacgaaa ccttagcaac ctagcggttt 480
 aatatagaaa caattttatt atgatacctt ccaataagag aaatgctaga attttaagca 540
 ttacaacgct attattgttg ttagtggttt tcgtagcgca aaatgcgaac ttcttgacgg 600
 tagagataaa agaggaaact tctaaagcat ttagtactaa tatggacaat atggctggag 660
 gatcttccag ggaatatgct gctatgccga cttctaccac gaataagggg agctctgaag 720
 tagacgaaga aattaatgaa ataaaacaga aggtgggact ccaacagccc atagcatcgg 780
 ttgatgatag tttgtcggcc attaaaaacg ataaagggtc gcgaataacc aaagctttta 840
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 gcacctgttc atatagcaag ggcagtaggg aactgcttga aaatgagtat cagtttatcc 960
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 gaggtaatga agaaatcaag aaactgcaca ctcaaggga acttttagaa tcattacaag 1140
 tctggagtga tggtaaattc tcggttgagc aacgtgaaaa accttccaat aattga 1196

<210> 34
 <211> 231
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 34
 Met Ile Pro Ser Asn Lys Arg Asn Ala Arg Ile Leu Ser Ile Thr Thr
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 Leu Leu Leu Leu Leu Val Phe Phe Val Ala Gln Asn Ala Asn Phe Leu
 20 25 30
 Thr Val Glu Ile Lys Glu Glu Thr Ser Lys Ala Phe Ser Thr Asn Met
 35 40 45
 Asp Asn Met Ala Gly Gly Ser Ser Arg Glu Tyr Ala Ala Met Pro Thr
 50 55 60

Ser Thr Thr Asn Lys Gly Ser Ser Glu Val Asp Glu Glu Ile Asn Glu
 65 70 75 80
 Ile Lys Gln Lys Val Gly Leu Gln Gln Pro Ile Ala Ser Val Asp Asp
 85 90 95
 Ser Leu Ser Ala Ile Lys Asn Asp Lys Gly Ser Arg Ile Thr Lys Ala
 100 105 110
 Phe Asn Val Gln Lys Glu Tyr Ser Leu Ile Leu Asp Leu Ser Pro Ile
 115 120 125
 Ile Ile Phe Ser Lys Ser Thr Cys Ser Tyr Ser Lys Gly Met Lys Glu
 130 135 140
 Leu Leu Glu Asn Glu Tyr Gln Phe Ile Pro Asn Tyr Tyr Ile Ile Glu
 145 150 155 160
 Leu Asp Lys His Gly His Gly Glu Glu Leu Gln Glu Tyr Ile Lys Leu
 165 170 175
 Val Thr Gly Arg Gly Thr Val Pro Asn Leu Leu Val Asn Gly Val Ser
 180 185 190
 Arg Gly Gly Asn Glu Glu Ile Lys Lys Leu His Thr Gln Gly Lys Leu
 195 200 205
 Leu Glu Ser Leu Gln Val Trp Ser Asp Gly Lys Phe Ser Val Glu Gln
 210 215 220
 Arg Glu Lys Pro Ser Asn Asn
 225 230

<210> 35

<211> 1889

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 35

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 caataccagg tacgactcct gatccaataa ttgaggcgca gaacgataat gatagtagtg 180
 atagtagcgg catagatttg atagccttct taagaaatgg accattataa agtttttgta 240
 tcgcatgtt tgaaaatgga aagtaaggaa cgtaatacaa attgacaagt agccgacatg 300
 aatgacgctc acttctctta tatatgttag gtagtatatg cattatagaa tttattcatt 360

```

gaagcaatgt gattcctcga taagtaagct ttttttctgt ctggcggcga accattagag 420
aacaaaagac cgagttaaga aaaagtcat aaaaaacttt tgaaaatgga tgagtgtctg 480
tataatggaa taggaaactt atgcaaagaa ataatagggt aagaaatttg ttacagtgc 540
cagtaataat ggctcgacaa ctcaaaagga atgcattatc tgcagggtctt gcttttgcag 600
gtaatgcaac ctcaaatgag tttgatgaac atttgcaaaa tgagggtgaa agagagaggg 660
aaattcaaaa gaaaaaaaaa ataaagcgaa ctcaatcaaa aaaatcgcca gatttgatta 720
ataaatctac ttttcaatca cgaacgatag gcagcaaaaa agagaaacat agacaactag 780
atccagagta tgaaattgtc atcgatggcc ctctaaggaa aatcaagccc taccatttta 840
cgtacaggac cttttgcaaa gagcgttgga gagataaaaa attggttgat gtctttatat 900
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gtaatagggt agataggctt acaagtggat taatgttttt ggcaaaaact ccgaaggagg 1260
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tatacgaatc aactgagact gaagaaggaa ccgaaaagaa aaagtgggtgc tacaaaacag 1860
agtatccaga atgggctctg agaagatag 1889

```

<210> 36

<211> 462

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 36

```

Met Gln Arg Asn Asn Arg Leu Arg Asn Leu Phe Thr Val Pro Val Ile
  1              5              10             15

```

```

Met Ala Arg Gln Leu Lys Arg Asn Ala Leu Ser Ala Gly Leu Ala Phe
          20              25             30

```

```

Ala Gly Asn Ala Thr Ser Asn Glu Phe Asp Glu His Leu Gln Asn Glu
          35              40             45

```

```

Val Glu Arg Glu Arg Glu Ile Gln Lys Lys Lys Lys Ile Lys Arg Thr
          50              55             60

```

```

Gln Ser Lys Lys Ser Pro Asp Leu Ile Asn Lys Ser Thr Phe Gln Ser
          65              70             75             80

```

Arg Thr Ile Gly Ser Lys Lys Glu Lys His Arg Gln Leu Asp Pro Glu
85 90 95

Tyr Glu Ile Val Ile Asp Gly Pro Leu Arg Lys Ile Lys Pro Tyr His
100 105 110

Phe Thr Tyr Arg Thr Phe Cys Lys Glu Arg Trp Arg Asp Lys Lys Leu
115 120 125

Val Asp Val Phe Ile Ser Glu Phe Arg Asp Arg Glu Ser Glu Tyr Tyr
130 135 140

Lys Arg Thr Ile Glu Asn Gly Asp Val His Ile Asn Asp Glu Thr Ala
145 150 155 160

Asp Leu Ser Thr Val Ile Arg Asn Gly Asp Leu Ile Thr His Gln Val
165 170 175

His Arg His Glu Pro Pro Val Thr Ser Arg Pro Ile Lys Val Ile Phe
180 185 190

Glu Asp Asp Asn Ile Met Val Ile Asp Lys Pro Ser Gly Ile Pro Val
195 200 205

His Pro Thr Gly Arg Tyr Arg Phe Asn Thr Ile Thr Lys Met Leu Gln
210 215 220

Asn Asn Leu Gly Phe Val Val Asn Pro Cys Asn Arg Leu Asp Arg Leu
225 230 235 240

Thr Ser Gly Leu Met Phe Leu Ala Lys Thr Pro Lys Gly Ala Asp Asn
245 250 255

Ile Gly Asp Gln Leu Lys Ala Arg Glu Val Thr Lys Glu Tyr Val Ala
260 265 270

Lys Val Val Gly Glu Phe Pro Glu Thr Glu Val Ile Val Glu Lys Pro
275 280 285

Leu Lys Leu Ile Glu Pro Arg Leu Ala Leu Asn Ala Val Cys Gln Met
290 295 300

Asp Glu Lys Gly Ala Lys His Ala Lys Thr Val Phe Asn Arg Ile Ser
305 310 315 320

Tyr Asp Gly Lys Thr Ser Ile Val Lys Cys Lys Pro Leu Thr Gly Arg
325 330 335

Ser His Gln Ile Arg Val His Leu Gln Tyr Leu Gly His Pro Ile Ala
340 345 350

Asn Asp Pro Ile Tyr Ser Asn Asp Glu Val Trp Gly Asn Asn Leu Gly
355 360 365

Lys Gly Gly Gln Ala Asp Phe Asp Ile Val Ile Thr Lys Leu Asp Glu
370 375 380

Ile Gly Lys Arg Lys Pro Ala Lys Ser Trp Phe His Ser Asn Gly Gly
385 390 395 400

Tyr Gly Glu Val Leu Arg Gln Glu Lys Cys Ser Ile Cys Glu Ser Asp
405 410 415

Leu Tyr Thr Asp Pro Gly Pro Asn Asp Leu Asp Leu Trp Leu His Ala
420 425 430

Tyr Leu Tyr Glu Ser Thr Glu Thr Glu Glu Gly Thr Glu Lys Lys Lys
435 440 445

Trp Cys Tyr Lys Thr Glu Tyr Pro Glu Trp Ala Leu Arg Arg
450 455 460

<210> 37

<211> 1364

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 37

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ctgatattca gaaaaaacac ccatacatgt tgaaaaataa tgcattgtga aaaaaagtg 180
ttgaaaaatg tatgcatctt aggaaaaact gaattttcct taggttgctg ctcctcctct 240
agaaggatgc tgtggccttt gacctgggcg gaaattctct ctgtttccct ctagctgagg 300
gaaacagaac tggtagcagt tcgttcggcg caggccgcgt gagcctatac caccgaatat 360
tatcctagcg cagagagtaa cactggcaaa gtcaaaaagta aatgccatgt aaaatgtata 420
ggttacgcag tagactatct aatatatacc tttttattta gcagtgtttc gaaaaataca 480
gcaagagaat aagcaacaag atgtctgccg tcccaagtgt ccaagtatgt taaataattt 540
aaacgatgtc acgaatttgt gagggatatt gaaaccatgc agtgagataa tttcaattta 600
agaaccatat cacctgaata agacgggtgg ggcaagcact agatgcgaat catagtttta 660
gaacaacgga tcaccatttc acacgttaaa gaccgagtag aaataaccaa taaattgtgt 720
gggaaaaatat tatacttaat ttctctgtgg agtaaagtaa tgagcgtctt ttgcgggtctt 780
atttattcat tcgctcccct tgcaatgaat tttgaacaga atgctccaaa gaggaagtgc 840
cagggtacct cacttgtttc acccttttac acagttcata atatttttga ggattttgaa 900

```

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aggtcaacgg ttctccaatc actttgggtg aaccagaaat cctaagattc aagggtctacg 1080
aaccattatt gttggttggt ttggacaagt tctccaacat cgatatcaga gttagagtca 1140
ctgggtgggtg tcatgtttct caagtctacg ccatcagaca agctattgct aagggttttag 1200
tcgcttacca ccaaaagtac gttgacgaac aatccaagaa cgaattgaag aaggccttca 1260
cctcttacga cagaactttg ttgatcgctg attctagaag accagaacca aagaaattcg 1320
gtggttaaggg tgctcgttct agattccaaa aatcttaccg ttaa 1364

```

<210> 38

<211> 143

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 38

```

Met Ser Ala Val Pro Ser Val Gln Thr Phe Gly Lys Lys Lys Ser Ala
  1              5              10              15

```

```

Thr Ala Val Ala His Val Lys Ala Gly Lys Gly Leu Ile Lys Val Asn
          20              25              30

```

```

Gly Ser Pro Ile Thr Leu Val Glu Pro Glu Ile Leu Arg Phe Lys Val
          35              40              45

```

```

Tyr Glu Pro Leu Leu Leu Val Gly Leu Asp Lys Phe Ser Asn Ile Asp
          50              55              60

```

```

Ile Arg Val Arg Val Thr Gly Gly Gly His Val Ser Gln Val Tyr Ala
          65              70              75              80

```

```

Ile Arg Gln Ala Ile Ala Lys Gly Leu Val Ala Tyr His Gln Lys Tyr
          85              90              95

```

```

Val Asp Glu Gln Ser Lys Asn Glu Leu Lys Lys Ala Phe Thr Ser Tyr
          100             105             110

```

```

Asp Arg Thr Leu Leu Ile Ala Asp Ser Arg Arg Pro Glu Pro Lys Lys
          115             120             125

```

```

Phe Gly Gly Lys Gly Ala Arg Ser Arg Phe Gln Lys Ser Tyr Arg
          130             135             140

```

<210> 39

<211> 1088

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 39

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ttcaaaatac gagtaaagga gacccatggt gtggattagt aaggggagtg tggcaacttc 60
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acgcatggag gctttctacaa aacagcgtgc cgttttgatg gcatgagcag ggggcgcaaa 180
ggaaacaccg gtaaactcgc caagaccttg ttggccacgt agcctcaaag gttgaattga 240
cacttgctta cagaacttga aaagtacaaa aggaggtcac ataaaacagt aagcttgaga 300
agctttaaga tatggtgcga atcgttacag aatattcctt gcagaaataa tggcgggtcc 360
gttctcttct gaagaagtta ccgccctact gaagcattgc tgtacgatcg tgtaattgtga 420
tgtgtgttcg actggaaagc ggagaacatt atgaagtaaa aggacaatca gcacgccttc 480
cagactttta agaaacattg atggagccat tgatatcggc accgtacctt acaacaacaa 540
aatgtctgct tcctgctacg cttgatgctg cctgtatttt ttgcaagatt attaaaagta 600
tgtcacatta ctaataaaga gcttacactc acaccaatga tggcgatagt ctctatgtag 660
tacatataca taaagcagaa tactaacaat cgatccgcta tgcaacaggc gaaattccat 720
ccttcaaatt gattgaaaca aagtactcgt atgctttctt ggacatccaa cctactgctg 780
aaggtcatgc tttaatcatt cctaagtacc atggtgcgaa gttgcatgac atccccgacg 840
aattccttac cgatgctatg ccgattgcc aagagactggc caaggcaatg aagttggaca 900
cttataatgt gttgcagaat aatggtaaaa ttgcgcatca agaagtcgac cagctccact 960
tccatttgat tcctaagaga gatgagaaaa gtggtttgat tgtaggggtg ccagcccaag 1020
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ccgattag                                     1088

```

<210> 40

<211> 158

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 40

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Met Glu Pro Leu Ile Ser Ala Pro Tyr Leu Thr Thr Thr Lys Met Ser
  1              5              10              15

Ala Pro Ala Thr Leu Asp Ala Ala Cys Ile Phe Cys Lys Ile Ile Lys
      20              25              30

Ser Glu Ile Pro Ser Phe Lys Leu Ile Glu Thr Lys Tyr Ser Tyr Ala
      35              40              45

Phe Leu Asp Ile Gln Pro Thr Ala Glu Gly His Ala Leu Ile Ile Pro
      50              55              60

Lys Tyr His Gly Ala Lys Leu His Asp Ile Pro Asp Glu Phe Leu Thr
      65              70              75              80

Asp Ala Met Pro Ile Ala Lys Arg Leu Ala Lys Ala Met Lys Leu Asp
      85              90              95

```

Thr Tyr Asn Val Leu Gln Asn Asn Gly Lys Ile Ala His Gln Glu Val
 100 105 110

Asp His Val His Phe His Leu Ile Pro Lys Arg Asp Glu Lys Ser Gly
 115 120 125

Leu Ile Val Gly Trp Pro Ala Gln Glu Thr Asp Phe Asp Lys Leu Gly
 130 135 140

Lys Leu His Lys Glu Leu Leu Ala Lys Leu Glu Gly Ser Asp
 145 150 155

<210> 41

<211> 578

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 41

aaaggtggtt ggagactttg tgttgtagct tagaatttct tccactatat gaaagccaag 60
 acctcttctc ctctttcgac acttcgttta ttccacttt cccttattta gtattcatcg 120
 ttcagaatgc tttctttatt tcacgacggt taccacaccc gtacaccctt atctcatttc 180
 accagtacct ttccttatta gattcatctt attttatttt aggattttta ggtcattgta 240
 cgacgcgtgt cgcaccatgg aaaaggtgtc gcagctgcga tgctatccat ttacccggtca 300
 tcattgctgg cagaaatccc atcttcctct gctggggtga tttatatata tggagagtta 360
 acgaatgtaa tattttctgaa tgtaaataa ttgttatccg tcattattgt ttcacttctc 420
 tctttgaaat ttcgcttggt ttctgttttc atcttatatt ttacttcaat cctaagatag 480
 tcatatcgac ttaattccaa atgagagcta agtggagaaa gaagagaact agaagactta 540
 agagaaagag acggaagggt agagccagat ccaaataa 578

<210> 42

<211> 25

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 42

Met Arg Ala Lys Trp Arg Lys Lys Arg Thr Arg Arg Leu Lys Arg Lys
 1 5 10 15

Arg Arg Lys Val Arg Ala Arg Ser Lys
 20 25

<210> 43

<211> 1268

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 43

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gctctttaat attgcaacgg cttgtaacgg gcgccatgat gacattcaga attataccac 180
tactatatga aaaaatgaaa agaggccctg ctttgaaccc gtacatttta ttctataata 240
ttgcactctg ggtttgcctg acggcagcga gtccaacaca aagtctggca tatgctacga 300
attttccacc atggattcag cacccaaaca tttgaatttt ttttcatgtc gattgtgaaa 360
ttttactgaa gatgagggta aatagaggcc tgcaatcgtc atcatatgag aaatggatat 420
attgaaaatc tactcacatc tcttttttgg gggtttggtg gtacagttag aacacgataa 480
agaaccaaat aggactaaaa atggtatgta gagatgaata tacatgaaac ggacgtgata 540
taatgtgcta tggagaagaaa aagtctcctt taatgtctgc aggataaata atcaagtggg 600
ctgaagaaaa tttacagcta cagtattact gcaaaccttg caggcaaata tcagagagat 660
ctcaccagct acaacttggg aacagaaatt tataagttta tggcacttgt taaaattggt 720
tggaggtttt cgaaattata atattggtct tcagaaacct ggaaccacat gtgaactatt 780
ttttttggat aatgcattgc acagagcgta ttagtgtata cgagaatcta aaaatttgaa 840
actggctcat aaaaacagga acttttacta acagttatga ttttttggtc ccattttctt 900
atcaataggc cggcggttaa gcttacgaac taagaaccaa atccaaggaa caattagctt 960
ctcaattggt tgacttgaaa aaggagtgg ctgaattgaa ggtccaaaag ttgtccagac 1020
catctttgcc aaagatcaag accgtcagaa agagtatcgc ctgtgtcttg accgtcatca 1080
acgaacaaca aagagaagct gttagacaat tatacaaggg taagaagtac caaccaaagg 1140
acttgagagc caagaagacc agagctttga gaagagcttt gaccaaattc gaagcttccc 1200
aagttaccga aaagcaaaga aagaagcaaa tcgctttccc acaaagaaag tacgctatca 1260
aggcttaa                                     1268

```

<210> 44

<211> 120

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 44

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Met Ala Gly Val Lys Ala Tyr Glu Leu Arg Thr Lys Ser Lys Glu Gln
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Leu Ala Ser Gln Leu Val Asp Leu Lys Lys Glu Leu Ala Glu Leu Lys
      20              25             30

Val Gln Lys Leu Ser Arg Pro Ser Leu Pro Lys Ile Lys Thr Val Arg
      35              40             45

Lys Ser Ile Ala Cys Val Leu Thr Val Ile Asn Glu Gln Gln Arg Glu
      50              55             60

Ala Val Arg Gln Leu Tyr Lys Gly Lys Lys Tyr Gln Pro Lys Asp Leu
      65              70             75             80

```

Arg Ala Lys Lys Thr Arg Ala Leu Arg Arg Ala Leu Thr Lys Phe Glu
85 90 95

Ala Ser Gln Val Thr Glu Lys Gln Arg Lys Lys Gln Ile Ala Phe Pro
100 105 110

Gln Arg Lys Tyr Ala Ile Lys Ala
115 120

<210> 45
<211> 2660
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 45

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acaataatgt	taacagtagt	agaaataatt	taaacaatcg	cgtgaactcg	ggatcttcaa	1740
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<210> 46

<211> 719

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 46

```

Met His Tyr Val Val Leu Glu Leu Gln Val Ala His Leu Pro Asp Thr
  1              5              10              15

```

```

Pro Lys Asp Gln Cys Arg Ile Ala Asn Ile Ala Phe Gln Ile Val Asn
          20              25              30

```

```

Ala Glu Thr Leu Val Cys His Tyr Gly Thr Asn Ser Leu Pro Ser Ile
      35              40              45

```

```

Glu Val Asn Gly Thr Thr Lys Ser Leu Glu Ser Ala Met Val Gln Leu
      50              55              60

```

```

Asp Lys Asp Ile His Asp Val Ile Gly Asn Asp Asp Phe Val Leu Val
      65              70              75              80

```

```

Ser Leu Tyr Ser Thr Trp His Ile Arg Val Thr Leu Pro Arg Gln Ala
          85              90              95

```

```

Arg Asp Asp Gly Phe Ile Leu Thr Ser Tyr Leu Gln His Pro Lys Val
      100              105              110

```

```

Phe Asp Leu Trp Lys Glu Phe Asp Arg Trp Cys Val Asn His Pro Glu
      115              120              125

```

```

Ile Leu Gly Gln Lys Lys Ala Ile Ser Asn Asn Asn Cys Asn Thr Lys

```

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	165	170 175
Pro Glu Ile Tyr Ser Leu Leu Lys Arg Thr Thr Asp Ile Leu Ile Gln		
	180	185 190
Leu His Lys Lys Cys Thr Ser Pro Glu Asp Met Glu Ser Val Leu Thr		
	195	200 205
Lys Pro Tyr Asp Ser His Thr Asp Ile Arg Ala Phe Leu Gln Glu Lys		
	210	215 220
Ser Lys Ile Leu Tyr Met Asn Asn Leu Pro Pro Asp Thr Thr Gln Ser		
	225	230 235 240
Glu Leu Glu Ser Trp Phe Thr Gln Tyr Gly Val Arg Pro Val Gly Phe		
	245	250 255
Trp Thr Val Lys Asn Ile Val Glu Asp Thr Ser Asn Val Asn Asn Asn		
	260	265 270
Trp Ser Leu Asn Asn Ser Pro Tyr Val Glu Asp Gln Asp Ser Ile Ser		
	275	280 285
Gly Phe Val Val Phe Gln Thr His Glu Glu Ala Thr Glu Val Leu Ala		
	290	295 300
Leu Asn Gly Arg Ser Ile Leu Ser Asn Leu Ala Asn Thr Lys Gln Pro		
	305	310 315 320
Arg Val Val Glu His Val Leu Glu Leu Gln Pro Ser Ser Thr Gly Val		
	325	330 335
Leu Asp Lys Ala Gln Glu Ile Leu Ser Pro Phe Pro Gln Ser Lys Asn		
	340	345 350
Lys Pro Arg Pro Gly Asp Trp Asn Cys Pro Ser Cys Gly Phe Ser Asn		
	355	360 365
Phe Gln Arg Arg Thr Ala Cys Phe Arg Cys Ser Phe Pro Ala Pro Ser		
	370	375 380
Asn Ser Gln Ile His Thr Ala Asn Ser Asn Asn Asn Val Asn Ser Ser		